

```

XX AC AAR28486;
XX DT 22-MAR-1993 (first entry)
XX DE Casoxin D-like vasodilatory peptide #2.
XX KW Vasodilation.
XX OS Synthetic.
XX PN JF04275299-A.
XX PD 30-SEP-1992.
XX PF 01-MAR-1991; 91JP-0077441.
XX PR 01-MAR-1991; 91JP-0077441.
XX PA (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX DR WPI; 1992-376305/46.
XX PT Physiologically active peptide(s) useful as vasodilators - prepd.
XX PS by solid peptide synthesis using peptide synthesizer
XX DT Disclosure; Page 5; 6pp; Japanese.
XX CC This peptide and its deriv in which the N-terminal Val is deleted
XX CC both have casoxin D-like activity as vasodilators.
XX CC See also AAR28484-R28489.
XX SQ Sequence 6 AA;
      Query Match 40.0%; Score 4; DB 13; Length 6;
      Best Local Similarity 100.0%; Pred. No. 9.3e+05;
      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VMFP 10
Db 1 VMFP 4

RESULT 59
AAW31463
ID AAW31463 standard; Protein; 6 AA.
XX AC AAW31463;
XX DT 04-AUG-1998 (first entry)
XX DE Transcriptional activator peptide fragment LS123.
XX KW Activating sequence; Gal4; transcriptional activator; RNA polymerase;
XX KW Protein-protein interaction; gene therapy; therapeutic; holoenzyme;
XX KW Gall1; DNA binding domain.
XX OS Synthetic.
XX PN WO9744447-A2.
XX PD 27-NOV-1997.
XX PF 02-MAY-1997; 97WO-US07338.
XX PR 01-MAY-1997; 97US-0017016.
XX PR 03-MAY-1996; 96US-0017016.
XX PA (HARD ) HARVARD COLLEGE.
XX PI Lu X, Ptashne M, Wu Y;
XX DR WPI; 1998-018502/02.
DR
```

```

DR N-PSDB; AAV02561.
XX New transcriptional activator containing DNA binding domain bound to
XX peptide - useful for controlling gene expression, especially in gene
XX therapy, and in protein-protein interaction assays, does not inhibit
XX other transcription activators
XX PS Example 1; Page 26; 55pp; English.
XX CC AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW39053-W39076
XX CC are fragments used in an assay to determine novel transcriptional
XX CC activators. The method involves the production of transcriptional
XX CC activators comprising of a DNA-binding group and a 6-25 amino acid
XX CC peptide that is covalently bonded to the DNA binding group and does not
XX CC represent a fragment of a natural transcription activator.
XX CC Protein-protein interactions are identified in the assay by fusing a
XX CC DNA-binding domain to a library of DNA fragments and introducing this and
XX CC a fusion of target protein and a polypeptide containing a region of Gal4
XX CC which interacts with Gal1p into a cell containing Gal1p and identifying
XX CC members of the library that interact with the target from activation of
XX CC transcription. Such constructs are used to activate transcription in a
XX CC cell, e.g. for controlling gene activity, particularly in gene therapy
XX CC (e.g. recognizing a site close to a selected therapeutic gene).
XX CC Transcription can be activated without blocking other transcriptional
XX CC activators. They probably act by interacting with a component of the RNA
XX CC polymerase II holoenzyme, Gal11, the strongest known yeast activator,
XX CC which provides a more sensitive assay allowing detection of even weak
XX CC protein-protein interactions. Such activators do not create toxicity
XX CC problems even when overexpressed.
XX SQ Sequence 6 AA;
      Query Match 40.0%; Score 4; DB 19; Length 6;
      Best Local Similarity 100.0%; Pred. No. 9.3e+05;
      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 1 PLPP 4

RESULT 60
AAW31465
ID AAW31465 standard; Protein; 6 AA.
XX AC AAW31465;
XX DT 04-AUG-1998 (first entry)
XX DE Transcriptional activator peptide fragment LS126.
XX KW Activating sequence; Gal4; transcriptional activator; RNA polymerase;
XX KW Protein-protein interaction; gene therapy; therapeutic; holoenzyme;
XX KW Gall1; DNA binding domain.
XX OS Synthetic.
XX PN WO9744447-A2.
XX PD 27-NOV-1997.
XX PF 02-MAY-1997; 97WO-US07338.
XX PR 01-MAY-1997; 97US-0017016.
XX PR 03-MAY-1996; 96US-0017016.
XX PA (HARD ) HARVARD COLLEGE.
XX PI Lu X, Ptashne M, Wu Y;
XX DR WPI; 1998-018502/02.
DR N-PSDB; AAV02563.
XX
```

PT New transcriptional activator containing DNA binding domain bound to
PT peptide - useful for controlling gene expression, especially in gene
PT therapy, and in protein-protein interaction assays, does not inhibit
PT other transcription activators
XX
XX Example 1; Page 26; 55pp; English.
XX
CC AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW39053-W39076
CC are fragments used in an assay to determine novel transcriptional
CC activators. The method involves the production of transcriptional
CC activators comprising of a DNA-binding group and a 6-25 amino acid
CC peptide that is covalently bonded to the DNA binding group and does not
CC represent a fragment of a natural transcription activator.
CC Protein-protein interactions are identified in the assay by fusing a
CC DNA-binding domain to a library of DNA fragments and introducing this and
CC a fusion of target protein and a polypeptide containing a region of Gal4
CC which interacts with Gal4P into a cell containing Gal4P and identifying
CC members of the library that interact with the target for activation of
CC transcription. Such constructs are used to activate transcription in a
CC cell, e.g. for controlling gene activity, particularly in gene therapy
CC (e.g. recognizing a site close to a selected therapeutic gene).
CC Transcription can be activated without blocking other transcriptional
CC activators. They probably act by interacting with a component of the RNA
CC polymerase II holoenzyme, Gal4, the strongest known yeast activator,
CC which provides a more sensitive assay allowing detection of even weak
CC protein-protein interactions. Such activators do not create toxicity
CC problems even when overexpressed.
XX
XX Sequence 6 AA;
SQ
Query Match 40.0%; Score 4; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 LPPT 6
DB 3 LPPT 6
RESULT 61
AAR60997
ID AAR60997 standard; peptide; 7 AA.
XX
AC AAR60997;
XX
DT 25-MAR-2003 (updated)
DT 14-APR-1995 (first entry)
XX
DE Fragment of the 3BP1 protein that binds to SH3 of Abl kinase.
XX
KW CD4; T cell; surface antigen; receptor; MHC class II antigen;
KW protein-tyrosine kinase; p56lck; TCR/CD3 complex; PI 3-kinase;
KW PI 4-kinase; lipid kinase; T cell receptor complex; 3BP1; SH3;
KW Abl kinase.
XX
OS Synthetic.
XX
XX WO9418832-A1.
XX
XX 01-SEP-1994.
XX
XX 25-FEB-1994; 94WO-US01840.
XX
XX 26-FEB-1993; 93US-0023915.
XX
XX (DAND) DANA FARBER CANCER INST INC.
XX
XX Cantley L, Kanteti P, Rudd CE;
XX
XX WPI; 1994-293868/36.
XX
XX Method for inhibiting or reducing signal transduction - utilizes
PT peptide or corresp. nucleic acid which decreases association of

PT PI 3- or 4- kinase with CD4/p56lck
XX
XX Example; Page 32; 46pp; English.
XX
CC In order for certain T cells to make an optimal response to antigen,
CC it is necessary for the T cell surface antigen CD4 to couple to the
CC protein-tyrosine kinase p56lck. (CD4-p56lck is known to associate
CC with and functionally synergise with the TCR/CD3 complex.) CD4-p56lck
CC complex in T cells associates with two lipid kinases: PI 3-kinase
CC and PI 4-kinase, which suggests that these lipid kinases are also
CC involved in intracellular signalling via the T cell receptor complex.
CC The interaction of a lipid kinase, such as PI 3-kinase or PI 4-
CC kinase, with CD4-p56lck, may be blocked by administering a peptide.
CC This peptide may be a fragment of the cytoplasmic domain of CD4
CC (eg AAR60987-R60991), a fragment of p56lck (eg AAR60992, AAR60993),
CC a fragment of PI 3-kinase (eg AAR60994, AAR60995), or a fragment of
CC PI 4-kinase. Other proline-rich peptides that bind to SH3 binding
CC sequences can also be used, such as the fragment of
CC 3BP1 protein that binds to the SH3 of the Abl kinase (AAR60997), or
CC a sequence found in the SOS protein (AAR60999).
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 7 AA;
SQ
Query Match 40.0%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PLPP 5
DB 3 PLPP 6
RESULT 62
AAW11128
ID AAW11128 standard; peptide; 7 AA.
XX
AC AAW11128;
XX
XX 27-JUN-1997 (first entry)
XX
DE Src SH3 domain-binding peptide preferred core sequence.
XX
XX Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
KW protein tyrosine kinase; signal transduction; RNA processing;
KW trafficking; translation.
XX
OS Synthetic.
XX
XX WO9603649-A1.
XX
XX 08-FEB-1996.
XX
XX 24-JUL-1995; 95WO-US09382.
XX
XX 07-JUN-1995; 95US-0483555.
XX
XX 22-JUL-1994; 94US-0278865.
XX
XX (UYNC-) UNIV NORTH CAROLINA.
XX
XX Der CJ, Kay BK, Quilliam LA, Sparks AB, Thorn JM;
XX
XX WPI; 1996-117151/12.
XX
XX Peptide with binding affinity for Src homology region 3 (SH3)
PT domains of proteins - useful for e.g. modulating signal transduction
PT pathways at the cellular level, esp. protein tyrosine
PT kinase-mediated
XX
XX Disclosure; Page 62; 116pp; English.
XX
XX AAW11128 represents a preferred core sequence of a set of peptides
CC that bind to the Src SH3 domain. The SH3 binding peptides are useful in

CC modulating signal transduction pathways at the cellular level
 CC (especially protein tyrosine kinase-mediated), modulating oncogenic
 CC protein activity, or providing compounds for the development of drugs
 CC with the ability to modulate broad classes, as well as specific classes,
 CC of proteins involved in signal transduction and also for regulating the
 CC processing, trafficking or translation of RNA. Conjugates of the peptides
 CC with detectable labels or imaging agents are useful for imaging cells,
 CC tissues and organs in which Src or Src-related proteins are expressed.
 XX
 SQ Sequence 7 AA;

Query Match 40.0%; Score 4; DB 17; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
 Db 2 PLPP 5

RESULT 63
 AAW17010
 ID AAW17010 standard; peptide; 7 AA.
 XX
 AC AAW17010;
 XX
 DT 27-JUN-1997 (first entry)
 XX
 DE SRC SH3 domain-binding consensus peptide.
 XX
 KW Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
 KW protein tyrosine kinase; signal transduction; RNA processing;
 KW trafficking; translation.
 XX
 OS Synthetic.
 XX
 PN WO9603649-A1.
 XX
 PD 08-FEB-1996.
 XX
 PF 24-JUL-1995; 95WO-US09382.
 XX
 PR 07-JUN-1995; 95US-0483555.
 PR 22-JUL-1994; 94US-0278865.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX
 PI Der CJ, Kay BK, Quilliam LA, Sparks AB, Thorn JM;
 XX
 DR WPI; 1996-117151/12.
 XX
 PT Peptide with binding affinity for Src homology region 3 (SH3)
 PT domains of proteins - useful for e.g. modulating signal transduction
 PT pathways at the cellular level, esp. protein tyrosine
 PT kinase-mediated
 XX
 PS Example 14; Page 58; 116pp; English.
 XX
 CC AAW17010 is the consensus sequence of a set of SRC SH3-binding
 CC peptides derived from a biased peptide library, exhibiting selective
 CC SH3 binding. SH3 binding peptides are useful in modulating signal
 CC transduction pathways at the cellular level (especially protein tyrosine
 CC kinase-mediated), modulating oncogenic protein activity, or providing
 CC compounds for the development of drugs with the ability to modulate
 CC broad classes, as well as specific classes, of proteins involved in
 CC signal transduction and also for regulating the processing, trafficking
 CC or translation of RNA. Conjugates of the peptides with detectable
 CC labels or imaging agents are useful for imaging cells, tissues and
 CC organs in which Src or Src-related proteins are expressed.
 XX
 SQ Sequence 7 AA;

Query Match 40.0%; Score 4; DB 17; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
 Db 2 PLPP 5

RESULT 64
 AAW07013
 ID AAW07013 standard; peptide; 7 AA.
 XX
 AC AAW07013;
 XX
 DT 17-JAN-1997 (first entry)
 XX
 DE Synthetic peptide used in GalNac-transferase activity SPA.
 XX
 KW SPA; scintillation proximity assay; antigen; bead coating; capture;
 KW antibody; N-acetyl galactosamine transferase; GalNac transferase;
 KW activity; enzyme; O-linked glycosylation.
 XX
 OS Synthetic.
 XX
 PN WO9615258-A1.
 XX
 PD 23-MAY-1996.
 XX
 PF 08-NOV-1995; 95WO-US13483.
 XX
 PR 16-NOV-1994; 94US-0340283.
 XX
 PA (UPJO) UPJOHN CO.
 XX
 PI Elhammer AP;
 XX
 DR WPI; 1996-268220/27.
 XX
 PT Scintillation proximity assay for N-acetyl:galactosaminyl activity
 PT - esp. for large scale screening of cpds. for their effect on enzyme
 PT activity
 XX
 PS Claim 14; Page 17; 29pp; English.
 XX
 CC AAW06985-W07180 are antigenic peptides derived from either the
 CC product of the human c-myc oncogene or the FLAG peptide (DYKDDK).
 CC The peptides are useful for coating beads used in a scintillation
 CC proximity assay for N-acetyl:galactosamine (GalNac)-transferase (GNT)
 CC activity. The assay involves fewer steps than known assays and is
 CC quicker, producing excellent signal-to-noise ratios. The
 CC assay is capable of screening large numbers of cpds. for their
 CC ability to affect GNT activity and is thus useful for identifying
 CC inhibitors and promoters of glycosylation (in partic. O-linked
 CC glycosylation).
 XX
 SQ Sequence 7 AA;

Query Match 40.0%; Score 4; DB 17; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
 Db 4 PLPP 7

RESULT 65
 AAW25486
 ID AAW25486 standard; peptide; 7 AA.
 XX
 AC AAW25486;
 XX
 DT 27-MAR-1998 (first entry)

XX SH3 domain binding peptide consensus motif.
 DE Cortactin; SH3 domain; binding peptide; Src homology region 3;
 XX tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLGgamma; p53bp2; Crk; Yes; Grb2.
 KW
 XX Synthetic.
 OS Unidentified.
 OS
 XX WO9730074-A1.
 PN
 XX 21-AUG-1997.
 XX
 XX 14-FEB-1997; 97WO-US02298.
 PF
 XX 16-FEB-1996; 96US-0602999.
 XX
 XX (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 PA
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX
 XX WPI; 1997-424972/39.
 DR
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX
 XX Disclosure; Page 8; 131pp; English.
 PS
 XX The present sequence represents a Src homology region 3 (SH3) binding
 CC peptide consensus motif. SH3 binding peptides are selected from: (a)
 CC peptides which bind the SH3 domain of Cortactin; (b) peptides which bind
 CC the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of
 CC Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which
 CC bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain
 CC of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding
 CC peptides can be used in the method to identify inhibitors of their
 CC binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 40.0%; Score 4; DB 18; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPP 5
 Db 2 PLPP 5
 ||||
 ||||
 RESULT 66
 AAW10774
 ID AAW10774 standard; peptide; 7 AA.
 XX
 AC AAW10774;
 XX
 XX 25-MAR-2003 (updated)
 DT 10-NOV-1997 (first entry)
 XX
 XX Ferritin motif #17 important for selective binding affinity.

KW Functional surrogate; analyte; affinity receptor; immunoreactive group;
 KW mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia;
 KW cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin;
 KW pregnancy; infectious disease; ferritin; myosin light chain; troponin;
 KW follicle stimulating hormone; human; growth hormone; immunoglobulin E;
 KW prolactin; parathyroid hormone; placental lactogen; hepatitis antigen;
 KW antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus;
 KW Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen;
 KW carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
 XX
 OS Synthetic.
 XX
 XX WO9641172-A1.
 PN
 XX 19-DEC-1996.
 PD
 XX 07-JUN-1996; 96WO-US10498.
 PF
 XX 07-JUN-1995; 95US-0476375.
 XX
 XX (CYTO-) CYTOGEN CORP.
 PA
 XX Lee-owen FV, Carter JM;
 PI
 XX WPI; 1997-077284/07.
 DR
 XX Labelled functional surrogate of an analyte - useful as competitor
 PT molecule in affinity assays, esp. for detecting large macromolecules
 PT such as ferritin
 PT
 XX Claim 56; Page 56; 156pp; English.
 PS
 XX This sequence represents a peptide motif derived from ferritin which is
 CC important for selective binding affinity. Peptides containing motifs
 CC such as this may be used as functional surrogates in the conjugate of
 CC the invention. The novel labelled conjugate comprises at least one
 CC label attached to a functional surrogate of an analyte of interest.
 CC The surrogate is capable of competing effectively with the analyte
 CC for a limiting amount of an affinity receptor for the analyte. The
 CC conjugate exhibits an activity that is altered upon interaction with
 CC the affinity receptor and this activity can be measured and related to
 CC the amount of the analyte present in a sample. Functional surrogates
 CC such as this have an immunoreactive group that allows the surrogate to
 CC compete effectively and with the analyte for a limiting amount of its
 CC affinity receptor. Functional surrogates are able to mimic naturally
 CC occurring analytes. They can be labelled for use in standard competitive
 CC affinity assays (esp. homogenous immunoassays) for detecting large
 CC macromolecules such as polypeptides, polysaccharides, polynucleotides,
 CC glycoproteins and lipid-containing macromolecules, as well as small
 CC haptens. Typical diagnostic analytes for detection include cardiac or
 CC tumour markers, allergens, hormones related to fertility-pregnancy or
 CC analytes associated with infectious disease. In particular, the assays
 CC are useful for detecting ferritin, follicle stimulating hormone, human
 CC growth hormone, immunoglobulin E, prolactin, parathyroid hormone, human
 CC placental lactogen, hepatitis antigens or antibodies against them, human
 CC chorionic gonadotropin, human luteinising hormone, cytomegalovirus,
 CC Chlamydia, streptococcus a, rubella, toxoplasma, herpes virus, DK-MB,
 CC myoglobin, myosin light chain, troponin, carcinoembryonic antigen,
 CC alpha-fetoprotein, prostate-specific antigen and CA125 (a tumour marker).
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 40.0%; Score 4; DB 18; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 TVMF 9
 Db 3 TVMF 6
 ||||
 ||||
 RESULT 67

AAW79781
 ID AAW79781 standard; peptide; 7 AA.
 AC AAW79781;
 XX
 DT 18-JAN-1999 (first entry)
 XX
 DE Proline-rich peptide which binds with Src SH3 domain.
 XX
 KW electrochemical; potentiometric; specific binding pair; assay;
 KW competition; analysis; purification; proline-rich; Src SH3.
 XX
 OS Unidentified.
 XX
 PN W09835232-A2.
 XX
 PD 13-AUG-1998.
 XX
 XX 06-FEB-1998; 98WO-US02440.
 XX
 PF 16-SEP-1997; 97US-0059049.
 PR 06-FEB-1997; 97US-0036919.
 XX
 XX (NOVA-) NOVALON PHARM CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 PA
 PI Fowlkes DM, Thorp HH;
 XX
 DR WPI; 1998-467163/40.
 XX
 XX Apparatus for electrochemically detecting binding - for use in
 PT biochemical analyses, drug development and protein purification
 PT assays
 XX
 PS Example 6; Page 55; 104pp; English.
 XX
 CC The invention relates to a method and apparatus for performing an
 CC electrochemical assay for detecting specific binding between members
 CC of a biological binding pair. The apparatus detects specific binding
 CC between a first member immobilised on an electrode and a second member
 CC which is biologically labelled, in the presence of an electrochemical
 CC mediator. The method may be used for performing binding and competitive
 CC binding assays. It may be used in performing high throughput screening
 CC assays for detecting inhibition of specific binding between the members
 CC of the binding pair for use in drug development, biochemical analyses
 CC and protein purification assays.
 CC The present sequence is an example of a peptide which is used in labelled
 CC form as a second binding member in the above assay. The peptide acts as a
 CC surrogate ligand for the first member. Specifically, the peptide
 CC is a proline-rich peptide which binds with Src SH3 domain.
 XX
 SQ Sequence 7 AA;
 Query Match 40.0%; Score 4; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPP 5
 DB 2 PLPP 5
 RESULT 68
 AAY41611
 ID AAY41611 standard; peptide; 7 AA.
 AC AAY41611;
 XX
 DT 02-DEC-1999 (first entry)
 XX
 DE Mammalian ion channel proline rich motif containing peptide #5.
 KW SH3 domain; binding motif; potassium channel; protein tyrosine kinase;

KW proline rich.
 XX
 OS Rattus sp.
 XX
 PN US955259-A.
 XX
 PD 21-SEP-1999.
 XX
 XX 19-DEC-1996; 96US-0769745.
 PF 19-DEC-1996; 96US-0769745.
 PR 19-DEC-1996; 96US-0769745.
 XX
 PA (UYBR-) UNIV BRANDEIS.
 XX
 PI Holmes TC, Levitan IB;
 XX
 DR WPI; 1999-560490/47.
 XX
 XX Identification of compounds that modulate potassium ion channel binding
 PT with protein tyrosine kinase SH3 domains -
 PT
 PS Disclosure; Column 8; 18pp; English.
 XX
 CC A method has been developed for determining if a compound modulates the
 CC binding of a potassium ion channel to the SH3 domain of a protein
 CC tyrosine kinase by contacting the channel with a polypeptide comprising
 CC the SH3 domain and the compound to be assessed and measuring channel-SH3
 CC binding. The method is useful for assessing the ability of a compound to
 CC modulate the formation of channel-SH3 domain complexes to improve the
 CC understanding of mechanisms of potassium channel blockage and assess the
 CC ability of potential therapeutics to inhibit blockage. AAY41607 to
 CC AAY41644 represent mammalian ion channel peptides with proline-rich
 CC motifs.
 XX
 SQ Sequence 7 AA;
 Query Match 40.0%; Score 4; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPP 5
 DB 2 PLPP 5
 RESULT 69
 AAY17016
 ID AAY17016 standard; peptide; 7 AA.
 XX
 AC AAY17016;
 XX
 DT 20-JUL-1999 (first entry)
 XX
 DE Heat shock protein (hsp) binding peptide.
 XX
 KW Conjugate peptide; heat shock protein; hsp; phage display library; virus;
 KW surface protein; tethering peptide; chaperone process; cytokine; cancer;
 KW neoplastic disease; infectious disease; bacterium; immune system; fungus;
 KW acquired immune deficiency; autoimmune disease.
 XX
 OS Synthetic.
 XX
 PN W09922761-A1.
 XX
 PD 14-MAY-1999.
 XX
 PF 22-OCT-1998; 98WO-US22335.
 XX
 PR 31-OCT-1997; 97US-0961707.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX
 PI Hartl U, Hoe MH, Houghton A, Mayhew M, Moroi Y;

PI Overfelli O, Rothman JE;
 DR WPI; 1999-313177/26.
 XX
 XX Identifying peptides which bind heat shock proteins
 PT Examples; Page 24; 155pp; English.
 XX
 XX The invention relates to conjugate peptides engineered to noncovalently
 CC bind to heat shock proteins (hsp). A method of identifying a hsp binding
 CC peptide comprises (a) contacting a phage display library having
 CC bacteriophage expressing, in a surface protein, inserted peptides with a
 CC hsp target, and bound to a benzquinone ansamycin antibiotic (BAA), in a
 CC physiologic binding buffer; (b) isolating a phage binding to the hsp
 CC target; and (c) identifying the inserted peptide expressed. The peptides
 CC which bind to a hsp can be used as tethering peptides for a hsp which may
 CC serve as an accessory in a chaperone process and/or may comprise a
 CC cytokine. They can also be coupled to antigens to induce an immune
 CC response. Such compositions can be used for treating neoplastic disease,
 CC e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,
 CC virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a
 CC disease of the immune system, e.g. acquired immune deficiencies or
 CC autoimmune diseases.
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 40.0%; Score 4; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPP 5
 Db 4 PLPP 7
 AAB17226
 ID AAB17226 standard; Peptide; 7 AA.
 XX
 AC AAB17226;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE SH3 antagonist peptide sequence SEQ ID NO:282.
 XX
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX
 PN WO200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 25-OCT-1999; 99WO-US25044.
 XX
 PR 23-OCT-1998; 98US-0105371.
 PR 22-OCT-1999; 99US-0428082.
 XX
 PA (ANGE-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham J, Boone TC;
 XX
 DR WPI; 2000-350702/30.
 XX
 XX Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -
 PT

XX Claim 39; Page 295; 608pp; English.
 PS
 XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cycostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAB69443
 CC to AAB69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 40.0%; Score 4; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPP 5
 Db 2 PLPP 5
 AAB17228
 ID AAB17228 standard; Peptide; 7 AA.
 XX
 AC AAB17228;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE SH3 antagonist peptide sequence SEQ ID NO:284.
 XX
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX
 PN WO200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 25-OCT-1999; 99WO-US25044.
 XX
 PR 23-OCT-1998; 98US-0105371.
 PR 22-OCT-1999; 99US-0428082.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham J, Boone TC;
 XX
 DR WPI; 2000-350702/30.
 XX
 XX Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -
 XX
 PS Claim 39; Page 296; 608pp; English.

XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P*3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 7 AA;
 Query Match 40.0%; Score 4; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPP 5
 DB 2 PLPP 5
 RESULT 72
 AAB17229
 ID AAB17229 standard; Peptide; 7 AA.
 AC AAB17229;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE SH3 antagonist peptide sequence SEQ ID NO:285.
 XX
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX
 PN WO200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 25-OCT-1999; 99WO-US25044.
 XX
 PR 23-OCT-1998; 98US-0105371.
 XX
 PR 22-OCT-1999; 99US-0428082.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham J, Boone TC;
 XX
 DR WPI; 2000-350702/30.
 XX
 PT Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -
 XX
 PS Claim 39; Page 296; 608pp; English.
 XX
 CC The present invention describes composition of matter (I) comprising an

CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P*3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 7 AA;
 Query Match 40.0%; Score 4; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLPP 5
 DB 2 PLPP 5
 RESULT 73
 AAB17232
 ID AAB17232 standard; Peptide; 7 AA.
 AC AAB17232;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE SH3 antagonist peptide sequence SEQ ID NO:288.
 XX
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX
 PN WO200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 25-OCT-1999; 99WO-US25044.
 XX
 PR 23-OCT-1998; 98US-0105371.
 XX
 PR 22-OCT-1999; 99US-0428082.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham J, Boone TC;
 XX
 DR WPI; 2000-350702/30.
 XX
 PT Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -
 XX
 PS Claim 39; Page 297; 608pp; English.
 XX
 CC The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

CC independently selected from - (L1)c-P1, - (L1)c-P1-(L2)d-P2,
 CC - (L1)c-P1-(L2)d-P2-(L3)e-P3, or - (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX
 XX
 SQ Sequence 7 AA;
 Query Match 40.0%; Score 4; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LPPT 6
 Db |||||
 3 LPPT 6
 RESULT 74
 AAB17233
 ID AAB17233 standard; Peptide; 7 AA.
 AC AAB17233;
 DT 31-OCT-2000 (first entry)
 DE SH3 antagonist peptide sequence SEQ ID NO:289.
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; tumour metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 OS Synthetic.
 XX
 XX WO200024782-A2.
 XX
 XX 04-MAY-2000.
 XX
 XX 25-OCT-1999; 99WO-US25044.
 XX
 XX 23-OCT-1998; 98US-0105371.
 PR 22-OCT-1999; 99US-0428082.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Feige U, Liu C, Cheetham J, Boone TC;
 XX WPI; 2000-350702/30.
 XX
 XX Novel composition of matter comprising an Fc domain and
 XX pharmacologically active peptides, useful for treating cancer and
 XX autoimmune diseases -
 XX
 XX Claim 39; Page 297; 608pp; English.
 XX
 XX The present invention describes composition of matter (I) comprising an
 XX Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-P1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from - (L1)c-P1, - (L1)c-P1-(L2)d-P2,
 CC - (L1)c-P1-(L2)d-P2-(L3)e-P3, or - (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC - (L1)c-P1-(L2)d-P2-(L3)e-P3, or - (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each

CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX
 XX
 SQ Sequence 7 AA;
 Query Match 40.0%; Score 4; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LPPT 6
 Db |||||
 3 LPPT 6
 RESULT 75
 AAB17267
 ID AAB17267 standard; Peptide; 7 AA.
 AC AAB17267;
 DT 31-OCT-2000 (first entry)
 DE Src antagonist peptide sequence SEQ ID NO:323.
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 OS Synthetic.
 XX
 XX WO200024782-A2.
 XX
 XX 04-MAY-2000.
 XX
 XX 25-OCT-1999; 99WO-US25044.
 XX
 XX 23-OCT-1998; 98US-0105371.
 PR 22-OCT-1999; 99US-0428082.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Feige U, Liu C, Cheetham J, Boone TC;
 XX WPI; 2000-350702/30.
 XX
 XX Novel composition of matter comprising an Fc domain and
 XX pharmacologically active peptides, useful for treating cancer and
 XX autoimmune diseases -
 XX
 XX Claim 39; Page 308; 608pp; English.
 XX
 XX The present invention describes composition of matter (I) comprising an
 XX Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-P1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from - (L1)c-P1, - (L1)c-P1-(L2)d-P2,
 CC - (L1)c-P1-(L2)d-P2-(L3)e-P3, or - (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each

CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX

SQ Sequence 7 AA;

Query Match 40.0%; Score 4; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
| | | |
Db 2 PLPP 5

Search completed: November 25, 2003, 19:27:13
Job time : 26.5233 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 16.0465 Seconds
(without alignments)
114.943 Million cell updates/sec

Title: US-09-641-801-25

Perfect score: 10

Sequence: 1 QELPTVMFP 10

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	10	100.0	10	15	US-10-281-652-25
2	10	100.0	10	15	US-10-281-652-34
3	6	60.0	16	12	US-10-161-791-227
4	5	50.0	7	12	US-10-286-457-359
5	5	50.0	9	12	US-10-062-109A-382
6	5	50.0	9	12	US-10-062-109A-458
7	5	50.0	9	12	US-10-062-109A-563
8	5	50.0	9	12	US-10-005-480A-382
9	5	50.0	9	12	US-10-005-480A-458
10	5	50.0	9	12	US-10-005-480A-563
11	5	50.0	10	9	US-09-794-346-1
12	5	50.0	12	15	US-10-148-936-1
13	5	50.0	13	9	US-09-938-315-93
14	5	50.0	13	10	US-09-897-107-69
15	5	50.0	13	12	US-10-161-791-90
					Sequence 25, Appl
					Sequence 34, Appl
					Sequence 227, Appl
					Sequence 359, Appl
					Sequence 382, Appl
					Sequence 458, Appl
					Sequence 563, Appl
					Sequence 382, Appl
					Sequence 458, Appl
					Sequence 563, Appl
					Sequence 1, Appl
					Sequence 93, Appl
					Sequence 69, Appl
					Sequence 90, Appl

Sequence 93, Appl
Sequence 38, Appl
Sequence 355, Appl
Sequence 437, Appl
Sequence 213, Appl
Sequence 1351, Appl
Sequence 31396, A
Sequence 17, Appl
Sequence 147, Appl
Sequence 11, Appl
Sequence 4, Appl
Sequence 45, Appl
Sequence 9, Appl
Sequence 286, Appl
Sequence 9, Appl
Sequence 286, Appl
Sequence 30, Appl
Sequence 82, Appl
Sequence 30, Appl
Sequence 82, Appl
Sequence 11, Appl
Sequence 165, Appl
Sequence 456, Appl
Sequence 517, Appl
Sequence 620, Appl
Sequence 34, Appl
Sequence 29, Appl
Sequence 26, Appl
Sequence 3, Appl
Sequence 648, Appl
Sequence 34, Appl
Sequence 29, Appl
Sequence 11, Appl
Sequence 49, Appl
Sequence 490, Appl
Sequence 505, Appl
Sequence 569, Appl
Sequence 588, Appl
Sequence 675, Appl
Sequence 28, Appl
Sequence 22, Appl
Sequence 636, Appl
Sequence 3283, Appl
Sequence 108, Appl
Sequence 124, Appl
Sequence 516, Appl
Sequence 701, Appl
Sequence 920, Appl
Sequence 1297, Appl
Sequence 28, Appl
Sequence 60, Appl
Sequence 61, Appl
Sequence 8, Appl
Sequence 9, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 141, Appl
Sequence 178, Appl
Sequence 70, Appl
Sequence 70, Appl
Sequence 27, Appl
Sequence 19, Appl
Sequence 27, Appl
Sequence 260, Appl
Sequence 50, Appl
Sequence 57, Appl
Sequence 84, Appl
Sequence 408, Appl
Sequence 95, Appl

89 4 40.0 12 11 US-09-791-389-95 Sequence 95, Appl
90 4 40.0 12 11 US-09-945-917-9 Sequence 9, Appl
91 4 40.0 12 11 US-09-745-078A-26 Sequence 26, Appl
92 4 40.0 12 12 US-10-155-883B-25 Sequence 25, Appl
93 4 40.0 12 12 US-09-845-917A-9 Sequence 3, Appl
94 4 40.0 12 12 US-10-286-457-226 Sequence 226, App
95 4 40.0 12 12 US-10-286-457-323 Sequence 323, App
96 4 40.0 12 12 US-10-374-624-26 Sequence 26, Appl
97 4 40.0 12 12 US-10-161-791-253 Sequence 253, App
98 4 40.0 12 12 US-10-161-791-254 Sequence 254, App
99 4 40.0 12 12 US-10-161-791-267 Sequence 267, App
100 4 40.0 12 15 US-10-158-596A-25 Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-10-281-652-25
; Sequence 25, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-25

Query Match 100.0%; Score 10; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0009; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

Qy 1 QLPPTVMFP 10
 |||||
Db 1 QLPPTVMFP 10
 |||||
RESULT 2
US-10-281-652-34
; Sequence 34, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-34

Query Match 100.0%; Score 10; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLPPTVMFP 10
 |||||
Db 6 QLPPTVMFP 15
 |||||

RESULT 3
US-10-161-791-227
; Sequence 227, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 227:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-227

Query Match 60.0%; Score 6; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPPTVM 8

```

Db          9 LPPTVM 14
|||||
RESULT 4
US-10-286-457-359
; Sequence 359, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 359
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-359

Query Match          50.0%; Score 5; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPPT 6
Db      2 PLPPT 6
|||||

RESULT 5
US-10-062-109A-382
; Sequence 382, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 382
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-382

Query Match          50.0%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LPPTV 7
Db      1 LPPTV 5
|||||

RESULT 6
US-10-062-109A-458
; Sequence 458, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 458
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-458

Query Match          50.0%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LPPTV 7
Db      1 LPPTV 5
|||||

RESULT 7
US-10-062-109A-563
; Sequence 563, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 563
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-563

Query Match          50.0%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LPPTV 7
Db      1 LPPTV 5
|||||

```

```
RESULT 8
US-10-005-480A-382
; Sequence 382, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 382
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-382

Query Match      50.0%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPPTV 7
Db 1 LPPTV 5

RESULT 9
US-10-005-480A-458
; Sequence 458, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 458
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-458

Query Match      50.0%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPPTV 7
Db 1 LPPTV 5

RESULT 10
US-10-005-480A-563
; Sequence 563, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 563
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-563

Query Match      50.0%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPPTV 7
Db 1 LPPTV 5

RESULT 11
US-09-794-346-1
; Sequence 1, Application US/09794346
; Patent No. US20010031857A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Memno Peptides, Process for Their Preparation and Use Thereof
; FILE REFERENCE: 02481.1728
; CURRENT APPLICATION NUMBER: US/09/794,346
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: EP 00104114.4
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: PCT/EP 01/01661
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: artificial sequence
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: Memmonella echinata, FH
; OTHER INFORMATION: 1, DSM 1319
US-09-794-346-1

Query Match      50.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
Db 6 QPLPP 10

RESULT 12
US-10-148-936-1
; Sequence 1, Application US/10148936
; Publication No. US20030113819A1
; GENERAL INFORMATION:
```

RESULT 10

US-10-005-480A-563

APPLICANT: Horton, Jeffrey
APPLICANT: Smith, John
APPLICANT: Teear, Michelle
APPLICANT: Kendall, Jonathan
APPLICANT: Michael, Nigel
TITLE OF INVENTION: Reagent and Method for Delivery of Molecules into Cells
FILE REFERENCE: PA9963
CURRENT APPLICATION NUMBER: US/10/148,936
PRIORITY FILING DATE: 2000-12-04
PRIORITY FILING DATE: 2000-12-04
PRIORITY FILING DATE: 2000-12-04
PRIORITY FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 12
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: synthetic oligomer
US-10-148-936-1

Query Match 50.0%; Score 5; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
Db 4 PLPPT 8

RESULT 13
US-09-938-315-93
Sequence 93, Application US/09938315
Patent No. US20020091085A1
GENERAL INFORMATION:
APPLICANT: KAY, BRIAN K.
SPARKS, ANDREW B.
THORN, JUDITH M.
QUILLIAM, LAWRENCE A.
DER, CHANNING J.
TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,315
FILING DATE: 23-Aug-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-007-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids

TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-09-938-315-93

Query Match 50.0%; Score 5; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
Db 5 PLPPT 9

RESULT 14
US-09-897-107-69
Sequence 69, Application US/09897107
Patent No. US20020137094A1
GENERAL INFORMATION:
APPLICANT: YAMAGISHI, Akihiko
TITLE OF INVENTION: METHOD FOR IMPROVING THERMOSTABILITY OF PROTEINS, PROTEINS HA
FILE REFERENCE: 210383USO
CURRENT APPLICATION NUMBER: US/09/897,107
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: JP2000-201920
PRIOR FILING DATE: 2000-07-04
PRIOR APPLICATION NUMBER: JP2001-164332
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.1
SEQ ID NO 69
LENGTH: 13
TYPE: PRT
ORGANISM: Escherichia coli
US-09-897-107-69

Query Match 50.0%; Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
Db 1 QPLPP 5

RESULT 15
US-10-161-791-90
Sequence 90, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-90

Query Match 50.0%; Score 5; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
Db 8 PLPPT 12

RESULT 16
US-10-161-791-93
; Sequence 93, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-93

Query Match 50.0%; Score 5; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
Db 5 PLPPT 9

RESULT 17
US-10-079-167-38
; Sequence 38, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: McShane, Helen
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Reece, William
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: Vaccination Method
; FILE REFERENCE: 2907.1000-001
; CURRENT APPLICATION NUMBER: US/10/079,167
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04116
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: GB 00 23203.3
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 14
; TYPE: PPT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-079-167-38

Query Match 50.0%; Score 5; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
Db 5 QPLPP 9

RESULT 18
US-10-161-791-355
; Sequence 355, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
```

APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
CURRENT APPLICATION DATA:
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/10/161,791
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-355

Query Match 50.0%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
Db 9 PLPPT 13

RESULT 19
US-10-161-791-437
Sequence 437, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
CURRENT APPLICATION DATA:
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 437:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-437

Query Match 50.0%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
Db 2 QPLPP 6

RESULT 20
US-10-161-791-213
Sequence 213, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
CURRENT APPLICATION DATA:
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 213:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-213

Query Match 50.0%; Score 5; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
| | | | |
Db 5 PLPPT 9

RESULT 21

US-10-225-567A-1351
; Sequence 1351, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1351
; LENGTH: 16
; TYPE: PPT
; ORGANISM: Homo sapiens
US-10-225-567A-1351

Query Match 50.0%; Score 5; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
| | | | |
Db 10 PLPPT 14

RESULT 22

US-10-029-386-31396
; Sequence 31396, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34286
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31396
; LENGTH: 17
; TYPE: PPT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL118558.2

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.4
US-10-029-386-31396

Query Match 50.0%; Score 5; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
| | | | |
Db 8 QPLPP 12

RESULT 23

US-09-964-201A-17
; Sequence 17, Application US/09964201A
; Publication No. US20030091575A1
; GENERAL INFORMATION:
; APPLICANT: Kenten, John H
; APPLICANT: Tramontano, Alfonso
; APPLICANT: Pilon, Aprile L
; APPLICANT: Lohnas, Gerald L
; APPLICANT: Roberts, Steven F
; TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
; FILE REFERENCE: U.S. Patent Application No. US20030091575A1 09\026,276
; CURRENT APPLICATION NUMBER: US/09/964,201A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 19
; TYPE: PPT
; ORGANISM: Mycobacterium tuberculosis
US-09-964-201A-17

Query Match 50.0%; Score 5; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
| | | | |
Db 6 QPLPP 10

RESULT 24

US-09-308-511-11
; Sequence 11, Application US/09308511
; Patent No. US20020103145A1
; GENERAL INFORMATION:
; APPLICANT: BOT and BONA
; TITLE OF INVENTION: IMMUNIZATION OF INFANTS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue &
; Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/308,511
; FILING DATE: 19-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Clark, Richard S.
REGISTRATION NUMBER: 26,154
REFERENCE/DOCKET NUMBER: 29889-165/29528
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2558
TELEFAX: 212-765-2519
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mycobacteria
FEATURE:
NAME/KEY:
LOCATION: 350...369
OTHER INFORMATION: Heat Shock Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-308-511-11

Query Match 50.0%; Score 5; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
Db 6 QPLPP 10

RESULT 25
US-10-161-791-147
Sequence 147, Application US/10161791
Publication No. US2003018683A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: GUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-147

Query Match 50.0%; Score 5; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
Db 7 PLPPT 11

RESULT 26
US-10-092-219-11
Sequence 11, Application US/10092219
Publication No. US2002015114A1
GENERAL INFORMATION:
APPLICANT: Domin, Jan
TITLE OF INVENTION: No. US2002015114A1e1 Lipid Kinase
FILE REFERENCE: 1064HG/50947
CURRENT APPLICATION NUMBER: US/10/092,219
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: PCT/GB98/00244
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: 09/355,160
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 9701652.1
PRIOR FILING DATE: 1997-01-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 6
TYPE: PRT
ORGANISM: Homo sapiens
US-10-092-219-11

Query Match 40.0%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 2 PLPP 5

RESULT 27
US-09-019-679-4
Sequence 4, Application US/09019679
Patent No. US20020012943A1
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M
APPLICANT: Thorp, H. Holden
TITLE OF INVENTION: Electrochemical Probes for Detection of Molecular
FILE OF INVENTION: Interactions and Drug Discovery
FILE REFERENCE: 97082-E
CURRENT APPLICATION NUMBER: US/09/019,679
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: 60/036,919
EARLIER FILING DATE: 1997-02-06
EARLIER APPLICATION NUMBER: 60/059,049
EARLIER FILING DATE: 1997-09-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 7


```
;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Src SH3
; OTHER INFORMATION: binding motif
US-09-019-679-4
    Query Match          40.0%; Score 4; DB 9; Length 7;
    Best Local Similarity 100.0%; Pred. No. 6e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      2 PLPP 5
      |||||

RESULT 28
US-09-879-957-45
; Sequence 45, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. US20020034755A1h
; KAY, Brian K.
; FOWLKES, Dana M.
; MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-879-957-45
    Query Match          40.0%; Score 4; DB 9; Length 7;
    Best Local Similarity 100.0%; Pred. No. 6e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
      . |||||

;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Src SH3
; OTHER INFORMATION: binding motif
US-09-019-679-4
    Query Match          40.0%; Score 4; DB 9; Length 7;
    Best Local Similarity 100.0%; Pred. No. 6e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      2 PLPP 5
      |||||

RESULT 29
US-09-938-315-9
; Sequence 9, Application US/09938315
; Patent No. US20020091085A1
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; SPARKS, ANDREW B.
; THORN, JUDITH M.
; QUILLIAM, LAWRENCE A.
; DER, CHANNING J.
; TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,315
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4380-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-938-315-9
    Query Match          40.0%; Score 4; DB 9; Length 7;
    Best Local Similarity 100.0%; Pred. No. 6e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      2 PLPP 5
      |||||

RESULT 30
US-10-052-578-286
; Sequence 286, Application US/10052578
; Publication No. US20030134787A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Onathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
```

```
; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 286
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-052-578-286

Query Match          40.0%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      4 PLPP 7

RESULT 31
US-10-053-520-286
; Sequence 286, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Overfelli, Quathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 286
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-520-286

Query Match          40.0%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      4 PLPP 7

RESULT 32
US-10-161-791-9
; Sequence 9, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.

; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-9

Query Match          40.0%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      2 PLPP 5

RESULT 33
US-10-053-498B-286
; Sequence 286, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Overfelli, Quathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 286
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-053-498B-286

Query Match          40.0%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 4 PLPP 7

RESULT 34
US-09-745-078A-30
; Sequence 30, Application US/09745078A
; Publication No. US20030050434A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathak
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-09-745-078A-30

Query Match          40.0%; Score 4; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
Db 5 PPTV 8

RESULT 35
US-10-052-578-82
; Sequence 82, Application US/10052578
; Publication No. US20030134787A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathak
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-053-520-82

Query Match          40.0%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 4 PLPP 7

RESULT 36
US-10-053-520-82
; Sequence 82, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathak
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-053-520-82

Query Match          40.0%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 4 PLPP 7

RESULT 37
US-10-374-624-30
; Sequence 30, Application US/10374624
; Publication No. US20030166561A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/10/374,624
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/745,078A
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
;
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-10-374-624-30

Query Match 40.0%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPTV 7
Db 5 PPTV 8

RESULT 38
US-10-053-498B-82
; Sequence 82, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathak
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-053-498B-82

Query Match 40.0%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 4 PLPP 7

RESULT 39
US-08-854-825-43
; Sequence 43, Application US/08854825
; Publication No. US20020115061A1
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; APPLICANT: Cerny, Andreas
; TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T
; NUMBER OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Leydig, Voit & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

;
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-10-374-624-30

Query Match 40.0%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPTV 7
Db 5 PPTV 8

RESULT 38
US-10-053-498B-82
; Sequence 82, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathak
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-053-498B-82

Query Match 40.0%; Score 4; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 1 PLPP 4

RESULT 40
US-09-938-315-11
; Sequence 11, Application US/09938315
; Patent No. US20020091085A1
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; APPLICANT: SPARKS, ANDREW B.
; APPLICANT: THORN, JUDITH M.
; APPLICANT: QUILLIAM, LAWRENCE A.
; APPLICANT: DER, CHANNING J.
; TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,315
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELETYPE: 248555 OPAT UR
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
```

```

; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-938-315-11

Query Match          40.0%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY      2 PLPP 5
Db      ||||
        2 PLPP 5

RESULT 41
US-09-780-053-165
; Sequence 165, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-165

Query Match          40.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY      4 PPTV 7
Db      ||||
        6 PPTV 9

RESULT 42
US-09-780-053-456
; Sequence 456, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 456
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-456

Query Match          40.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY      4 PPTV 7
Db      ||||
        6 PPTV 9

```

```

; ORGANISM: Homo Sapiens
US-09-780-053-456

Query Match          40.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY      4 PPTV 7
Db      ||||
        5 PPTV 8

RESULT 43
US-09-780-053-517
; Sequence 517, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 517
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-517

Query Match          40.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY      4 PPTV 7
Db      ||||
        5 PPTV 8

RESULT 44
US-09-780-053-620
; Sequence 620, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 620
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-620

```

US-09-78Q-053-620

Query Match 40.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 PPTV 7
|||
Db 5 PPTV 8
|||

RESULT 45

US-09-945-917-34
; Sequence 34, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-945-917-34

Query Match 40.0%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 2 PLPP 5
|||
Db 4 PLPP 7
|||

RESULT 46

US-09-745-078A-29
; Sequence 29, Application US/09745078A
; Publication No. US20030050434A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/09/745,078A
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-09-745-078A-29

Query Match 40.0%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 PPTV 7
|||

Db 5 PPTV 8

RESULT 47

US-09-972-656-26
; Sequence 26, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-26

Query Match 40.0%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 LPPT 6
|||
Db 6 LPPT 9
|||

RESULT 48

US-09-932-165-3
; Sequence 3, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-BID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-3

Query Match 40.0%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 TVMF 9
|||
Db 6 TVMF 9
|||

RESULT 49

US-09-932-165-648
; Sequence 648, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 648
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-648

Query Match 40.0%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TVMF 9
Db 6 TVMF 9

RESULT 50

US-09-845-917A-34
; Sequence 34, Application US/09845917A
; Publication No. US20030167538A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845,917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-845-917A-34

Query Match 40.0%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 4 PLPP 7

RESULT 51

US-10-374-624-29

US-10-374-624-29
; Sequence 29, Application US/10374624
; Publication No. US20030166561A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/10/374,624
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/745,078A
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ3336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-10-374-624-29

Query Match 40.0%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPTV 7
Db 5 PPTV 8

RESULT 52

US-10-161-791-11
; Sequence 11, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US/08/602,999
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-11

Query Match          40.0%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      2 PLPP 5

RESULT 53
US-10-042-202-49
; Sequence 49, Application US/10042202
; Publication No. US20020136733A1
; GENERAL INFORMATION:
; APPLICANT: Adrian Vivian Sinton HILL, Michael AIDOO,
; Catherine Elizabeth Margaret ALLSOPP, Ajit LALVANI, Magdalena
; PLEBANSKI, Hilton Carter WHITTLE,
; TITLE OF INVENTION: MALARIA PEPTIDES
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSES: WENDEROTH, LIND & PONACK, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800,
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006-1021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPad for Windows 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/042,202
; FILING DATE: 11-Jan-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/714,175
; FILING DATE: 28-Jan-1997
; APPLICATION NUMBER: WO PCT/GB95/26982
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: GB 9406492.0
; FILING DATE: 31-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M Cheak, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER: 2002_0026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)-721-8200
; TELEFAX: (202)-721-8250
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-042-202-49

Query Match          40.0%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-11

Query Match          40.0%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      2 PLPP 5

RESULT 54
US-09-780-053-490
; Sequence 490, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83p5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.505U1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 490
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-490

Query Match          40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPTV 7
Db      6 PPTV 9

RESULT 55
US-09-780-053-505
; Sequence 505, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83p5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.505U1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 505
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-505

Query Match          40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


QY 4 PPTV 7
|||||
Db 5 PPTV 8

RESULT 56

US-09-780-053-569
; Sequence 569, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 569
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-569

Query Match 40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
|||||
Db 5 PPTV 8

RESULT 57

US-09-780-053-588
; Sequence 588, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 588
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-588

Query Match 40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
|||||
Db 6 PPTV 9

RESULT 58

US-09-780-053-675
; Sequence 675, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 675
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-675

Query Match 40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
|||||
Db 5 PPTV 8

RESULT 59

US-09-745-078A-28
; Sequence 28, Application US/09745078A
; Publication No. US20030050434A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/09/745,078A
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-09-745-078A-28

Query Match 40.0%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
|||||
Db 5 PPTV 8

```
RESULT 60
US-09-572-404B-22
; Sequence 22, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in EDG1 at 236-245 and may interact with Sequen
; OTHER INFORMATION: this patent.
US-09-572-404B-22

Query Match 40.0%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPPT 6
Db 1 LPPT 4

RESULT 61
US-09-572-404B-636
; Sequence 636, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 636
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in EFNB3 OR EPLG8 OR LERK8 at 213-222 and may in
; OTHER INFORMATION: with Sequence 635 in this patent.
US-09-572-404B-636

Query Match 40.0%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 7 PLPP 10

RESULT 62
US-09-572-404B-3283
; Sequence 3283, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
```

```
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3283
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DAF OR CD55 at 291-300 and may interact w
; OTHER INFORMATION: Sequence 3284 in this patent.
US-09-572-404B-3283

Query Match 40.0%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
Db 3 PPTV 6

RESULT 63
US-09-932-165-108
; Sequence 108, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAF, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Cat-F2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-108

Query Match 40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVMF 9
Db 6 TVMF 9

RESULT 64
US-09-932-165-124
; Sequence 124, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAF, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
```

```
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
; US-09-932-165-124

Query Match          40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred.No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 TVMF 9
Db      1 TVMF 4

RESULT 65
US-09-932-165-516
; Sequence 516, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 516
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
; US-09-932-165-516

Query Match          40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred.No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 TVMF 9
Db      1 TVMF 4

RESULT 66
US-09-932-165-701
; Sequence 701, Application US/09932165
; Publication No. US20030134784A1
```

```
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 701
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
; US-09-932-165-701

Query Match          40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred.No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 TVMF 9
Db      1 TVMF 4

RESULT 67
US-09-932-165-920
; Sequence 920, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 920
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
; US-09-932-165-920

Query Match          40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred.No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 6 TVMF 9
| | | |
Db 4 TVMF 7

RESULT 68

US-09-932-165-1297
; Sequence 1297, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-ETD, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AVA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 81P2H3 AND CatfF2B11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1297
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1297

Query Match 40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TVMF 9
| | | |
Db 3 TVMF 6

RESULT 69

US-10-374-624-28
; Sequence 28, Application US/10374624
; Publication No. US20030166561A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/10/374,624
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/745,078A
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-10-374-624-28

Query Match 40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPTV 7
| | | |
Db 5 PPTV 8

RESULT 70

US-10-192-381-60
; Sequence 60, Application US/10192381
; Publication No. US20030170807A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: WORLEY, Paul
; APPLICANT: TU, Jian
; APPLICANT: XIAO, Bo
; APPLICANT: LEAHY, Daniel
; APPLICANT: BENEKEN, Jutta
; APPLICANT: LANAHAN, Anthony
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS
; TITLE OF INVENTION: AMENDED)
; FILE REFERENCE: JHU1580-4
; CURRENT APPLICATION NUMBER: US/10/192,381
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US/09/377,285
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: US 60/138,426
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,493
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,494
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/097,334
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 60
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with Homer ligand peptide consensus
US-10-192-381-60

Query Match 40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
| | | |
Db 1 PLPP 4

RESULT 71

US-10-192-381-61
; Sequence 61, Application US/10192381
; Publication No. US20030170807A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: WORLEY, Paul
; APPLICANT: TU, Jian
; APPLICANT: XIAO, Bo
; APPLICANT: LEAHY, Daniel
; APPLICANT: BENEKEN, Jutta
; APPLICANT: LANAHAN, Anthony
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS
; TITLE OF INVENTION: AMENDED)
; FILE REFERENCE: JHU1580-4
; CURRENT APPLICATION NUMBER: US/10/192,381
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US/09/377,285
US-10-192-381-61

```
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: US 60/138,426
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,493
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,494
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/097,334
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with Homer ligand peptide consensus
US-10-192-381-61
```

```
Query Match 40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 PLPP 5
Db 1 PLPP 4
```

```
RESULT 72
US-10-078-547-8
; Sequence 8, Application US/10078547
; Publication No. US20020199211A1
; GENERAL INFORMATION:
; APPLICANT: Narayanaswamy Ramesh
; APPLICANT: Miguel A. de la Fuente
; APPLICANT: Ines M. Anton
; APPLICANT: Raif S. Geha
; TITLE OF INVENTION: WIP, A WASP-Associated Protein
; FILE REFERENCE: 1242.1022-005
; CURRENT APPLICATION NUMBER: US/10/078,547
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/599,287
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US98/27501
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/101,457
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/068,533
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: WIP sequence 352-361a.a., human
US-10-078-547-8
```

```
Query Match 40.0%; Score 4; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 PLPP 5
Db 5 PLPP 8
```

```
RESULT 73
US-10-078-547-9
; Sequence 9, Application US/10078547
; Publication No. US20020199211A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Narayanaswamy Ramesh
; APPLICANT: Miguel A. de la Fuente
; APPLICANT: Ines M. Anton
; APPLICANT: Raif S. Geha
; TITLE OF INVENTION: WIP, A WASP-Associated Protein
; FILE REFERENCE: 1242.1022-005
; CURRENT APPLICATION NUMBER: US/10/078,547
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/599,287
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US98/27501
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/101,457
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/068,533
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 10
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: WIP sequence 374-383 a.a., human
US-10-078-547-9
```

```
Query Match 40.0%; Score 4; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 PLPP 5
Db 5 PLPP 8
```

```
RESULT 74
US-10-078-547-11
; Sequence 11, Application US/10078547
; Publication No. US20020199211A1
; GENERAL INFORMATION:
; APPLICANT: Narayanaswamy Ramesh
; APPLICANT: Miguel A. de la Fuente
; APPLICANT: Ines M. Anton
; APPLICANT: Raif S. Geha
; TITLE OF INVENTION: WIP, A WASP-Associated Protein
; FILE REFERENCE: 1242.1022-005
; CURRENT APPLICATION NUMBER: US/10/078,547
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/599,287
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US98/27501
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/101,457
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/068,533
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 10
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: WASP sequence 338-347 a.a.
US-10-078-547-11
```

```
Query Match 40.0%; Score 4; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 PLPP 5
Db 5 PLPP 8
```

```
RESULT 75
US-10-078-547-12
; Sequence 12, Application US/10078547
; Publication NO. US20020199211A1
; GENERAL INFORMATION:
; APPLICANT: Narayanaswamy Ramesh
; APPLICANT: Miguel A. de la Fuente
; APPLICANT: Ines M. Anton
; APPLICANT: Raif S. Geha
; TITLE OF INVENTION: WIP, A WASP-Associated Protein
; FILE REFERENCE: 1242.1022-005
; CURRENT APPLICATION NUMBER: US/10/078,547
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/599,287
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US98/27501
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/101,457
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/068,533
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: WASP sequence 376-385 a.a.
US-10-078-547-12

Query Match          40.0%; Score 4; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
        ||||
Db       5 PLPP 8

Search completed: November 25, 2003, 20:37:02
Job time : 17.0465 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 8.0814 Seconds
(without alignments)
52.356 Million cell updates/sec

Title: US-09-641-801-25

Perfect score: 10

Sequence: 1 QLPPTVMFP 10

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents.AA:*
1: /cgn2_6/prodata/1/iaa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5S.COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCITUS.COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	100.0	10	4	US-09-641-803-25
2	10	100.0	15	4	US-09-641-803-34
3	6	60.0	16	3	US-08-602-999A-227
4	6	60.0	16	4	US-09-500-124-227
5	5	50.0	7	2	US-08-769-745-26
6	5	50.0	11	1	US-08-336-343A-24
7	5	50.0	11	3	US-08-652-877-34
8	5	50.0	11	3	US-08-476-515A-34
9	5	50.0	13	3	US-08-602-999A-90
10	5	50.0	13	3	US-08-602-999A-93
11	5	50.0	13	4	US-08-278-865-93
12	5	50.0	13	4	US-09-500-124-90
13	5	50.0	13	4	US-09-500-124-93
14	5	50.0	15	3	US-08-602-999A-355
15	5	50.0	15	3	US-08-602-999A-437
16	5	50.0	15	4	US-09-500-124-355
17	5	50.0	15	4	US-09-500-124-437
18	5	50.0	16	3	US-08-602-999A-213
19	5	50.0	16	4	US-09-500-124-213
20	5	50.0	19	4	US-09-026-276-17
21	5	50.0	20	2	US-08-363-276B-11
22	5	50.0	20	3	US-08-602-999A-147
23	5	50.0	20	3	US-08-755-034-11
24	5	50.0	20	4	US-09-500-124-147
25	5	50.0	20	5	PCT-US96-16718-11
26	5	50.0	20	5	PCT-US96-08995-11
27	4	40.0	6	4	US-09-355-160D-11

28	4	40.0	7	1	US-08-230-047-40	Sequence 40, Appl
29	4	40.0	7	2	US-08-340-283-38	Sequence 38, Appl
30	4	40.0	7	2	US-08-769-745-7	Sequence 7, Appl
31	4	40.0	7	3	US-08-602-999A-9	Sequence 9, Appl
32	4	40.0	7	4	US-08-278-865-9	Sequence 9, Appl
33	4	40.0	7	4	US-08-630-915A-45	Sequence 45, Appl
34	4	40.0	7	4	US-09-500-124-9	Sequence 9, Appl
35	4	40.0	7	5	PCT-US94-01640-11	Sequence 11, Appl
36	4	40.0	8	1	US-09-641-640-8	Sequence 8, Appl
37	4	40.0	8	2	US-08-612-857-8	Sequence 8, Appl
38	4	40.0	8	3	US-08-747-221B-43	Sequence 43, Appl
39	4	40.0	8	3	US-09-005-051-43	Sequence 43, Appl
40	4	40.0	9	1	US-08-214-650-43	Sequence 43, Appl
41	4	40.0	9	1	US-08-615-181-110	Sequence 110, Appl
42	4	40.0	9	2	US-08-146-028-441	Sequence 441, Appl
43	4	40.0	9	2	US-08-146-028-442	Sequence 442, Appl
44	4	40.0	9	2	US-08-146-028-443	Sequence 443, Appl
45	4	40.0	9	2	US-08-146-028-445	Sequence 445, Appl
46	4	40.0	9	2	US-08-146-028-446	Sequence 446, Appl
47	4	40.0	9	2	US-08-318-856A-49	Sequence 49, Appl
48	4	40.0	9	3	US-08-723-425A-441	Sequence 441, Appl
49	4	40.0	9	3	US-08-723-425A-442	Sequence 442, Appl
50	4	40.0	9	3	US-08-723-425A-443	Sequence 443, Appl
51	4	40.0	9	3	US-08-723-425A-445	Sequence 445, Appl
52	4	40.0	9	3	US-08-723-425A-446	Sequence 446, Appl
53	4	40.0	9	3	US-08-602-999A-11	Sequence 11, Appl
54	4	40.0	9	3	US-09-112-206-441	Sequence 441, Appl
55	4	40.0	9	3	US-09-112-206-442	Sequence 442, Appl
56	4	40.0	9	3	US-09-112-206-443	Sequence 443, Appl
57	4	40.0	9	3	US-09-112-206-445	Sequence 445, Appl
58	4	40.0	9	3	US-09-112-206-446	Sequence 446, Appl
59	4	40.0	9	4	US-08-278-865-11	Sequence 11, Appl
60	4	40.0	9	4	US-09-500-124-11	Sequence 11, Appl
61	4	40.0	10	1	US-08-230-047-12	Sequence 12, Appl
62	4	40.0	10	1	US-08-212-190A-8	Sequence 8, Appl
63	4	40.0	10	2	US-08-146-028-444	Sequence 444, Appl
64	4	40.0	10	2	US-08-769-745-5	Sequence 5, Appl
65	4	40.0	10	2	US-08-769-745-6	Sequence 6, Appl
66	4	40.0	10	2	US-08-900-321-8	Sequence 8, Appl
67	4	40.0	10	3	US-08-336-553A-12	Sequence 12, Appl
68	4	40.0	10	3	US-08-336-553A-43	Sequence 43, Appl
69	4	40.0	10	3	US-08-336-553A-65	Sequence 65, Appl
70	4	40.0	10	3	US-08-723-425A-444	Sequence 444, Appl
71	4	40.0	10	3	US-09-112-206-444	Sequence 444, Appl
72	4	40.0	10	4	US-08-439-157-12	Sequence 12, Appl
73	4	40.0	10	4	US-08-439-157-43	Sequence 43, Appl
74	4	40.0	10	4	US-08-439-157-65	Sequence 65, Appl
75	4	40.0	10	4	US-09-437-895-12	Sequence 12, Appl
76	4	40.0	10	4	US-09-437-895-43	Sequence 43, Appl
77	4	40.0	10	4	US-09-437-895-65	Sequence 65, Appl
78	4	40.0	10	5	PCT-US95-03610-8	Sequence 8, Appl
79	4	40.0	11	1	US-07-794-288D-24	Sequence 24, Appl
80	4	40.0	11	1	US-08-336-343A-25	Sequence 25, Appl
81	4	40.0	11	1	US-08-323-531-22	Sequence 22, Appl
82	4	40.0	11	1	US-08-198-094-22	Sequence 22, Appl
83	4	40.0	11	3	US-08-602-999A-260	Sequence 260, Appl
84	4	40.0	11	3	US-08-652-877-22	Sequence 22, Appl
85	4	40.0	11	3	US-08-652-877-32	Sequence 32, Appl
86	4	40.0	11	3	US-08-652-877-35	Sequence 35, Appl
87	4	40.0	11	3	US-08-652-877-36	Sequence 36, Appl
88	4	40.0	11	3	US-08-107-794A-22	Sequence 22, Appl
89	4	40.0	11	3	US-08-476-515A-22	Sequence 22, Appl
90	4	40.0	11	3	US-08-476-515A-32	Sequence 32, Appl
91	4	40.0	11	3	US-08-476-515A-35	Sequence 35, Appl
92	4	40.0	11	3	US-08-476-515A-36	Sequence 36, Appl
93	4	40.0	11	4	US-09-500-124-260	Sequence 260, Appl
94	4	40.0	11	5	PCT-US91-09055-7	Sequence 7, Appl
95	4	40.0	11	5	PCT-US93-07424-22	Sequence 22, Appl
96	4	40.0	11	5	PCT-US95-02087-22	Sequence 22, Appl
97	4	40.0	11	6	5258287-53	Patent No. 5258287
98	4	40.0	12	1	US-08-036-555B-50	Sequence 50, Appl
99	4	40.0	12	1	US-08-230-047-17	Sequence 17, Appl
100	4	40.0	12	1	US-07-794-288D-23	Sequence 23, Appl

ALIGNMENTS

```

RESULT 1
US-09-641-803-25
; Sequence 25, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641.803
; CURRENT FILING DATE: 2000-08-17
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-25

Query Match      100.0%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPPTVMFP 10
Db 1 QPLPPTVMFP 10

RESULT 2
US-09-641-803-34
; Sequence 34, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641.803
; CURRENT FILING DATE: 2000-08-17
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-34

Query Match      100.0%; Score 10; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.7e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPPTVMFP 10
Db 6 QPLPPTVMFP 15

```

```

RESULT 3
US-08-602-999A-227
; Sequence 227, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 227:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-227

Query Match      60.0%; Score 6; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPPTVM 8
Db 9 LPPTVM 14

RESULT 4
US-09-500-124-227
; Sequence 227, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467

```


;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/500,124
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/602,999
;; FILING DATE: 16-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Masrock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 227:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-09-500-124-227

Query Match 60.0%; Score 6; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPPTVM 8
|||
Db 9 LPPTVM 14

RESULT 5
US-08-769-745-26
;; Sequence 26, Application US/08769745
;; Patent No. 5955259
;; GENERAL INFORMATION:
;; APPLICANT: Holmes, Todd C.
;; APPLICANT: Levitan, Irwin B.
;; APPLICANT: Brandeis University
;; TITLE OF INVENTION: Mechanism for the Regulation of Ion
;; TITLE OF INVENTION: Channel Activity
;; FILE REFERENCE: BRU96-02
;; CURRENT APPLICATION NUMBER: US/08/769,745
;; CURRENT FILING DATE: 1996-12-19
;; NUMBER OF SEQ ID NOS: 41
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 26
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Mouse
US-08-769-745-26

Query Match 50.0%; Score 5; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
|||
Db 1 QPLPP 5

RESULT 6
US-08-336-343A-24
;; Sequence 24, Application US/08336343A
;; Patent No. 5677144
;; GENERAL INFORMATION:
;; APPLICANT: Ullrich, Axel
;; APPLICANT: Alves, Frauke
;; TITLE OF INVENTION: CKK-2, A No. 5677144el Receptor Tyrosine Kinase
;; NUMBER OF SEQUENCES: 43
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/336,343A
;; FILING DATE: 08-NOV-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7683-065
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-08-336-343A-24

Query Match 50.0%; Score 5; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
|||
Db 7 PLPPT 11

RESULT 7
US-08-652-877-34
;; Sequence 34, Application US/08652877
;; Patent No. 6187548
;; GENERAL INFORMATION:
;; APPLICANT: Akerstrom, Goran
;; APPLICANT: Juhlin, Claes
;; APPLICANT: Rask, Lars
;; APPLICANT: Crumley, Gregg R.
;; APPLICANT: Morse, Clarence C.
;; APPLICANT: Murray, Edward M.
;; APPLICANT: Hjaln, Goran
;; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
;; NUMBER OF SEQUENCES: 106
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Rhone-Poulenc Rorer Inc.
;; STREET: 500 Arcola Rd., 3C43
;; CITY: Collegeville
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19426-0107

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.5.1
; SOFTWARE: Word 6.0 (Patentin)
; CURRENT APPLICATION DATA: US/08/652,877
; APPLICATION NUMBER: US/08/652,877
; FILING DATE:
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15203
; FILING DATE: 22-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,314
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355E-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; US-08-652-877-34

```

```

Query Match 50.0%; Score 5; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 PLPPT 6
Db 7 PLPPT 11

```

```

RESULT 8
; US-08-476-515A-34
; Sequence 34, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjaln, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Martin Savitzky
; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 7.0 (Patentin)

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,515A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE94/00483
; FILING DATE: 24-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9301764-8
; FILING DATE: 24-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; US-08-476-515A-34

```

```

Query Match 50.0%; Score 5; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 PLPPT 6
Db 7 PLPPT 11

```

```

RESULT 9
; US-08-602-999A-90
; Sequence 90, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOMLKE, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie

```

REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-90

Query Match 50.0%; Score 5; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
DB 8 PLPPT 12

RESULT 10
US-08-602-999A-93
Sequence 93, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-93

Query Match 50.0%; Score 5; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
DB 5 PLPPT 9

RESULT 11
US-08-278-865-93
Sequence 93, Application US/08278865
Patent No. 6303574
GENERAL INFORMATION:
APPLICANT: KAY, BRIAN K.
APPLICANT: SPARKS, ANDREW B.
APPLICANT: THORN, JUDITH M.
APPLICANT: QUILLIAM, LAWRENCE A.
APPLICANT: DER, CHANNING J.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,865
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-007-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-278-865-93

Query Match 50.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
DB 5 PLPPT 9

RESULT 12
US-09-500-124-90
Sequence 90, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.

```
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 869-9741/8864
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-90

Query Match 50.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
Db 8 PLPPT 12

RESULT 13
US-09-500-124-93
; Sequence 93, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 869-9741/8864
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-90
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 869-9741/8864
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-93

Query Match 50.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
Db 5 PLPPT 9

RESULT 14
US-08-602-999A-355
; Sequence 355, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 869-9741/8864
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 355:
```

SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-355

Query Match 50.0%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
|||||
Db 9 PLPPT 13

RESULT 15

US-08-602-999A-437
Sequence 437, Application US/08602999A
Patent No. 6184205

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 437:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-437

Query Match 50.0%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
|||||
Db 2 QPLPP 6

RESULT 16

US-09-500-124-355
Sequence 355, Application US/09500124
Patent No. 6432920

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-355

Query Match 50.0%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
|||||
Db 9 PLPPT 13

RESULT 17

US-09-500-124-437
Sequence 437, Application US/09500124
Patent No. 6432920

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 437:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-437

Query Match 50.0%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
Db 2 QPLPP 6

RESULT 18
US-08-602-999A-213
; Sequence 213, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A

```

```

; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 213:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-213

Query Match 50.0%; Score 5; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
Db 5 PLPPT 9

RESULT 19
US-09-500-124-213
; Sequence 213, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 213:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid

```

```
;
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-213

Query Match 50.0%; Score 5; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6
Db 5 PLPPT 9

RESULT 20
US-09-026-276-17
; Sequence 17, Application US/09026276
; Patent No. 6319503
; GENERAL INFORMATION:
; APPLICANT: Kenten, John H
; APPLICANT: Trantomano, Alfonso
; APPLICANT: Pilon, April L
; APPLICANT: Lohnas, Gerald L
; APPLICANT: Roberts, Steven F
; TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
; FILE REFERENCE: U.S. Patent Application No. 6319503 09\026,276
; CURRENT APPLICATION NUMBER: US/09\026,276
; CURRENT FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-026-276-17

Query Match 50.0%; Score 5; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
Db 6 QPLPP 10

RESULT 21
US-08-363-276B-11
; Sequence 11, Application US/08363276B
; Patent No. 5969109
; GENERAL INFORMATION:
; APPLICANT: BONA ET AL.
; TITLE OF INVENTION: CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue &
; ADDRESSER: Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08\363,276B
; FILING DATE: 22-DECEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 07/486,546
; FILING DATE: 28-FEBRUARY-1990 (ABANDONED)
```

```
;
; APPLICATION NUMBER: USSN 07/687,376
; FILING DATE: 18-APRIL-1991 (ABANDONED)
; APPLICATION NUMBER: USSN 08/327,636
; FILING DATE: 24-OCTOBER-1994 (ABANDONED)
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Richard S
; REGISTRATION NUMBER: 26,154
; REFERENCE/DOCKET NUMBER: 29889-165/29528
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2558
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mycobacteria
; FEATURE:
; NAME/KEY:
; LOCATION: 350...369
; OTHER INFORMATION: Heat Shock Protein
US-08-363-276B-11

Query Match 50.0%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
Db 6 QPLPP 10

RESULT 22
US-08-602-999A-147
; Sequence 147, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08\602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
```

TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-147

Query Match 50.0%; Score 5; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
Db 7 PLPPT 11

RESULT 23
US-08-755-034-11
Sequence 11, Application US/08755034
Patent No. 6204250
GENERAL INFORMATION:
APPLICANT: BOT and BONA
TITLE OF INVENTION: IMMUNIZATION OF INFANTS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue &
ADDRESSEE: Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,034
FILING DATE: 22-NOVEMBER-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Richard S
REGISTRATION NUMBER: 26,154
REFERENCE/DOCKET NUMBER: 29889-165/29528
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2558
TELEFAX: 212-765-2519
TELEX:

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mycobacteria
FEATURE:
NAME/KEY:
LOCATION: 350...369
OTHER INFORMATION: Heat Shock Protein
US-08-755-034-11

Query Match 50.0%; Score 5; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5
Db 6 QPLPP 10

RESULT 24
US-09-500-124-147
Sequence 147, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-147

Query Match 50.0%; Score 5; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6
Db 7 PLPPT 11

RESULT 25
PCT-US95-16718-11
Sequence 11, Application PC/TUS9516718
GENERAL INFORMATION:
APPLICANT: MOUNT SINAI SCHOOL OF MEDICINE OF THE
APPLICANT: CITY UNIVERSITY OF NEW YORK
TITLE OF INVENTION: CHIMERIC ANTIBODIES
TITLE OF INVENTION: COMPRISING ANTIGEN BINDING SITES AND B AND T CELL EPITOPES


```
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue &
; ADDRESSEE: Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16718
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Richard S
; REGISTRATION NUMBER: 26,154
; REFERENCE/DOCKET NUMBER: 29889-165/29528
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2558
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mycobacteria
; FEATURE:
; NAME/KEY:
; LOCATION: 350...369
; OTHER INFORMATION: Heat Shock Protein
; PCT-US95-16718-11

Query Match 50.0%; Score 5; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
Db 6 QPLPP 10

RESULT 26
PCT-US96-08995-11
; Sequence 11, Application PC/TUS9608995
; GENERAL INFORMATION:
; APPLICANT: MOUNT SINAI SCHOOL OF MEDICINE OF THE CITY
; APPLICANT: UNIVERSITY OF NEW YORK
; TITLE OF INVENTION: PEGYLATED MODIFIED PROTEINS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
```

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/08995
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,421
; FILING DATE: 7-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Richard S
; REGISTRATION NUMBER: 26,154
; REFERENCE/DOCKET NUMBER: 29889-165/29528
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2558
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mycobacteria
; FEATURE:
; NAME/KEY:
; LOCATION: 350...369
; OTHER INFORMATION: Heat Shock Protein
; PCT-US96-08995-11

Query Match 50.0%; Score 5; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5
Db 6 QPLPP 10

RESULT 27
US-09-355-160D-11
; Sequence 11, Application US/09355160D
; Patent No. 6436671
; GENERAL INFORMATION:
; APPLICANT: Domin, Jan
; TITLE OF INVENTION: No. 6436671el Lipid Kinase
; FILE REFERENCE: 2332-1-004
; CURRENT APPLICATION NUMBER: US/09/355,160D
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/GB98/00244
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 9701652.1
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-355-160D-11

Query Match 40.0%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 2 PLPP 5

RESULT 28
US-08-230-047-40
; Sequence 40, Application US/08230047
```

; Patent No. 5541109
; GENERAL INFORMATION:
; APPLICANT: Searlross III, George H.
; APPLICANT: Ivashchenko, Yuri D.
; APPLICANT: Jaye, Michael C.
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230,047
; FILING DATE: 19-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A1465-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-230-047-40

Query Match 40.0%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 3 PLPP 6

RESULT 29
US-08-340-283-38
; Sequence 38, Application US/08340283
; Patent No. 5861318
; GENERAL INFORMATION:
; APPLICANT: Elhammer, Ake P.
; TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR
; TITLE OF INVENTION: N-ACETYLGLACTOSAMINYLTRANSFERASE ACTIVITY
; NUMBER OF SEQUENCES: 205
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia and Upjohn, Inc., Intellect. Prop. Law
; ADDRESSEE: (1920-32-1)
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,283
; FILING DATE:

; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Wootton, Thomas A.
; REGISTRATION NUMBER: 35,004
; REFERENCE/DOCKET NUMBER: 4828
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (616) 385-7914
; TELEFAX: (616) 385-6897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-340-283-38

Query Match 40.0%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 4 PLPP 7

RESULT 30
US-08-769-745-7
; Sequence 7, Application US/08769745
; Patent No. 5955259
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd C.
; APPLICANT: Levitan, Irwin B.
; APPLICANT: Brandeis University
; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; TITLE OF INVENTION: Channel Activity
; FILE REFERENCE: BRU96-02
; CURRENT APPLICATION NUMBER: US/08/769,745
; CURRENT FILING DATE: 1996-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rat
US-08-769-745-7

Query Match 40.0%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 2 PLPP 5

RESULT 31
US-08-602-999A-9
; Sequence 9, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

;; TITLE OF INVENTION: ISOLATING AND USING SAME
;; NUMBER OF SEQUENCES: 467
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/602,999A
;; FILING DATE: 16-FEB-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Misrock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; US-08-602-999A-9

Query Match 40.0%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 2 PLPP 5

RESULT 32
US-08-278-865-9
; Sequence 9, Application US/08278865
; Patent No. 6303574
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; APPLICANT: SPARKS, ANDREW B.
; APPLICANT: THORN, JUDITH M.
; APPLICANT: QUILLIAM, LAWRENCE A.
; APPLICANT: DER, CHANNING J.
; TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,865
; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Villacorta, Gilberto M.
;; REGISTRATION NUMBER: 34,038
;; REFERENCE/DOCKET NUMBER: 4980-007-0
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 413-3000
;; TELEFAX: (703) 413-2220
;; TELEX: 248855 OPAT UR
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; US-08-278-865-9

Query Match 40.0%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 2 PLPP 5

RESULT 33
US-08-630-915A-45
; Sequence 45, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: McCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-630-915A-45

Query Match 40.0%; Score 4; DB 4; Length 7;

```
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 2 PLPP 5

RESULT 34
US-09-500-124-9
; Sequence 9, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAN, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500.124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602.999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-9

Query Match 40.0%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 2 PLPP 5

RESULT 35
PCT-US94-01840-11
; Sequence 11, Application PC/TUS9401840
; GENERAL INFORMATION:
; APPLICANT: Christopher E. Rudd
; APPLICANT: Prasad Kanteti
```

```
; APPLICANT: Lewis Cantley
; TITLE OF INVENTION: CD4 MEDIATED MODULATION OF
; TITLE OF INVENTION: LIPID KINASES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01840
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/023,915
; FILING DATE: February 26, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/063001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
; PCT-US94-01840-11

Query Match 40.0%; Score 4; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 3 PLPP 6

RESULT 36
US-09-641-640-8
; Sequence 8, Application US/09641640
; Patent No. RE37952
; GENERAL INFORMATION:
; APPLICANT: SCHWEIGHOFFER, Fabien
; TOCQUE, Bruno
; TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/641,640
; FILING DATE: 15-Aug-2000
; CLASSIFICATION: <Unknown>
```

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,857
; FILING DATE: <Unknown>
; APPLICATION NUMBER: WO PCT/FR94/00542
; FILING DATE: 09-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: 38,619
; REFERENCE/DOCKET NUMBER: ST93044-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..8
; OTHER INFORMATION: /note= "3BP1 peptide"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-641-640-8

Query Match          40.0%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      3 PLPP 6

RESULT 37
US-08-612-857-8
; Sequence 8, Application US/08612857
; Patent No. 5831048
; GENERAL INFORMATION:
; APPLICANT: SCHWEIGHOFFER, Fabien
; APPLICANT: TOCQUE, Bruno
; TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/612,857
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93-10971
; FILING DATE: 15-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR94/00542
; FILING DATE: 09-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: 38,619
; REFERENCE/DOCKET NUMBER: ST93044-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
```

```
;
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..8
; OTHER INFORMATION: /note= "3BP1 peptide"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-612-857-8

Query Match          40.0%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      3 PLPP 6

RESULT 38
US-08-747-221B-43
; Sequence 43, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,221B
; FILING DATE: No. 6063610ember 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: PC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-08-747-221B-43

Query Match          40.0%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPTV 7
Db      2 PPTV 5
```

RESULT 39

US-09-005-051-43
; Sequence 43, Application US/09005051
; Patent No. 6291222

; GENERAL INFORMATION:

; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; ADDRESSEE: Heska Corporation

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/005,051

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/747,221

; FILING DATE: No. 6291222ember 12, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: FC-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 43:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: Peptide

US-09-005-051-43

Query Match 40.0%; Score 4; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPTV 7

Db 2 PPTV 5

RESULT 40

US-08-214-650-43

; Sequence 43, Application US/08214650

; Patent No. 5709995

; GENERAL INFORMATION:

; APPLICANT: Chisari, Francis V.

; APPLICANT: Cerny, Andreas

; TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T

; TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS C VIRUS

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leydig, Voit & Mayer

; STREET: Two Prudential Plaza, Suite 4900

; CITY: Chicago

; STATE: IL

; COUNTRY: USA

; ZIP: 60601

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,650

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Silvert, Donald J.

; REGISTRATION NUMBER: 37552

; REFERENCE/DOCKET NUMBER: 61230

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 616-5600

; TELEFAX: (312) 616-5700

; TELEX: 25-3533

; INFORMATION FOR SEQ ID NO: 43:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-214-650-43

Query Match 40.0%; Score 4; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5

Db 1 PLPP 4

RESULT 41

US-08-615-181-110

; Sequence 110, Application US/08615181

; Patent No. 5756666

; GENERAL INFORMATION:

; APPLICANT: MASAFUMI, TAKIGUCHI

; APPLICANT: MIWA, KIYOSHI

; TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE

; TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND

; TITLE OF INVENTION: CURING AIDS

; NUMBER OF SEQUENCES: 115

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/615,181

; FILING DATE: 04-APR-1996

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP94/01756

; FILING DATE: 19-OCT-1994

; APPLICATION NUMBER: JP 261302/1993

; FILING DATE: 19-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 10-796-0 PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-08-615-181-110

Query Match 40.0%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPPT 6
|||||
Db 1 LPPT 4

RESULT 42
US-08-146-028-441
Sequence 441, Application US/08146028
Patent No. 5891640
GENERAL INFORMATION:

APPLICANT: PROCESS FOR THE DETERMINATION OF PEPTIDES
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
NUMBER OF SEQUENCES: 453
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,028
INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-146-028-441

Query Match 40.0%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
|||||
Db 6 PLPP 9

RESULT 43
US-08-146-028-442
Sequence 442, Application US/08146028
Patent No. 5891640
GENERAL INFORMATION:

APPLICANT: PROCESS FOR THE DETERMINATION OF PEPTIDES
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
NUMBER OF SEQUENCES: 453
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,028
INFORMATION FOR SEQ ID NO: 442:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-146-028-442

Query Match 40.0%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
|||||
Db 5 PLPP 8

RESULT 44
US-08-146-028-443
Sequence 443, Application US/08146028
Patent No. 5891640
GENERAL INFORMATION:

APPLICANT: PROCESS FOR THE DETERMINATION OF PEPTIDES
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THE
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
NUMBER OF SEQUENCES: 453
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,028
INFORMATION FOR SEQ ID NO: 443:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-146-028-443

Query Match 40.0%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
|||||
Db 4 PLPP 7

RESULT 45
US-08-146-028-445
Sequence 445, Application US/08146028
Patent No. 5891640
GENERAL INFORMATION:

APPLICANT: PROCESS FOR THE DETERMINATION OF PEPTIDES
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THE
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
NUMBER OF SEQUENCES: 453

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,028
; INFORMATION FOR SEQ ID NO: 445:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-146-028-445

```

```

Query Match 40.0%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2 PLPP 5
Db 2 PLPP 5

```

```

RESULT 46
US-08-146-028-446
; Sequence 446, Application US/08146028
; Patent No. 5891640
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,028
; INFORMATION FOR SEQ ID NO: 446:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-146-028-446

```

```

Query Match 40.0%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2 PLPP 5
Db 1 PLPP 4

```

```

RESULT 47
US-08-318-856A-49
; Sequence 49, Application US/08318856A
; Patent No. 5972351
; GENERAL INFORMATION:
; APPLICANT: Adrian V.S. Hill, et al.
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
; TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
; TITLE OF INVENTION: ANTIGENS (AS AMENDED)
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1+
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,856A
; FILING DATE: October 3, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92 08 068.8
; FILING DATE: April 3, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92 17 704.7
; FILING DATE: August 20, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB93/00711
; FILING DATE: April 5, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee Cheng
; REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 263-PP1R1577US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 721-8200
; TELEFAX: (202) 721-8250
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-318-856A-49

```

```

Query Match 40.0%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2 PLPP 5
Db 5 PLPP 8

```

```

RESULT 48
US-08-723-425A-441
; Sequence 441, Application US/08723425A
; Patent No. 6165730
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
; NUMBER OF SEQUENCES: 453
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,425A

```


QY	Db	2 PLPP 5	5 PLPP 8
<p>* FILING DATE:</p> <p>CLASSIFICATION: 435</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: SADOFF, B.J.</p> <p>REGISTRATION NUMBER: 36,663</p> <p>REFERENCE/DOCKET NUMBER: 1487-13</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 703-816-4000</p> <p>TELEFAX: 703-816-4100</p> <p>INFORMATION FOR SEQ ID NO: 441:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 9 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: peptide</p> <p>US-08-723-425A-441</p>			
<p>Query Match 40.0%; Score 4; DB 3; Length 9;</p> <p>Best Local Similarity 100.0%; Pred. No. 2.5e+05;</p> <p>Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>			
QY	Db	2 PLPP 5	6 PLPP 9
<p>RESULT 49</p> <p>US-08-723-425A-442</p> <p>Sequence 442, Application US/08723425A</p> <p>Patent No. 6165730</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: DELEYS, ROBERT</p> <p>TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF</p> <p>TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT</p> <p>TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF</p> <p>TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...</p> <p>NUMBER OF SEQUENCES: 453</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: NIXON & VANDERHVE, P.C.</p> <p>STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR</p> <p>CITY: Arlington</p> <p>STATE: VA</p> <p>COUNTRY: USA</p> <p>ZIP: 22201</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: PatentIn Release #1.0, Version #1.30</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/723,425A</p> <p>FILING DATE:</p> <p>CLASSIFICATION: 435</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: SADOFF, B.J.</p> <p>REGISTRATION NUMBER: 36,663</p> <p>REFERENCE/DOCKET NUMBER: 1487-13</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 703-816-4000</p> <p>TELEFAX: 703-816-4100</p> <p>INFORMATION FOR SEQ ID NO: 443:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 9 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: peptide</p> <p>US-08-723-425A-443</p>			
<p>Query Match 40.0%; Score 4; DB 3; Length 9;</p> <p>Best Local Similarity 100.0%; Pred. No. 2.5e+05;</p> <p>Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>			
QY	Db	2 PLPP 5	4 PLPP 7
<p>RESULT 51</p> <p>US-08-723-425A-445</p> <p>Sequence 445, Application US/08723425A</p> <p>Patent No. 6165730</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: DELEYS, ROBERT</p> <p>TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF</p> <p>TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT</p> <p>TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF</p> <p>TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...</p> <p>NUMBER OF SEQUENCES: 453</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: NIXON & VANDERHVE, P.C.</p> <p>STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR</p> <p>CITY: Arlington</p> <p>STATE: VA</p> <p>COUNTRY: USA</p> <p>ZIP: 22201</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: PatentIn Release #1.0, Version #1.30</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/723,425A</p> <p>FILING DATE:</p> <p>CLASSIFICATION: 435</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: SADOFF, B.J.</p> <p>REGISTRATION NUMBER: 36,663</p> <p>REFERENCE/DOCKET NUMBER: 1487-13</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 703-816-4000</p> <p>TELEFAX: 703-816-4100</p> <p>INFORMATION FOR SEQ ID NO: 442:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 9 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: peptide</p> <p>US-08-723-425A-442</p>			
<p>Query Match 40.0%; Score 4; DB 3; Length 9;</p> <p>Best Local Similarity 100.0%; Pred. No. 2.5e+05;</p> <p>Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>			

STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,425A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1487-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 445:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-723-425A-445

Query Match 40.0%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 2 PLPP 5

RESULT 52
US-08-723-425A-446
Sequence 446, Application US/08723425A
Patent No. 6165730
GENERAL INFORMATION:
APPLICANT: DELEYS, ROBERT
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
NUMBER OF SEQUENCES: 453
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE, P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,425A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1487-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 446:
SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-723-425A-446

Query Match 40.0%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 1 PLPP 4

RESULT 53
US-08-602-999A-11
Sequence 11, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-11

Query Match 40.0%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 2 PLPP 5

RESULT 54

US-09-112-206-441
; Sequence 441, Application US/09112206
; Patent No. 6210903
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112,206
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,028
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 441:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-112-206-441

Query Match 40.0%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 6 PLPP 9

RESULT 55
US-09-112-206-442
; Sequence 442, Application US/09112206
; Patent No. 6210903
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112,206
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,028
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 442:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-112-206-442

Query Match 40.0%; Score 4; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PLPP 5
Db 5 PLPP 8
RESULT 56
US-09-112-206-443
; Sequence 443, Application US/09112206
; Patent No. 6210903
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THE
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112,206
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,028
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 443:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-112-206-443

Query Match 40.0%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 4 PLPP 7

RESULT 57
US-09-112-206-445
; Sequence 445, Application US/09112206
; Patent No. 6210903
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THE
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112,206
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,028
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 445:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-112-206-445

Query Match 40.0%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 2 PLPP 5

RESULT 58
US-09-112-206-446
; Sequence 446, Application US/09112206
; Patent No. 6210903
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112,206
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,028
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 446:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-112-206-446

Query Match 40.0%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 1 PLPP 4

RESULT 59
US-08-278-865-11
; Sequence 11, Application US/08278865
; Patent No. 6303574
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; APPLICANT: SPARKS, ANDREW B.
; APPLICANT: THORN, JUDITH M.
; APPLICANT: QUILLIAM, LAWRENCE A.
; APPLICANT: DER, CHANNING J.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

```

```

; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,865
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-278-865-11

Query Match 40.0%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 2 PLPP 5

RESULT 60
US-09-500-124-11
; Sequence 11, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999

```

;
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-11

Query Match 40.0%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 2 PLPP 5

RESULT 61
US-08-230-047-12
; Sequence 12, Application US/08230047
; Patent No. 5541109
; GENERAL INFORMATION:
; APPLICANT: Searfoss III, George H.
; APPLICANT: Ivashchenko, Yuri D.
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230,047
; FILING DATE: 19-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A1465-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-230-047-12

Query Match 40.0%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5

Db 7 PLPP 10

RESULT 62
US-08-212-190A-8
; Sequence 8, Application US/08212190A
; Patent No. 5652223
; GENERAL INFORMATION:
; APPLICANT: KOHN, Elise C.
; APPLICANT: LIOTTA, Lance A.
; APPLICANT: KIM, Young Sook
; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,190A
; FILING DATE: 14-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 15280-204US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-212-190A-8

Query Match 40.0%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 7 PLPP 10

RESULT 63
US-08-146-028-444
; Sequence 444, Application US/08146028
; Patent No. 5891640
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THE
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPE
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/08/146,028
; INFORMATION FOR SEQ ID NO: 444:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-146-028-444

Query Match 40.0%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 PLPP 5
|||
Db 3 PLPP 6

RESULT 64
US-08-769-745-5
; Sequence 5, Application US/08769745
; Patent No. 5955259
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd C.
; APPLICANT: Levitan, Irwin B.
; APPLICANT: Brandeis University
; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; TITLE OF INVENTION: Channel Activity
; FILE REFERENCE: BRU96-02
; CURRENT APPLICATION NUMBER: US/08/769,745
; CURRENT FILING DATE: 1996-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Rat
US-08-769-745-5

Query Match 40.0%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 PLPP 5
|||
Db 4 PLPP 7

RESULT 65
US-08-769-745-6
; Sequence 6, Application US/08769745
; Patent No. 5955259
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd C.
; APPLICANT: Levitan, Irwin B.
; APPLICANT: Brandeis University
; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; TITLE OF INVENTION: Channel Activity
; FILE REFERENCE: BRU96-02
; CURRENT APPLICATION NUMBER: US/08/769,745
; CURRENT FILING DATE: 1996-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapien
US-08-769-745-6

Query Match 40.0%; Score 4; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
QY 2 PLPP 5
|||
Db 4 PLPP 7

RESULT 66
US-08-900-321-8
; Sequence 8, Application US/08900321
; Patent No. 5981712
; GENERAL INFORMATION:
; APPLICANT: Kohn, Elise C.
; APPLICANT: Liotta, Lance A.
; APPLICANT: Kim, Young S.
; TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,321
; FILING DATE: 25-JUL-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,190
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-204100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-900-321-8

Query Match 40.0%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 PLPP 5
|||
Db 7 PLPP 10

RESULT 67
US-08-336-553A-12
; Sequence 12, Application US/08336553A
; Patent No. 6054264
; GENERAL INFORMATION:
; APPLICANT: CHIEN, DAVID Y.
; APPLICANT: KUO, GEORGE
; TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND
; TITLE OF INVENTION: REAGENTS FOR USE THEREIN
; NUMBER OF SEQUENCES: 75

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,553A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,400
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 22300-20947.00
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-336-553A-12

Query Match 40.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
Db 5 PPTV 8

RESULT 68
US-08-336-553A-43
; Sequence 43, Application US/08336553A
; Patent No. 6054264
; GENERAL INFORMATION:
; APPLICANT: CHIEN, DAVID Y.
; APPLICANT: KUO, GEORGE
; TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND
; TITLE OF INVENTION: REAGENTS FOR USE THEREIN
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,553A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,400
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 22300-20947.00
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-336-553A-65

Query Match 40.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
Db 5 PPTV 8
```

```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 22300-20947.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-336-553A-43

Query Match 40.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
Db 5 PPTV 8

RESULT 69
US-08-336-553A-65
; Sequence 65, Application US/08336553A
; Patent No. 6054264
; GENERAL INFORMATION:
; APPLICANT: CHIEN, DAVID Y.
; APPLICANT: KUO, GEORGE
; TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND
; TITLE OF INVENTION: REAGENTS FOR USE THEREIN
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,553A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,400
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 22300-20947.00
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-336-553A-65

Query Match 40.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 4 PPTV 7
Db 5 PPTV 8

RESULT 70
US-08-723-425A-444
; Sequence 444, Application US/08723425A
; Patent No. 6165730
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
; NUMBER OF SEQUENCES: 453
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,425A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 444:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-723-425A-444

Query Match 40.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred.No.1.le+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 3 PLPP 6

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,157
FILING DATE: 11-May-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/336,553A
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/060,400
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 22300-20947.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-08-439-157-12

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112,206
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,028
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 444:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-112-206-444

Query Match 40.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred.No.1.le+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 3 PLPP 6

RESULT 72
US-08-439-157-12
; Sequence 12, Application US/08439157
; Patent No. 6416944
; GENERAL INFORMATION:
; APPLICANT: CHIEN, DAVID Y.
; Kuo, GEORGE
; TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND
; REAGENTS FOR USE THEREIN
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,157
; FILING DATE: 11-May-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,553A
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/060,400
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 22300-20947.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-08-439-157-12

Query Match 40.0%; Score 4; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 4 PPTV 7
 Db 5 PPTV 8

RESULT 73
 US-08-439-157-43
 ; Sequence 43, Application US/08439157
 ; Patent No. 6416944
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIEN, DAVID Y.
 ; Kuo, George
 ; TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND
 ; REAGENTS FOR USE THEREIN

NUMBER OF SEQUENCES: 75
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/439,157
 FILING DATE: 11-May-1995
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/336,553A
 FILING DATE: 10-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: LEHNHARDT, SUSAN K.
 REGISTRATION NUMBER: 33,943
 REFERENCE/DOCKET NUMBER: 22300-20947.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792

INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 43:
 US-08-439-157-43

Query Match 40.0%; Score 4; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 4 PPTV 7
 Db 5 PPTV 8

RESULT 74
 US-08-439-157-65
 ; Sequence 65, Application US/08439157
 ; Patent No. 6416944
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIEN, DAVID Y.

Kuo, George
 ; TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND
 ; REAGENTS FOR USE THEREIN
 ; NUMBER OF SEQUENCES: 75
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/439,157
 FILING DATE: 11-May-1995
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/336,553A
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/060,400
 FILING DATE: 10-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: LEHNHARDT, SUSAN K.
 REGISTRATION NUMBER: 33,943
 REFERENCE/DOCKET NUMBER: 22300-20947.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141

INFORMATION FOR SEQ ID NO: 65:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 65:
 US-08-439-157-65

Query Match 40.0%; Score 4; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
 Db 5 PPTV 8

RESULT 75
 US-09-437-895-12
 ; Sequence 12, Application US/09437895
 ; Patent No. 6416946
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIEN, DAVID Y.
 ; Kuo, George

TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND
 REAGENTS FOR USE THEREIN
 NUMBER OF SEQUENCES: 75
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1018

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/437,895
; FILING DATE: 09-No. 6416946-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,553
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/060,400
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 22300-20947.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-437-895-12

Query Match      40.0%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      4 PPTV 7
Db      5 PPTV 8
```

```
Search completed: November 25, 2003, 20:30:01
Job time : 9.0814 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 4.11628 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-26

Perfect score: 6

Sequence: 1 PQSVLS 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	ID	Description
1	4	66.7	11	2 F33098	214k exoantigen (v
2	3	50.0	6	2 PT0560	T-cell receptor be
3	3	50.0	9	4 I57650	hemoglobin alpha c
4	3	50.0	12	2 A42324	cytochrome P450c27
5	3	50.0	12	2 S69095	ubiquinol-cytochro
6	3	50.0	13	2 S47361	T-cell antigen rec
7	3	50.0	13	2 B58864	dipeptidyl-peptida
8	3	50.0	14	1 QMWAFF	polistes mastopara
9	3	50.0	14	2 S11074	alcohol dehydrogen
10	3	50.0	15	2 PN0117	hemoglobin alpha c
11	3	50.0	15	2 S62620	protein disulfide-
12	3	50.0	15	2 PA0075	fructose-bisphosph
13	3	50.0	15	2 PA0102	fructose-bisphosph
14	3	50.0	15	2 S71300	ICU3 protein - Par
15	3	50.0	15	2 C84035	hypothetical prote
16	3	50.0	16	2 S11290	matrix protein M1
17	3	50.0	16	2 A44352	candidatepsin (EC
18	3	50.0	16	2 C61414	chymotrypsin (EC 3
19	3	50.0	16	2 G24687	T-cell receptor be
20	3	50.0	16	2 C28587	T-cell receptor be
21	3	50.0	16	2 G53284	T-cell receptor be
22	3	50.0	17	2 A34835	ribosomal protein
23	3	50.0	17	2 B44873	caldesmon rabbit
24	3	50.0	17	2 B61414	chymotrypsin (EC 3
25	3	50.0	18	2 S74195	epoxide hydrolase
26	3	50.0	19	2 S54848	succinyl-CoA synth
27	3	50.0	19	2 B53145	high conductance c
28	3	50.0	19	2 S20274	quinoline oxidized
29	3	50.0	20	2 S46205	comosain (EC 3.4.2

30	3	50.0	20	2 S46204	anain (EC 3.4.2.2
31	3	50.0	20	2 C49164	chromogranin-B - r
32	3	50.0	20	2 B46174	RNA-binding protei
33	3	50.0	20	2 S18582	hypothetical prote
34	3	50.0	20	2 T50757	pufK protein limpo
35	3	50.0	20	2 JU0330	hypothetical prote
36	3	50.0	20	2 A61414	chymotrypsin (EC 3
37	3	50.0	20	2 A99091	hypothetical prote
38	2	33.3	4	2 I40505	hypothetical prote
39	2	33.3	4	2 S17255	ribosomal protein
40	2	33.3	4	2 T30569	hypothetical prote
41	2	33.3	5	2 A60521	glycogen phosphory
42	2	33.3	5	2 T14908	hypothetical prote
43	2	33.3	5	2 S55237	zinc-binding prote
44	2	33.3	5	2 A60803	neuropeptide - sea
45	2	33.3	5	2 PT0278	Ig heavy chain CRD
46	2	33.3	5	2 S69237	surface protein te
47	2	33.3	5	4 A58728	serrawettin W2 - S
48	2	33.3	6	2 A35890	RNA-directed DNA p
49	2	33.3	6	2 B34835	dnaA protein - pse
50	2	33.3	6	2 A37765	hypothetical prote
51	2	33.3	6	2 S29637	jacalin beta-II ch
52	2	33.3	6	2 A49792	acylaminoacyl-pept
53	2	33.3	6	2 B26206	alpha-1,4-glucan-p
54	2	33.3	6	2 I59142	platelet-derived g
55	2	33.3	7	2 UN0859	peptidyl-dipeptida
56	2	33.3	7	2 PQ0663	membrane protein -
57	2	33.3	7	2 PT0087	ribulose-bisphosph
58	2	33.3	7	2 PN0150	omega-gliadine 1'
59	2	33.3	7	2 S70335	endosperm protein,
60	2	33.3	7	2 S71299	ICL2 protein - Par
61	2	33.3	7	2 S33244	neuromodulatory pe
62	2	33.3	7	2 S33245	neuromodulatory pe
63	2	33.3	7	2 S33246	neuromodulatory pe
64	2	33.3	7	2 PT0246	Ig heavy chain CRD
65	2	33.3	7	2 E30608	Ig kappa chain V-I
66	2	33.3	7	2 I48086	DNA topoisomerase
67	2	33.3	7	2 S29735	polysphosphate-gluc
68	2	33.3	8	2 B24749	neuroreceptor B - b
69	2	33.3	8	2 PC4131	hypothetical prote
70	2	33.3	8	2 A39308	glycine reductase
71	2	33.3	8	2 A37521	R-phycocerythrin ga
72	2	33.3	8	2 S68802	nitrate reductase
73	2	33.3	8	2 PL0162	paramyosin - north
74	2	33.3	8	2 A46306	spasmogenic toxin
75	2	33.3	8	2 JS0316	leucokinin VI - Ma
76	2	33.3	8	2 PT0298	Ig heavy chain CRD
77	2	33.3	8	2 A42057	fibroblast growth
78	2	33.3	8	2 PN0043	phosphatidylethano
79	2	33.3	8	2 I49404	prealbumin - weste
80	2	33.3	8	2 A5180	neutral proteinase
81	2	33.3	8	2 PC4372	telomeric and tetr
82	2	33.3	8	2 B47594	aspartate kinase (
83	2	33.3	8	2 T13818	cytochrome oxidase
84	2	33.3	9	2 D24180	fibrinogen beta ch
85	2	33.3	9	2 D58503	translation elonga
86	2	33.3	9	2 S02384	probable membrane
87	2	33.3	9	2 C36730	hutu protein - Kle
88	2	33.3	9	2 P50253	glycine cleavage s
89	2	33.3	9	2 C57444	neuropeptide Grb-A
90	2	33.3	9	2 A41978	calliWRamide1 -
91	2	33.3	9	2 S10920	venom protein HR-3
92	2	33.3	9	2 A60427	macrophage cytotox
93	2	33.3	9	2 S78426	52.5K protein - sp
94	2	33.3	9	2 G85802	hypothetical prote
95	2	33.3	10	1 XAVI6B	angiotensin-conver
96	2	33.3	10	1 ECLQ3M	tachykinin iii - m
97	2	33.3	10	1 GMR0L2	leucosulfakinin-II
98	2	33.3	10	2 C26997	unspecific monooxy
99	2	33.3	10	2 S33844	alpha-2-macroglobu
100	2	33.3	10	2 A46491	C3 homolog HX - in

ALIGNMENTS

RESULT 1

F33098
214K exoantigen (version 3) - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C;Accession: F33098
R;Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A;Reference number: A33098
A;Accession: F33098
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <NIC>

Query Match 66.7%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQSV 4
|||
Db 4 PQSV 7

RESULT 2

PT0560
T-cell receptor beta chain V-D-J region (126-1CE) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0560
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0560

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-6 <PEE>

A;Experimental source: day 18 fetal thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 50.0%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
|||
Db 2 SVL 4

RESULT 3

I57650
hemoglobin alpha chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 31-Jul-1997 #text_change 20-Apr-2000
C;Accession: I57650
R;Whitelaw, E.; Hogben, P.; Hanscombe, O.; Proudfoot, N.J.
Mol. Cell. Biol. 9, 241-251, 1989
A;Title: Transcriptional promiscuity of the human alpha-globin gene.
A;Reference number: I57650; MUID:89181576; PMID:2538719
A;Accession: I57650
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-9 <WHI>

A;Cross-references: GB:M23454; NID:G340922; PIDN:AAA52629.1; PID:G553329

A;Note: engineered sequence; this sequence was not determined in this report
C;Genetics:

A;Gene: GDB:HBA1

A;Cross-references: GDB:I19293

A;Map position: 16p13.3-16p13.3

Query Match 50.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
|||
Db 2 VLS 4

RESULT 4

A42324
cytochrome P450c27/25 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Feb-1996
C;Accession: A42324
R;Shayiq, R.M.; Avadhani, N.G.
J. Biol. Chem. 267, 2421-2428, 1992
A;Title: Sequence complementarity between the 5'-terminal regions of mRNAs for rat m3 ap
A;Reference number: A42324; MUID:92129322; PMID:1733943
A;Accession: A42324
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <SHA>
A;Note: sequence extracted from NCBI backbone (NCBIN:78404, NCBIPI:78410)

Query Match 50.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
|||
Db 3 VLS 5

RESULT 5

S69095
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein - Sulfolobus acid
N;Alternate names: Rieske iron-sulfur protein
C;Species: Sulfolobus acidocaldarius
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 03-Jun-2002
C;Accession: S69095
R;Schmidt, C.L.; Anemuller, S.; Teixeira, M.; Schaefer, G.
FEBS Lett. 359, 239-243, 1995
A;Title: Purification and characterization of the Rieske iron-sulfur protein from th
A;Reference number: S69095; MUID:95172243; PMID:7867807
A;Accession: S69095
A;Molecule type: protein
A;Residues: 1-12 <SCH>
C;Keywords: oxidoreductase

Query Match 50.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
|||
Db 2 SVL 4

RESULT 6

S47361
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47361
R;Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HUA-A0201 restricted recognition of influenza A is dominated by

A;Reference number: S47355

A;Accession: S47361

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:235685; NID:G527459; PIDN:CAA84754.1; PID:G527460
C;Keywords: T-cell receptor

Query Match 50.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
|||
Db 2 SVL 4
|||

RESULT 7
B56864
dipeptidyl-peptidase IV (EC 3.4.14.5) - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C;Accession: B56864
R;Plakidou-Dymock, S.; McGivan, J.D.
Biochim. Biophys. Acta 1145, 105-112, 1993
A;Title: The oligomeric structure of renal aminopeptidase N from bovine brush-border membrane vesicles
A;Reference number: A56864; MUID:93136203; PMID:8093665
C;Accession: B56864
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <P>
A;Experimental source: renal brush-border membrane vesicles
C;Keywords: dipeptidylpeptide hydrolase

Query Match 50.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
|||
Db 7 VLS 9
|||

RESULT 8
QWAPP
polistes mastoparan - paper wasp (Polistes jadwigae)
C;Species: Polistes jadwigae
C;Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 08-Dec-1995
C;Accession: A01780
R;Hirai, Y.; Ueno, Y.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
Biomed. Res. 1, 185-187, 1980
A;Title: A new mast cell degranulating peptide, polistes mastoparan, in the venom of Polistes wasps
A;Reference number: A01780
C;Accession: A01780
A;Molecule type: protein
A;Residues: 1-14 <HR>
C;Comment: This cytoactive peptide from wasp venom induces mast cell degranulation.
C;Superfamily: mastoparan
C;Keywords: amidated carboxyl end
F.14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 50.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
|||
Db 12 SVL 14
|||

RESULT 9
S11074
alcohol dehydrogenase (EC 1.1.1.1) - Baltic cod (fragments)
C;Species: Gadus morhua callarias (Baltic cod)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 31-Jan-1997
C;Accession: S11074
R;Egestad, B.; Estonius, M.; Danielsson, O.; Persson, B.; Cederlund, E.; Kaiser, R.; Hol

FRBS Lett. 269, 194-196, 1990
A;Title: Fast atom bombardment mass spectrometry and chemical analysis in determinati
A;Reference number: S11074; MUID:90353571; PMID:2387402
C;Accession: S11074

A;Molecule type: protein
A;Residues: 1-5,6-14 <EGE>
C;Keywords: acetylated amino end; alcohol metabolism; NAD; oxidoreductase
F.1/Modified site: acetylated amino end (Ala) #status experimental

Query Match 50.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
|||
Db 10 VLS 12
|||

RESULT 10

PN0117
hemoglobin alpha chain - red fox (fragment)
C;Species: Vulpes vulpes (red fox)

C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 19-May-2000
C;Accession: PN0117
R;Sukhomlinov, B.F.; Konoshenko, S.V.
Mol. Biol. (Mosk.) 5, 415-418, 1971

A;Title: Study on N-terminal sequence of the haemoglobin of Vulpes vulpes fox.
A;Reference number: PN0117
C;Accession: PN0117
A;Molecule type: protein
A;Residues: 1-15 <SUK>
C;Superfamily: globin; globin homology
C;Keywords: blood; erythrocyte; heme; heterotetramer; oxygen carrier

Query Match 50.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
|||
Db 1 VLS 3
|||

RESULT 11

S62620

protein disulfide-isomerase (EC 5.3.4.1) - castor bean (fragment)
C;Species: Ricinus communis (castor bean)

C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 17-Mar-1999
C;Accession: S62620
R;Coughlan, S.J.; Hastings, C.; Winfrey Jr., R.J.

Eur. J. Biochem. 235, 215-224, 1996
A;Title: Molecular characterisation of plant endoplasmic reticulum: identification of

A;Reference number: S62620; MUID:96202938; PMID:8631332
C;Accession: S62620
A;Status: preliminary

A;Molecule type: protein
A;Residues: 1-15 <COU>
C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 50.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
|||
Db 9 SVL 11
|||

RESULT 12

PA00075

fructose-bisphosphate aldolase (EC 4.1.2.13) I - fungus (Fusarium sporotrichioides) (
N;Alternate names: aldolase; fructose-1,6-biophosphate triosephosphate-lase
C;Species: Fusarium sporotrichioides

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C;Accession: PA0075; PA0077
 R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 Submitted to JIPID, October 1994
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
 A;Reference number: PA0051
 A;Accession: PA0075
 A;Molecule type: protein
 A;Residues: 1-15 <CHO>
 A;Note: this form (I) had a molecular weight of 30.6K and an isoelectric point of 5.3
 A;Accession: PA0077
 A;Molecule type: protein
 A;Residues: 1-15 <CH2>
 A;Note: this form (II) had a molecular weight of 31.6K and an isoelectric point of 5.4
 C;Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 50.0%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
 |||
 Db 5 VLS 7

RESULT 13
 PA0102
 fructose-bisphosphate aldolase (EC 4.1.2.13) III - fungus (Fusarium sporotrichioides) (fragment)
 C;Species: Fusarium sporotrichioides
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C;Accession: PA0102
 R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 Submitted to JIPID, October 1994
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
 A;Reference number: PA0051
 A;Accession: PA0102
 A;Molecule type: protein
 A;Residues: 1-15 <CHO>
 C;Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 50.0%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
 |||
 Db 5 VLS 7

RESULT 14
 S71300
 ICL3 protein - Paramecium tetraurelia (fragment)
 C;Species: Paramecium tetraurelia
 C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
 C;Accession: S71300
 R;Madeddu, L.; Klotz, C.; Le Caer, J.P.; Beisson, J.
 Eur. J. Biochem. 238, 121-128, 1996
 A;Title: Characterization of centrin genes in Paramecium.
 A;Reference number: S71298; MUID:96248429; PMID:8665928
 A;Accession: S71300
 A;Molecule type: protein
 A;Residues: 1-15 <MAD>
 A;Experimental source: strain d4-2
 C;Genetics:
 A;Genetic code: SGC5

Query Match 50.0%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQS 3
 |||
 Db 2.PQS 4

RESULT 15
 C84035
 hypothetical protein BH3083 [imported] - Bacillus halodurans (strain C-125)
 C;Species: Bacillus halodurans
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C;Accession: C84035
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; I
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: C84035
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-15 <STO>
 A;Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BA06802.1; GSPDB:(
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: BH3083

Query Match 50.0%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
 |||
 Db 10 VLS 12

RESULT 16
 S11290
 matrix protein M1 - influenza A virus (strain A/FPV/Rostock/34 [H7N1]) (fragment)
 C;Species: influenza A virus
 C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 18-Jun-1993
 C;Accession: S11290
 R;Robertson, J.S.
 Nucleic Acids Res. 6, 3745-3757, 1979
 A;Title: 5' and 3' terminal nucleotide sequences of the RNA genome segments of influ
 A;Reference number: S11286; MUID:80034428; PMID:493121
 A;Accession: S11290
 A;Molecule type: genomic RNA
 A;Residues: 1-16 <ROB>
 A;Cross-references: EMBL:J02112
 C;Genetics:
 A;Map position: segment 7
 C;Superfamily: influenza virus matrix protein M1

Query Match 50.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
 |||
 Db 11 VLS 13

RESULT 17
 A44352
 candidapepsin (EC 3.4.21.24), white-opaque switching regulated - yeast (Candida albi
 C;Species: Candida albicans
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Nov-1996
 C;Accession: A44352
 R;Morrow, B.; Srikantha, T.; Soll, D.R.
 Mol. Cell. Biol. 12, 2997-3005, 1992
 A;Title: Transcription of the gene for a pepsinogen, PEPI, is regulated by white-opa
 A;Reference number: A44352; MUID:92318916; PMID:1620110
 A;Accession: A44352
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-16 <MOR>
 C;Keywords: aspartic proteinase; hydrolase

Query Match 50.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
 |||
 Db 8 SVL 10

RESULT 18
 C61414
 chymotrypsin (EC 3.4.21.1) - slider turtle (fragment)
 C:Species: Pseudemys scripta (slider)
 C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999
 C:Accession: C61414
 R:Bhargava, A. K.; Barnard, E.A.
 J. Mol. Evol. 2, 187-198, 1973
 A:Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence deter
 A:Reference number: A61414; MUID:76146602; PMID:4807189
 A:Accession: C61414
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-16 <BHA>
 C:Keywords: hydrolase; protein digestion; serine proteinase

Query Match 50.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
 |||
 Db 9 VLS 11

RESULT 19
 G24687
 T-cell receptor beta-1 chain J-B1.4 segment - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
 C:Accession: G24687
 R:Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
 A:Title: Organization and sequences of the diversity, joining, and constant region genes
 A:Reference number: A94081; MUID:86094276; PMID:3866244
 A:Accession: G24687
 A:Molecule type: DNA
 A:Residues: 1-16 <NOY>
 A:Cross-references: GB:M14158; NID:G338844; PIDN:AAA60671.1; PID:G553683
 C:Keywords: T-cell receptor

Query Match 50.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
 |||
 Db 14 SVL 16

RESULT 20
 C28587
 T-cell receptor beta-2 chain J-B2.4 segment - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
 C:Accession: C28587
 R:Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
 A:Title: Organization and sequences of the diversity, joining, and constant region genes
 A:Reference number: A94081; MUID:86094276; PMID:3866244
 A:Accession: C28587
 A:Molecule type: DNA
 A:Residues: 1-16 <TOY>
 A:Cross-references: GB:M14159; NID:G338852; PIDN:AAA60678.1; PID:G553689

C:Keywords: T-cell receptor

Query Match 50.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
 |||
 Db 14 SVL 16

RESULT 21
 G53284
 T-cell receptor beta 2 chain J region, Jbeta2.4 - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C:Accession: G53284
 R:Harindranath, N.; Alexander, C.B.; Mage, R.G.
 Mol. Immunol. 28, 881-888, 1991
 A:Title: Evolutionarily conserved organization and sequences of germline diversity an
 A:Reference number: A53284; MUID:91342695; PMID:1678859
 A:Accession: G53284
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-16 <HAR>
 A:Cross-references: GB:S60737; NID:G233916; PIDN:AA19523.1; PID:G233923
 A:Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60745)
 C:Keywords: T-cell receptor

Query Match 50.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
 |||
 Db 14 SVL 16

RESULT 22
 A34835
 ribosomal protein L34 - Pseudomonas aeruginosa (fragment)
 C:Species: Pseudomonas aeruginosa
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Jun-1993
 C:Accession: A34835
 R:Yee, T.W.; Smith, D.W.
 Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
 A:Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from
 A:Reference number: A34835; MUID:90160310; PMID:2106132
 A:Accession: A34835
 A:Molecule type: DNA
 A:Residues: 1-17 <YEE>
 A:Cross-references: GB:M30125
 C:Genetics:
 A:Gene: rpmH
 C:Superfamily: Escherichia coli ribosomal protein L34.
 C:Keywords: protein biosynthesis; ribosome

Query Match 50.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
 |||
 Db 11 VLS 13

RESULT 23
 B44873
 caldesmon - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 04-Mar-2000
 C:Accession: B44873
 R:Ikebe, M.; Hornick, T.

```

Arch. Biochem. Biophys. 288, 538-542, 1991
A;Title: Determination of the phosphorylation sites of smooth muscle caldesmon by protei
A;Reference number: A44873; MUID:91378498; PMID:1898046
A;Accession: S54873
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <IKS>
A;Experimental source: skeletal myosin
A;Note: sequence extracted from NCBI backbone (NCBIP:63202)
C;Superfamily: caldesmon

Query Match 50.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4
Db 6 QSV 8

RESULT 24
B61414
Chymotrypsin (EC 3.4.21.1) - painted turtle (fragment)
C;Species: Chrysemys picta (painted turtle)
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 07-May-1999
C;Accession: B61414
R;Bhargava, A.K.; Barnard, E.A.
J. Mol. Evol. 2, 187-198, 1973
A;Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determ
A;Reference number: A61414; MUID:76146602; PMID:4807189
A;Accession: B61414
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <BHA>
C;Keywords: hydrolase; serine proteinase

Query Match 50.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
Db 9 VLS 11

RESULT 25
S74195
epoxide hydrolase (EC 3.3.2.3), microsomal - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 17-Mar-1999
C;Accession: S74195
R;Arava, Z.; Hellman, U.; Hansson, R.
Eur. J. Biochem. 231, 855-861, 1995
A;Title: Characterisation of taurochenodeoxycholic acid 6-alpha-hydroxylase from pig liv
A;Reference number: S66455; MUID:95377322; PMID:7649186
A;Accession: S74195
A;Molecule type: protein
A;Residues: 1-18 <ARA>
A;Experimental source: liver
C;Superfamily: epoxide hydrolase
C;Keywords: ether hydrolase

Query Match 50.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
Db 8 SVL 10

RESULT 26
S54848

Arch. Biochem. Biophys. 288, 538-542, 1991
A;Title: Determination of the phosphorylation sites of smooth muscle caldesmon by protei
A;Reference number: A44873; MUID:91378498; PMID:1898046
A;Accession: S54848
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <LTA>
A;Cross-references: EMBL:X84052
C;Genetics:
A;Gene: sucd
C;Superfamily: succinate-CoA ligase (ADP-forming) alpha chain
C;Keywords: acid-thiol ligase; ATP; phosphohistidine; phosphoprotein; tricarboxylic a

succinyl-CoA synthetase (EC 6.2.1.-) alpha subunit - Pseudomonas aeruginosa (fragment
C;Species: Pseudomonas aeruginosa
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 17-Jul-1998
A;Accession: S54848
R;Liao, X.; Lightfoot, J.; Charlebois, I.; Ouellet, C.; Morency, M.J.; Dewar, K.; Shi
submitted to the EMBL Data Library, January 1995
A;Description: Physical mapping of 44 loci including acoA, aimE, ampC, ampR, arcA, a
prP, ppbB, ppbC, phes, phoA, phoB, phoS, ponA, proS, pyoS1, qin, rpoB, rpoH, rpsB, s
A;Reference number: S54841
A;Accession: S54848
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-19 <LTA>
A;Cross-references: EMBL:X84052
C;Genetics:
A;Gene: sucd
C;Superfamily: succinate-CoA ligase (ADP-forming) alpha chain
C;Keywords: acid-thiol ligase; ATP; phosphohistidine; phosphoprotein; tricarboxylic a

Query Match 50.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
Db 2 SVL 4

RESULT 27
B53145
high conductance calcium-activated potassium channel, maxi-K channel - bovine (fragme
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 18-Jul-2001
C;Accession: B53145
R;Knaus, H.G.; Garcia-Calvo, M.; Kaczorowski, G.J.; Garcia, M.L.
J. Biol. Chem. 269, 3921-3924, 1994
A;Title: Subunit composition of the high conductance calcium-activated potassium cha
A;Reference number: A53145; MUID:94140798; PMID:7508434
A;Accession: B53145
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <KNA>
A;Note: sequence extracted from NCBI backbone (NCBIP:144547)
C;Superfamily: fruit fly calcium-activated potassium channel sio

Query Match 50.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
Db 11 SVL 13

RESULT 28
S20274
guanine oxidoreductase - Rhodococcus sp.
C;Species: Rhodococcus sp.
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S20274
R;Peschke, B.; Lingens, F.
Biol. Chem. Hoppe-Seyler 372, 1081-1088, 1991
A;Title: Microbial metabolism of guanine and related compounds. XII. Isolation and
ase from Pseudomonas putida 86.
A;Reference number: S20274; MUID:92162192; PMID:1789933
A;Accession: S20274
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <PES>

Query Match 50.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


QY 3 SVL 5
|||
Db 17 SVL 19

RESULT 29

S46205
comosain (EC 3.4.22.-) - pineapple (fragment)
C:Species: Ananas comosus (pineapple)
C:Date: 16-Feb-1995 #sequence_revision 01-Nov-1996 #text_change 07-May-1999
C:Accession: S46205
R:Napper, A.D.; Bennett, S.P.; Borowski, M.; Holdridge, M.B.; Leonard, M.J.C.; Rogers, E.
Biochem. J. 301, 727-735, 1994
A:Title: Purification and characterization of multiple forms of the pineapple-stem-deriv
A:Reference number: S46204; MUID:94330946; PMID:8053898
A:Accession: S46205
A:Molecule type: protein
A:Residues: 1-20 <NAP>
C:Superfamily: papain
C:Keywords: cysteine proteinase; hydrolase

Query Match 50.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POS 3
|||
Db 2 POS 4

RESULT 30

S46204
ananain (EC 3.4.22.31) - pineapple (fragment)
C:Species: Ananas comosus (pineapple)
C:Date: 16-Feb-1995 #sequence_revision 01-Nov-1996 #text_change 07-May-1999
C:Accession: S46204
R:Napper, A.D.; Bennett, S.P.; Borowski, M.; Holdridge, M.B.; Leonard, M.J.C.; Rogers, E.
Biochem. J. 301, 727-735, 1994
A:Title: Purification and characterization of multiple forms of the pineapple-stem-deriv
A:Reference number: S46204; MUID:94330946; PMID:8053898
A:Accession: S46204
A:Molecule type: protein
A:Residues: 1-20 <NAP>
C:Superfamily: papain
C:Keywords: cysteine proteinase; hydrolase

Query Match 50.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POS 3
|||
Db 2 POS 4

RESULT 31

C49164
Chromogranin-B - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-May-1997
C:Accession: C49164
R:Nielsen, E.; Wellinder, B.S.; Madsen, O.D.
Endocrinology 129, 3147-3156, 1991
A:Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides th
A:Reference number: A49164; MUID:92063871; PMID:1954895
A:Accession: C49164
A:Status: preliminary
A:Molecule type: Protein
A:Residues: 1-20 <NIE>
A:Note: sequence extracted from NCBI backbone (NCBIP:66369)
C:Superfamily: chromogranin B precursor

Query Match 50.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POS 3
|||
Db 2 POS 4

RESULT 32

B46174
RNA-binding protein TIAR - human (fragment)
N:Alternate names: cytotoxic granule-associated RNA-binding protein; TIA-1 related pr
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jul-1998
C:Accession: B46174
R:Kawakami, A.; Tian, Q.; Duan, X.; Streuli, M.; Schlossman, S.F.; Anderson, P.
Proc. Natl. Acad. Sci. U.S.A. 89, 8681-8685, 1992
A:Title: Identification and functional characterization of a TIA-1-related nucleolysi
A:Reference number: A46174; MUID:92409580; PMID:1326761
A:Accession: B46174
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-20 <KAW>
A:Note: sequence extracted from NCBI backbone (NCBIN:114067, NCBIP:114068)
C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleopro

Query Match 50.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
|||
Db 16 SVL 18

RESULT 33

S18582
hypothetical protein X (pufQ 3' region) - Rhodobacter sphaeroides
C:Species: Rhodobacter sphaeroides
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-May-1994
C:Accession: S18582; S32855
R:Hunter, C.N.; McGlynn, P.; Ashby, M.K.; Burgess, J.G.; Olsen, J.D.
Mol. Microbiol. 5, 2849-2861, 1991
A:Title: DNA sequencing and complementation/deletion analysis of the bchA-puf operon
A:Reference number: S18580; MUID:92140030; PMID:1779756
A:Accession: S18582
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-20 <HUN>
A:Cross-references: EMBL:X68795

Query Match 50.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
|||
Db 14 SVL 16

RESULT 34

T50757
pufK protein [imported] - Rhodobacter sphaeroides
C:Species: Rhodobacter sphaeroides
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C:Accession: T50757
R:Choudhary, M.; Kaplan, S.
Nucleic Acids Res. 28, 862-867, 2000
A:Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroide
A:Reference number: Z25222; MUID:20115911; PMID:10648776
A:Accession: T50757
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-20 <CHO>
 A:Cross-references: ENBL:AF195122; PIDN:AAF24301.1
 A:Experimental source: strain 2.4.1
 C:Genetics:
 A:Gene: pufK

Query Match 50.0%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVL 5
 |||
 Db 14 SVL 16

RESULT 35

JU0330
 hypothetical protein, 2.4K (lytA 5' region) - Streptococcus pneumoniae
 C:Species: Streptococcus pneumoniae
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 24-Feb-1995
 C:Accession: JU0330
 R:Diaz, E.; Garcia, J.L.
 Gene 90, 157-162, 1990
 A:Title: Characterization of the transcription unit encoding the major pneumococcal auto
 A:Reference number: JU0329; MUID:90337339; PMID:1974230
 A:Accession: JU0330
 A:Molecule type: DNA
 A:Residues: 1-20 <DIA>
 A:Experimental source: strain M31
 C:Genetics:
 A:Start codon: GTG

Query Match 50.0%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
 |||
 Db 5 VLS 7

RESULT 36

A61414
 Chymotrypsin (EC 3.4.21.1) - snapping turtle (fragment)
 C:Species: Chelydra serpentina (snapping turtle)
 C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999
 C:Accession: A61414
 R:Bhargava, A.K.; Barnard, E.A.
 J. Mol. Evol. 2, 187-198, 1973
 A:Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence deter
 A:Reference number: A61414; MUID:76146602; PMID:4807189
 A:Accession: A61414
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <BRA>
 C:Keywords: hydrolase; protein digestion; serine proteinase

Query Match 50.0%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
 |||
 Db 9 VLS 11

RESULT 37

A99091
 hypothetical protein spr1755 [imported] - Streptococcus pneumoniae (strain R6)
 C:Species: Streptococcus pneumoniae
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
 C:Accession: A99091

R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.
 Y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A:Reference number: A97872; MUID:21429245; PMID:11544234
 A:Accession: A99091
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-20 <KUR>
 A:Cross-references: GB:AE007317; PIDN:AAL00558.1; PID:GI5459436; GSPDB:GN00174
 C:Genetics:
 A:Gene: spr1755

Query Match 50.0%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
 |||
 Db 5 VLS 7

RESULT 38

I40505
 hypothetical protein 3 (4 aa) - Bacillus stearothermophilus
 C:Species: Bacillus stearothermophilus
 C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999
 C:Accession: I40505
 R:Waye, M.M.; Winter, G.
 Eur. J. Biochem. 158, 505-510, 1996
 A:Title: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA
 A:Reference number: I40503; MUID:86274732; PMID:3525162
 A:Accession: I40505
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-4 <RES>
 A:Cross-references: EMBL:X04193; NID:G40233; PIDN:CAA27783.1; PID:G580944

Query Match 33.3%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LS 6
 |||
 Db 2 LS 3

RESULT 39

S17255
 ribosomal protein YmL1, mitochondrial, questionable - yeast (Saccharomyces cerevisia
 C:Species: Saccharomyces cerevisiae
 A:Variety: strain 07173
 C:Date: 23-Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-May-1997
 C:Accession: S17255
 R:Grohmann, L.; Graack, H.R.; Kruff, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa,
 FEBS Lett. 284, 51-56, 1991
 A:Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit f
 A:Reference number: S17255; MUID:91285106; PMID:2060626
 A:Accession: S17255
 A:Molecule type: protein
 A:Residues: 1-4 <GRO>
 C:Comment: A coding region for this protein could not be identified in the genome of
 C:Genetics:
 A:Genome: nuclear
 C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 33.3%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SV 4

Db 1 SV 2
||

RESULT 40

T30569
hypothetical protein - Emericella nidulans
C:Species: Emericella nidulans, Aspergillus nidulans
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C:Accession: T30569
R:Morrice, J.; Mackenzie, D.A.; Parr, A.J.; Archer, D.B.
Curr. Genet. 34, 379-385, 1998
A:Title: Isolation and characterization of the acetyl-CoA carboxylase gene from Aspergillus
C:Reference number: Z20869; MUID:99087906; PMID:9871120
A:Accession: T30569
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-4 <MOR>
A:Cross-references: EMBL:Y15996; NID:e1285512; PID:e1218041; PIDN:CAA75927.1

Query Match

Best Local Similarity 33.3%; Score 2; DB 2; Length 4;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4
||
Db 3 SV 4

RESULT 41

A60521
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N:Alternate names: glycogen phosphorylase b
C:Species: Liza ramada
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
C:Accession: A60521
R:Bonamura, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A:Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle
C:Reference number: A60521; MUID:90227907; PMID:2109669
A:Accession: A60521
A:Molecule type: protein
A:Residues: 1-5 <BON>
A:Superfamily: phosphorylase
C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F:3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experimental

Query Match

Best Local Similarity 33.3%; Score 2; DB 2; Length 5;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4
||
Db 3 SV 4

RESULT 42

Ti4908
hypothetical protein - parsley
C:Species: Petroselinum crispum (parsley)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: Ti4908
R:Kircher, S.; Ledger, S.; Hayaashi, H.; Weishaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
A:Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of
C:Reference number: Z18261; MUID:98265918; PMID:9604882
A:Accession: Ti4908
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-5 <KIR>
A:Cross-references: EMBL:Y10809; NID:g3336901; PIDN:CAA71767.1; PID:g3336902
A:Experimental source: Hamburger Schnitt

Query Match

Best Local Similarity 33.3%; Score 2; DB 2; Length 5;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4
||
Db 3 SV 4

RESULT 43

S55237
zinc-binding protein ZBP14 - maize (fragment)
C:Species: Zea mays (maize)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C:Accession: S55237
R:Robinson, K.; Jones, D.; Howell, S.; Soneji, Y.; Martin, S.; Aitken, A.
Biochem. J. 307, 287-292, 1995
A:Title: Expression and characterization of maize ZBP14, a member of a new family of
C:Reference number: S55237; MUID:95234046; PMID:7717986
A:Accession: S55237
A:Molecule type: protein
A:Residues: 1-5 <ROB>

Query Match

Best Local Similarity 33.3%; Score 2; DB 2; Length 5;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
||
Db 4 VL 5

RESULT 44

A60803
neuropeptide - sea anemone (Anthopleura elegantissima)
C:Species: Anthopleura elegantissima
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: A60803
R:Graff, D.; Grimmelikhuijzen, C.J.P.
Brain Res. 442, 354-358, 1988
A:Title: Isolation of <Glu-Ser-Lu-Arg-Trp-NH-2>, a novel neuropeptide from sea anemone
C:Reference number: A60803; MUID:88222764; PMID:2897223
A:Accession: A60803
A:Molecule type: protein
A:Residues: 1-5 <GRA>
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:5/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 33.3%; Score 2; DB 2; Length 5;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QS 3
||
Db 1 QS 2

RESULT 45

PT0278
Ig heavy chain CRD3 region (clone 4-88) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0278
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
C:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0278
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
 ||
 Db 4 VL 5

RESULT 46
 S69237
 surface protein tetrabrachion heavy chain - Staphylothermus marinus (fragment)
 C/Species: Staphylothermus marinus
 C/Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
 C/Accession: S69237
 R/Peters, J.; Nitsch, M.; Kuehlmoorgen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; Engelh
 J. Mol. Biol. 245, 385-401, 1995
 A/Title: Tetrabrachion: a filamentous archaeobacterial surface protein assembly of unusa
 A/Reference number: S69237; MUID:95139068; PMID:7837271
 A/Accession: S69237
 A/Molecule type: protein
 A/Residues: 1-5 <PET>
 A/Experimental source: strain F1, DSM 3639
 C/Keywords: cell wall; glycoprotein; heat-stable protein

Query Match 33.3%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6
 ||
 Db 4 LS 5

RESULT 47
 A58728
 serrawettin W2 - Serratia marcescens
 C/Species: Serratia marcescens
 C/Date: 10-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 12-Feb-1998
 C/Accession: A58728
 R/Matsuyama, T.; Kaneda, K.; Nakagawa, Y.; Isa, K.; Hara-Hotta, H.; Yano, I.
 J. Bacteriol. 174, 1769-1776, 1992
 A/Title: A novel extracellular cyclic lipopeptide which promotes flagellum-dependent and
 A/Reference number: A58728; MUID:92193260; PMID:1548227
 A/Accession: A58728
 A/Status: unencoded polypeptide
 A/Molecule type: protein
 A/Residues: 1-5 <MAT>
 A/Experimental source: strain NS 25
 C/Comment: A surfactant lipopeptide promoting flagellum-independent surface translocation
 C/Keywords: blocked amino end; blocked carboxyl end; D-amino acid; lipoprotein; unencode
 F/1/Modified site: D-leucine (Ileu) #status experimental
 F/4/Modified site: D-phenylalanine (Phe) #status experimental
 F/1-5/Cross-link: 3-hydroxydecanoyl amino end, ester carboxyl end (Leu-Ile) #status expe

Query Match 33.3%; Score 2; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6
 ||
 Db 1 LS 2

RESULT 48
 A35890
 RNA-directed DNA polymerase (EC 2.7.7.49) 66K chain - human immunodeficiency virus type
 C/Species: human immunodeficiency virus type 1, HIV-1
 C/Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 31-Dec-1993
 C/Accession: A35890
 R/Bathurst, I.C.; Moen, L.K.; Lujan, M.A.; Gibson, H.L.; Feucht, P.H.; Pichuanes, S.; C
 Biochem. Biophys. Res. Commun. 171, 589-595, 1990

A/Title: Characterization of the human immunodeficiency virus type-1 reverse transcript
 A/Reference number: A35890; MUID:90386627; PMID:1698361
 A/Accession: A35890
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-6 <BAT>
 C/Keywords: nucleotidyltransferase

Query Match 33.3%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
 ||
 Db 5 VL 6

RESULT 49
 B34835
 dnaA protein - Pseudomonas aeruginosa (fragment)
 C/Species: Pseudomonas aeruginosa
 C/Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
 C/Accession: B34835
 R/Yee, T.W.; Smith, D.W.
 Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
 A/Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from
 A/Reference number: A34835; MUID:90160310; PMID:2106132
 A/Accession: B34835
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-6 <YEE>
 A/Cross-references: GB:M30125; NID:gl51419; PIDN:AAA25916.1; PID:gl51421
 C/Keywords: DNA binding

Query Match 33.3%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4
 ||
 Db 2 SV 3

RESULT 50
 A37765
 hypothetical protein (csma 5' region) - Chloroflexus aurantiacus (fragment)
 C/Species: Chloroflexus aurantiacus
 C/Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 30-Sep-1993
 C/Accession: A37765
 R/theroux, S.J.; Redlinger, T.E.; Fuller, R.C.; Robinson, S.J.
 J. Bacteriol. 172, 4497-4504, 1990
 A/Title: Gene encoding the 5.7-kilodalton chlorosome protein of Chloroflexus auranti.
 A/Reference number: A37765; MUID:90330558; PMID:2376566
 A/Accession: A37765
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-6 <THE>
 A/Cross-references: GB:M33964

Query Match 33.3%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQ 2
 ||
 Db 1 PQ 2

RESULT 51
 S29637
 jacalin beta-II chain - Artocarpus champeden (fragment)
 C/Species: Artocarpus champeden
 C/Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998

C;Accession: S29637
 B;Ngoc, L.D.; Brillard, M.; Hoebeke, J.
 Biochim. Biophys. Acta 1156, 219-222, 1993
 A;Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD
 A;Reference number: S29635; MUID:931152601; PMID:8427879
 A;Accession: S29637
 A;Molecule type: protein
 A;Residues: 1-6 <NGO>
 A;Experimental source: seed
 A;Complex: heterotetramer; two alpha and two beta chains
 C;Function:
 A;Description: seed storage protein
 A;Note: lectin for D-galactosyl-beta-1->3-N-acetylgalactosamine
 C;Keywords: heterotetramer; lectin; seed; storage protein

Query Match 33.3%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QS 3
 ||
 3 QS 4

Db

RESULT 52
 A49792
 acylaminoacyl-peptidase (EC 3.4.19.1) - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
 A;Accession: A49792
 R;Krishna, R.G.; Chin, C.C.Q.; Wold, F.
 Anal. Biochem. 199, 45-50, 1991
 A;Title: N-terminal sequence analysis of N(alpha)-acetylated proteins after unblocking w
 A;Reference number: A49792; MUID:92222120; PMID:1807161
 A;Accession: A49792
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-6 <KRI>
 A;Keywords: acetylated amino end; hydrolase; omega peptidase
 F;1/Modified site: acetylated amino end (Met) #status experimental

Query Match 33.3%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
 ||
 5 VL 6

Db

RESULT 53
 B26206
 alpha-1,4-glucan-protein synthase (UDP-forming) (EC 2.4.1.112) - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 13-Sep-1996
 C;Accession: B26206; A26206
 R;Lerner, J.; Sanger, F.
 J. Mol. Biol. 11, 491-500, 1965
 A;Title: The amino acid sequence of the phosphorylation site of muscle uridine diphospho
 A;Reference number: A26206
 A;Accession: B26206
 A;Molecule type: protein
 A;Residues: 1-6 <IAR>
 A;Experimental source: muscle
 A;Note: Lys-1 was also found
 C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
 F;4/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 33.3%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4
 ||
 4 SV 5

Db

RESULT 54
 I59142
 platelet-derived growth factor B chain - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C;Accession: I59142
 R;Pech, M.; Gazit, A.; Arnstein, P.; Aaronson, S.A.
 Proc. Natl. Acad. Sci. U.S.A. 86, 2693-2697, 1989
 A;Title: Generation of fibrosarcomas in vivo by a retrovirus that expressed the norma
 A;Reference number: I59142; MUID:89202393; PMID:2649890
 A;Accession: I59142
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-6 <RES>
 A;Cross-references: GB:M26180; NID:G516624; PIDN:AAA39905.1; PID:G516625

Query Match 33.3%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
 ||
 5 VL 6

Db

RESULT 55
 JN0859
 peptidyl-dipeptidase A inhibitory peptide C105 - striped bonito
 C;Species: Sarda orientalis (striped bonito)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 C;Accession: JN0859
 R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
 Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
 A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory
 A;Reference number: JN0859; MUID:94080036; PMID:7764272
 A;Accession: JN0859
 A;Molecule type: protein
 A;Residues: 1-7 <MAT>
 A;Experimental source: intestine
 C;Comment: The carboxyl-terminus is essential for the protein's expression of angiot
 C;Superfamily: bradykinin-potentiating peptide
 C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 33.3%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4
 ||
 1 SV 2

Db

RESULT 56
 PQ0663
 membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)
 C;Species: porcine epidemic diarrhea virus
 C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999
 C;Accession: PQ0663
 R;Brigden, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.
 J. Gen. Virol. 74, 1795-1804, 1993
 A;Title: Sequence determination of the nucleocapsid protein gene of the porcine epide
 issible gastroenteritis virus.
 A;Reference number: JQ2191; MUID:93389433; PMID:8397280
 A;Accession: PQ0663
 A;Molecule type: mRNA
 A;Residues: 1-7 <BRI>
 A;Cross-references: GB:Z14976; NID:G311650; PIDN:CAA78699.1; PID:G584083
 C;Comment: This virus is coronavirus related to human coronavirus 229E.
 C;Keywords: membrane protein

Query Match 33.3%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
||
Db 3 VL 4

RESULT 57

PT0087
ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - Arabidopsis thaliana (frag

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 24-Nov-1999
C;Accession: PT0087
R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.

submitted to JIPID, December 1995
A;Description: Two dimensional electrophoresis of plant proteins and standardization of

A;Reference number: PN0173
A;Accession: PT0087
A;Molecule type: protein

A;Residues: 1-7 <TSU>

A;Experimental source: leaf

C;Keywords: acetylated amino end; carbon-carbon lyase; carboxy-lyase

F;1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 33.3%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQ 2
||
Db 2 PQ 3

RESULT 58

PN0150

omega-gliadine 1' - Aegilops longissima (fragment)

C;Species: Aegilops longissima

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PN0150

R;Odintsova, T.I.; Egorov, T.A.

Biokhimia 55, 509-516, 1990

A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of

A;Reference number: PN0146; MUID:90283493; PMID:2354218

A;Accession: PN0150

A;Molecule type: protein

A;Residues: 1-7 <ODI>

A;Experimental source: strain K-907

Query Match 33.3%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6
||
Db 4 LS 5

RESULT 59

S70335

endosperm protein, 40K - rye (fragment)

C;Species: Secale cereale (rye)

C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998

C;Accession: S70335

R;Rocher, A.; Calero, M.; Soriano, F.; Mendez, E.

Biochim. Biophys. Acta 1295, 13-22, 1996

A;Title: Identification of major rye secalins as coeliac immunoreactive proteins.

A;Reference number: S70327; MUID:96283789; PMID:8679669

A;Accession: S70335

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <ROC>

Query Match 33.3%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QS 3
||
Db 5 QS 6

RESULT 60

S71299

IC12 protein - Paramecium tetraurelia (fragment)

C;Species: Paramecium tetraurelia

C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999

C;Accession: S71299

R;Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.

Eur. J. Biochem. 238, 121-128, 1996

A;Title: Characterization of centrin genes in Paramecium.

A;Reference number: S71298; MUID:96248429; PMID:8665928

A;Accession: S71299

A;Molecule type: protein

A;Residues: 1-7 <MAD>

A;Experimental source: strain d4-2

C;Genetics:

A;Genetic code: SGC5

Query Match 33.3%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQ 2
||
Db 5 PQ 6

RESULT 61

S33244

neuromodulatory peptide Wamide-1 - giant African snail

C;Species: Achatina fulica (giant African snail)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C;Accession: S33244

R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A;Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia

A;Reference number: S33244; MUID:93265912; PMID:8495720

A;Accession: S33244

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <MIN>

Query Match 33.3%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4
||
Db 5 SV 6

RESULT 62

S33245

neuromodulatory peptide Wamide-2 - giant African snail

C;Species: Achatina fulica (giant African snail)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C;Accession: S33245

R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A;Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia

A;Reference number: S33244; MUID:93265912; PMID:8495720

A;Accession: S33245

A;Status: preliminary

A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 33.3%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4
||
Db 5 SV 6

RESULT 63

S33246

neuromodulatory peptide Wamide-3 - giant African snail

C:Species: Achatina fulica (giant African snail)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C:Accession: S33246

R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A>Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of *Achatina fulica*

A:Reference number: S33244; PMID:93265912; PMID:8495720

A:Accession: S33246

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <MIN>

Query Match 33.3%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4
||
Db 5 SV 6

RESULT 64

PT0246

Ig heavy chain CRD3 region (clone 2-103D) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0246

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A:Reference number: PT0222; PMID:91108337; PMID:1899102

A:Accession: PT0246

A:Molecule type: DNA

A:Residues: 1-7 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
||
Db 3 VL 4

RESULT 65

E30608

Ig kappa chain V-III region (Gag) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996

C:Accession: E30608

R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solid

J. Immunol. 142, 3158-3163, 1989

A>Title: Structural and idiotypic characterization of the L chains of human IgM autoanti

A:Reference number: A30601; PMID:89215279; PMID:2496160

A:Accession: E30608

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <MIN>

A:Keywords: heterotetramer; immunoglobulin

A:Reference number: A30601; PMID:89215279; PMID:2496160

A:Accession: E30608

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <GON>

C:Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QS 3
||
Db 6 QS 7

RESULT 66

I48086

DNA topoisomerase II alpha - Chinese hamster (fragment)

C:Species: Cricetulus griseus (Chinese hamster)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C:Accession: I48086

R:Ng, S.W.; Eder, J.P.; Schnipper, L.E.; Chan, V.T.W.

J. Biol. Chem. 270, 25850-25858, 1995

A>Title: Molecular cloning and characterization of the promoter for the Chinese hamst

A:Reference number: I48086; PMID:96029684; PMID:7592770

A:Accession: I48086

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-7 <RES>

A:Cross-references: EMBL:U34196; NID:G1041231; PIDN:IACS2315.1; PID:G1041232

Query Match 33.3%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6
||
Db 3 LS 4

RESULT 67

S29735

polyphosphate-glucose phosphotransferase (EC 2.7.1.63) - Propionibacterium freudenrei

C:Species: Propionibacterium freudenreichii subsp. shermanii

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002

C:Accession: S29735

R:Phillips, N.F.B.; Horn, P.J.; Wood, H.G.

Arch. Biochem. Biophys. 300, 309-319, 1993

A>Title: The polyphosphate- and ATP-dependent glucokinase from Propionibacterium sher

A:Reference number: S29735; PMID:93143332; PMID:8380966

A:Accession: S29735

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <PHI>

C:Keywords: phosphotransferase

Query Match 33.3%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
||
Db 3 VL 4

RESULT 68

B24749

neuropeptide B - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2000

C:Accession: B24749

R:Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.

Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985

A>Title: Isolation, sequencing, synthesis, and pharmacological characterization of tw

A:Reference number: A94074; PMID:86067985; PMID:3865193

A:Accession: B24749
A:Molecule type: protein
A:Residues: 1-8 <YAN>
C:Superfamily: unassigned animal peptides
C:Keywords: neuropeptide

Query Match 33.3%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQ 2
||
Db 5 PQ 6

RESULT 69

PC4131
hypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PC4131
R:Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
Gene 167, 87-91, 1995
A:Title: Sequencing and characterization of the downstream region of the genes encoding y for biosynthesis of heme d1
A:Reference number: JC4552; MUID:96144254; PMID:8566817
A:Accession: PC4131
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <KAW>
A:Cross-references: DDBJ:D50473; NID:g1217594
A>Note: this ORF is not annotated in GenBank entry PSENIRC, release 113.0

Query Match 33.3%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6
||
Db 4 LS 5

RESULT 70

A39308
glycine reductase [EC 1.4.99.-] sulphydryl protein C, alpha chain - Clostridium sticklandii
C:Species: Clostridium sticklandii
C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 15-Aug-1997
C:Accession: A39308
R:Stadman, T.C.; Davis, J.N.
J. Biol. Chem. 266, 22147-22153, 1991
A:Title: Glycine reductase protein C. Properties and characterization of its role in the
A:Reference number: A39308; MUID:92042141; PMID:1939235
A:Accession: A39308
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <STA>
C:Function:
A:Description: glycine reductase complex catalyzes the reductive deamination of glycine
C:Keywords: ATP; oxidoreductase

Query Match 33.3%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
||
Db 4 VL 5

RESULT 71

A37521
R-phycoerythrin gamma-E chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri

C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: A37521; J22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Accession: A37521
A:Molecule type: protein
A:Residues: 1-8 <KLO>

Query Match 33.3%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6
||
Db 1 LS 2

RESULT 72

S68802
nitrate reductase (NADH) inhibitor - spinach (fragment)
C:Species: Spinacia oleracea (spinach)
C:Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 30-Jan-1998
C:Accession: S68802
R:Bachmann, M.; Huber, J.L.; Liao, P.C.; Gage, D.A.; Huber, S.C.
FEBS Lett. 387, 127-131, 1996
A:Title: The inhibitor protein of phosphorylated nitrate reductase from spinach (Spir)
A:Reference number: S68802; MUID:96244508; PMID:8674533
A:Accession: S68802
A:Molecule type: protein
A:Residues: 1-8 <BAC>
A:Experimental source: leaves; strain cv. Bloomsdale

Query Match 33.3%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6
||
Db 3 LS 4

RESULT 73

PL0162
paramyosin - northern quahog (fragment)
C:Species: Mercenaria mercenaria (northern quahog)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 11-May-2000
C:Accession: PL0162
R:Watabe, S.; Teuchiya, T.; Hartshorne, D.J.
Comp. Biochem. Physiol. B 94, 813-821, 1989
A:Title: Phosphorylation of paramyosin.
A:Reference number: PL0162; MUID:90107385; PMID:2532591
A:Accession: PL0162
A:Molecule type: protein
A:Residues: 1-8 <WAR>

A:Experimental source: white adductor muscle
A>Note: the sequence is the phosphorylated tryptic peptide
C:Comment: This protein is thought to exist as a dimer of two subunits, termed alpha
om the carboxyl-terminal end of the molecule. Only alpha-paramyosin is phosphorylate
C:Keywords: muscle; phosphoprotein
F:5/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 33.3%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4
||
Db 5 SV 6

RESULT 74

A46306
spasmogenic toxin PNVI - spider (Phoneutria nigriventer) (fragment)
C:Species: Phoneutria nigriventer
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999
C:Accession: A46306
R:Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.; Novello, J.
Toxicol 31, 377-384, 1993
A:Title: Biochemical characterization of a vascular smooth muscle contracting polypeptide
A:Reference number: A46306; MUID:93276438; PMID:8503129
A:Accession: A46306
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <MAR>

Query Match 33.3%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QS 3
||
Db 6 QS 7

RESULT 75
JS0316
leucokinin VI - Madeira cockroach
C:Species: Leucophaea maderae (Madeira cockroach)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Accession: JS0316
R:Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987
A:Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic
A:Reference number: JS0315
A:Accession: JS0316
A:Molecule type: protein
A:Residues: 1-8 <HOL>
C:Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
C:Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 33.3%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QS 3
||
Db 1 QS 2

Search completed: November 25, 2003, 19:36:10
Job time : 4.11628 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 2.12791 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-26

Perfect score: 6

Sequence: 1 PQSVLS 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	50.0	10	1 LPK2 LOCOMI	P41488 locusta mig
2	3	50.0	11	1 ES1 RAT	P56571 rattus norv
3	3	50.0	13	1 TEM4 RANTE	P56917 rana tempor
4	3	50.0	13	1 TEMF_RANTE	P56921 rana tempor
5	3	50.0	14	1 MAST_POLJA	P01517 polistes ja
6	3	50.0	15	1 ACT_FINPS	P18085 pinus pinas
7	3	50.0	16	1 H5_COTJA	P18638 coturnix co
8	3	50.0	19	1 AL22 HORSE	P81217 equus cabal
9	3	50.0	20	1 FRE3_LITIN	P56249 litoria inf
10	3	50.0	20	1 MAX8_BOMMX	P83087 bombina max
11	3	50.0	20	1 MIL7_BOVIN	P35451 bos taurus
12	3	50.0	20	1 PUPK_RHOSH	P53121 rhodobacter
13	3	33.3	4	1 RM01_YEAST	P36515 saccharomyc
14	2	33.3	4	1 ACPH_RABIT	P25154 oryctolagus
15	2	33.3	7	1 UH11_RAT	P56576 rattus norv
16	2	33.3	7	1 WWA1_ACHFUF	P35919 achatina fu
17	2	33.3	7	1 WWA2_ACHFUF	P35920 achatina fu
18	2	33.3	7	1 WWA3_ACHFUF	P35921 achatina fu
19	2	33.3	8	1 CAD1_ENTFA	P13268 enterococcu
20	2	33.3	8	1 COM2_CONPU	P58785 conus purpu
21	2	33.3	8	1 CPD1_ENTFA	P13269 enterococcu
22	2	33.3	8	1 LCK6_LEUMA	P19988 leucophaea
23	2	33.3	8	1 NPB_BOVIN	P15507 bos taurus
24	2	33.3	8	1 UH09_RAT	P56575 rattus norv
25	2	33.3	9	1 AL10_CARMA	P81813 carcinus ma
26	2	33.3	9	1 BS43_SERPL	P83375 serratia pl
27	2	33.3	9	1 FAR1_CALVO	P41856 calliphora
28	2	33.3	9	1 FIBB_ERIPA	P19346 erythrocebu
29	2	33.3	9	1 HUTU_KLEAE	P12381 klebsiella
30	2	33.3	9	1 OXYT_BUFRE	P42995 bufo regula
31	2	33.3	9	1 OXYT_RAJCL	P42994 raja clavav
32	2	33.3	10	1 BPP2_BOTIN	P30422 bothrops in
33	2	33.3	10	1 BPP2_BOTJA	P01022 bothrops ja

34	2	33.3	10	1 ESI_LACCA	P81758 lactobacill
35	2	33.3	10	1 PAR6_PANRE	P82660 panagrellus
36	2	33.3	10	1 GONI_CLUPA	P81749 clupea pall
37	2	33.3	10	1 GS09_BACSU	P80243 bacillus su
38	2	33.3	10	1 LSK2_LEUMA	P80339 leucophaea
39	2	33.3	10	1 MALE_KLEPN	Q05564 klebsiella
40	2	33.3	10	1 RRPL_PHODV	P35946 phocine dis
41	2	33.3	10	1 TKL2_LOCOMI	P16224 locusta mig
42	2	33.3	10	1 TKL3_LOCOMI	P30249 locusta mig
43	2	33.3	10	1 TKU1_UREUN	P40751 urechis uni
44	2	33.3	10	1 UPA2_HUMAN	P30088 homo sapien
45	2	33.3	10	1 UPA5_HUMAN	P30091 homo sapien
46	2	33.3	11	1 BPP3_BOTIN	P30423 bothrops in
47	2	33.3	11	1 BPP4_BOTIN	P30424 bothrops in
48	2	33.3	11	1 CEP1_ACHFUF	P22790 achatina fu
49	2	33.3	11	1 FAR9_CALVO	P41864 calliphora
50	2	33.3	11	1 PQOC_PSEPL	P55173 pseudomonas
51	2	33.3	11	1 RANC_RANPI	P89951 rana pipien
52	2	33.3	11	1 T2P1_PROVU	P31031 proteus vul
53	2	33.3	11	1 TKNA_CHICK	P19850 gallus gall
54	2	33.3	11	1 TKNA_GADMO	P28498 gadus morhu
55	2	33.3	11	1 TKNA_HORSE	P01290 equus cabal
56	2	33.3	12	1 FIF1_SARBU	P83349 sarcophaga
57	2	33.3	12	1 FRE1_LITIN	P82021 litoria inf
58	2	33.3	12	1 HCV1_CARMA	P83176 carcinus ma
59	2	33.3	12	1 PKA4_PERFU	P82690 periplaneta
60	2	33.3	12	1 TW2A_METNA	P86652 methanosarc
61	2	33.3	12	1 V2SK_WSSV	P82004 white spot
62	2	33.3	13	1 BOML_PSEGU	P42991 pseudophryn
63	2	33.3	13	1 CHEP_PARID	P47218 parapolybia
64	2	33.3	13	1 CRBL_VESMA	P17232 vespa manda
65	2	33.3	13	1 FIUB_RABIT	P14478 oryctolagus
66	2	33.3	13	1 HEAL_RANES	P24415 rana escul
67	2	33.3	13	1 IDHC_PIG	P20304 sus scrofa
68	2	33.3	13	1 LMA1_LOCOMI	P38496 locusta mig
69	2	33.3	13	1 NEUT_RANTE	P41536 rana tempor
70	2	33.3	13	1 PEDI_HYDAT	P80578 hydra atten
71	2	33.3	13	1 SA2A_ONCMY	P82238 oncorhynch
72	2	33.3	13	1 SA2B_ONCMY	P82239 oncorhynch
73	2	33.3	13	1 TEME_RANTE	P56920 rana tempor
74	2	33.3	13	1 UN12_CLOPA	P81353 clostridium
75	2	33.3	14	1 VG16_BACSU	P80867 bacillus su
76	2	33.3	14	1 CX1A_CONBE	P58623 conus betul
77	2	33.3	14	1 HCYA_MEGOR	Q10583 megathura c
78	2	33.3	14	1 KLP5_SCARA	P58396 scaptocosa
79	2	33.3	14	1 LPW_CITFR	P30356 citrobacter
80	2	33.3	14	1 LPW_ECOLI	P21654 vespa basai
81	2	33.3	14	1 MAST_VESBA	P17238 vespa orien
82	2	33.3	14	1 MAST_VESOR	P80526 fasciola he
83	2	33.3	14	1 NSJ2_FASHE	P40449 cucumis sat
84	2	33.3	14	1 PSAG_CUCSA	P80640 zea mays (m
85	2	33.3	14	1 UC34_MAIZE	P81352 clostridium
86	2	33.3	14	1 UN07_CLOPA	P81337 malva parvi
87	2	33.3	15	1 APP3_MALPA	P81663 pinus pinas
88	2	33.3	15	1 ATP2_PINPS	P82076 litoria cae
89	2	33.3	15	1 CDN4_LITCE	P19917 pseudomonas
90	2	33.3	15	1 DCMU_PSECH	P12665 cricetidae
91	2	33.3	15	1 IRBP_CRISP	P22582 psophocarpu
92	2	33.3	15	1 LEC1_PSOQC	P22585 psophocarpu
93	2	33.3	15	1 LEC2_PSOQC	P22583 psophocarpu
94	2	33.3	15	1 LEC3_PSOQC	P22583 psophocarpu
95	2	33.3	15	1 LPL_THETH	P21234 thermus the
96	2	33.3	15	1 MCA2_RHOOP	P56870 rhodococcus
97	2	33.3	15	1 NIS1_ANAVA	Q44507 anabaena va
98	2	33.3	15	1 PH3_PRUSE	P22265 prunus sero
99	2	33.3	15	1 PRP_MYCBO	P80149 mycobacteri
100	2	33.3	15	1 RKG6_CARCR	P21586 caretta car

ALIGNMENTS

RESULT 1

```

LPK2 LOCMI
ID LPK2_LOCMI STANDARD; PRT; 10 AA.
AC P4148;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrokinin 2 (LOM-PK-2) (FXPRL-amide).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE
RN TISSUE=Brain;
RC MEDLINE=94094539; PubMed=7903606;
RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustapyrokinin II from
RT Locusta migratoria, another member of the FXPRL-amide peptide
RT family."
RL Comp. Biochem. Physiol. 106C:103-109(1993).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTIONS ACTIVITY (MYOTROPIC
CC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro: IPR001484; PYROKININ.
DR PROSITE: PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4
|||
DB 1 QSV 3

RESULT 2
ES1_RAT
ID ES1_RAT STANDARD; PRT; 11 AA.
AC P56571;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ES1 protein, mitochondrial (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheller C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -1- SUBCELLULAR LOCATION: Mitochondrial (Potential).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
CC (SPOT P2) IS: 8.9. ITS MW IS: 25 kDa.
CC -1- SIMILARITY: BELONGS TO THE ES1 FAMILY.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1142 MW; D862272D32C72DC2 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
|||

```

```

Db 7 VLS 9

RESULT 3
TEMA_RANTE
ID TEMA_RANTE STANDARD; PRT; 13 AA.
AC P56917;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin A.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Skin secretion.
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria."
RL Eur. J. Biochem. 242:788-792(1996).
CC -1- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1398 MW; 2653612B9DECD408 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
|||
DB 8 VLS 10

RESULT 4
TEMA_RANTE
ID TEMA_RANTE STANDARD; PRT; 13 AA.
AC P56921;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin F.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria."
RL Eur. J. Biochem. 242:788-792(1996).
CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
CC GRAM-POSITIVE BACTERIA.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1370 MW; 2653612B9DECC338 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 13;

```

Best Local Similarity 100.0%; Pred. No. 8.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 4 VLS 6
Db 8 VLS 10

RESULT 5
MAST_FOLJA STANDARD; PRT; 14 AA.
ID MAST_FOLJA
AC P01517;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Polistes mastoparan.
OS Polistes jadwigae (Paper wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Polistinae; Polistes.
OX NCBI_TaxID=7457;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Hirai Y., Ueno Y., Yasuhara T., Yoshida H., Nakajima T.;
RT "A new mast cell degranulating peptide, polistes mastoparan, in the
RT venom of Polistes jadwigae.";
RL Biomed. Res. 1:185-187(1980).
CC -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
DR PIR; A01780; QMWAPP.
KW Mast cell degranulation; Amidation.
FT MOD_RES 14 14
SQ SEQUENCE 14 AA; 1636 MW; 26472A53BF4778D8 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.6e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 3 SVL 5
Db 12 SVL 14

RESULT 6
ACT_PINPS STANDARD; PRT; 15 AA.
ID ACT_PINPS
AC P81085;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Actin (Water stress responsive protein 5) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=98418576; PubMed=9747804;
RA Costa P., Bahran N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water-deficit-responsive proteins in maritime pine.";
RL Plant Mol. Biol. 38:587-596(1998).
RN [2]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED

CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- INDUCTION: By water stress.
CC -!- SIMILARITY: Belongs to the actin family.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; actin; 1.
DR PROSITE; PS00406; ACTINS_1; PARTIAL.
DR PROSITE; PS01132; ACTINS_ACT LIKE; PARTIAL.
DR PROSITE; PS00432; ACTINS_2; PARTIAL.
KW Structural protein.
FT NON_TER 1 15
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1574 MW; 4712F0146D5B4DE3 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.2e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 4 VLS 6
Db 7 VLS 9

RESULT 7
H5_COTJA STANDARD; PRT; 16 AA.
ID H5_COTJA
AC P18638;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Histone H5 (Fragment).
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE.
RX MEDLINE=76277939; PubMed=962913;
RA Selligy V., Roy C., Dove M., Yaguchi M.;
RT "Species variability of N-terminal sequence of avian erythrocyte-
RT specific histone H5.";
RL Biochem. Biophys. Res. Commun. 71:196-202(1976).
CC -!- FUNCTION: HISTONE H5 PERFORMS THE SAME FUNCTION AS H1, BEING
CC NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER
CC ORDER STRUCTURES, AND REPLACES HISTONE H1 IN CERTAIN CELLS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: ERYTHROID CELLS.
CC -!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
KW Chromosomal protein; Nuclear protein; DNA-binding; DNA condensation.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1665 MW; DB528219B3074D3C CRC64;

Query Match 50.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.7e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 4 VLS 6
Db 5 VLS 7

RESULT 8
AL22_HORSE STANDARD; PRT; 19 AA.
ID AL22_HORSE
AC P81217;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dander allergen Equ c 2.0102 (fragment).
OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin;
 RX MEDLINE=98237590; PubMed=9578478;
 RA Bulone V., Krogstad-Johnsen T., Smeestad-Paulsen B.;
 RT "Separation of horse dander allergen proteins by two-dimensional
 electrophoresis -- molecular characterization and identification of
 Equ c 2.0101 and Equ c 2.0102 as lipocalin proteins.";
 RL Eur. J. Biochem. 253:202-211(1998).
 RN [2]
 RP MASS SPECTROMETRY.
 RC TISSUE=Hair; dandruff;
 RX MEDLINE=21257838; PubMed=11358533;
 RA Goubiran Botros H., Poncet P., Rabillon J., Fontaine T., Laval J.-M.,
 RA David B.;
 RT "Biochemical characterization and surfactant properties of horse
 allergens";
 RL Eur. J. Biochem. 268:3126-3136(2001).
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -!- MASS SPECTROMETRY: MW=16000; METHOD=Electrospray.
 CC -!- MISCELLANEOUS: Allergen of horse dander.
 CC -!- SIMILARITY: Belongs to the lipocalin family.
 CC -!- CAUTION: C 2.0101 AND C 2.0102 MIGHT BE TWO VARIANTS OF THE
 CC SAME PROTEIN.
 DR InterPro: IPR000566; Lipocalin_cytFABP.
 DR PROSITE: PS00213; LIPOCALIN; PARTIAL.
 KW Transport; Lipocalin; Allergen.
 FT NON TER 19
 SQ SEQUENCE 19 AA; 2195 MW; A8E86FAFC9322C26 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 POS 3
 DB 4 POS 6

RESULT 9
 PRE3 LITIN
 ID PRE3_LITIN STANDARD; PRT; 20 AA.
 AC P56249;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Frenatin 3.
 OS Litoria infrafronata (Giant tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=61195;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=97368637; PubMed=9225251;
 RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "The structures of the frenatin peptides from the skin secretion of
 the giant tree frog Litoria infrafronata";
 RL J. Pept. Sci. 2:117-124(1996).
 CC -!- FUNCTION: Wide spectrum antimicrobial peptide.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral
 CC glands.
 KW Amphibian defense peptide; Antibiotic.
 SQ SEQUENCE 20 AA; 1956 MW; 7E4ABE30EA17B20C CRC64;

Query Match 50.0%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SVL 5
 DB 4 SVL 6

RESULT 10
 MAX8 BOMMX
 ID MAX8_BOMMX STANDARD; PRT; 20 AA.
 AC P83087;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Maximin 8.
 OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
 OX NCBI_TaxID=161274;
 RN [1]
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
 RC TISSUE=Skin secretion;
 RA Chen T.B., McClean S., Orr D.P., Boursen A.J., Rao P.F., Shaw C.;
 RT "Isolation and structural characterisation of antimicrobial peptides
 from the venom of the Chinese large-webbed bell toad (Bombina
 maxima).";
 RL Submitted (JUN-2001) to the SWISS-PROT data bank.
 CC -!- FUNCTION: Has antimicrobial activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
 KW Amphibian defense peptide; Antibiotic.
 SQ SEQUENCE 20 AA; 1977 MW; EC7541AD6BE2F949 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 VLS 6
 DB 5 VLS 7

RESULT 11
 MIL17 BOVIN
 ID MIL17_BOVIN STANDARD; PRT; 20 AA.
 AC P35451;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE 17 kDa milk glycoprotein (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Milk;
 RX MEDLINE=93308294; PubMed=8320368;
 RA Soerensen E.S., Petersen T.E.;
 RT "Purification and characterization of three proteins isolated from
 the proteose peptone fraction of bovine milk.";
 RL J. Dairy Res. 60:189-197(1993).
 CC -!- PTM: N-GLYCOSYLATED.
 CC -!- SIMILARITY: TO CAMEL WHEY PROTEIN.
 KW Glycoprotein; Milk.
 FT NON TER 1
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2233 MW; 4CCA589404C62C27 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQS 3
Db |||
5 PQS 7

RESULT 12

PUFK RHOSH
ID PUFK RHOSH STANDARD; PRT; 20 AA.
AC Q53121; O08033;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcriptional regulatory protein pufK.
GN PUFK
OS Rhodospirillum rubrum (Rhodospirillum rubrum)
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE=96349111; PubMed=8760918;
RA Gong L., Kaplan S.;
RT "Translational control of puf operon expression in Rhodobacter
RT sphaeroides 2.4.1";
RL Microbiology 142:2057-2069(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RA McGlynn P.;
RT "R. sphaeroides genes bchC, bchX, bchY, bchZ and pufQ";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]

RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE=20115911; PubMed=10648776;
RA Choudhary M., Kaplan S.;
RT "DNA sequence analysis of the photosynthesis region of Rhodobacter
RT sphaeroides 2.4.1";
RL Nucleic Acids Res. 28:862-867(2000).

CC -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF PUFK.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; S82643; AAB46798.1; -.
DR EMBL; AJ010302; CAB38751.1; -.
DR EMBL; AF195122; AAF24301.1; -.
DR PIR; T50757; T50757.
KW Transcription regulation.
SQ SEQUENCE 20 AA; 2262 MW; 764DBD64B9DD990C CRC64;

Query Match 50.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
Db |||
14 SVL 16

RESULT 13

RM01 YEAST
ID RM01 YEAST STANDARD; PRT; 4 AA.
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein L1 (YmL1) (Fragment).
GN MRPL1

OS Saccharomycetes cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.

RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria";
RL FEBS Lett. 284:51-56(1991).
DR PIR; S17255; S17255.
DR SGD; L0002681; MRPL1.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4
Db |||
1 SV 2

RESULT 14

ACPH RABIT
ID ACPH RABIT STANDARD; PRT; 6 AA.
AC P25154;

DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)
DE (APH) (Acylaminoacyl-peptidase) (Fragment).
GN APEH.

OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]

RP TISSUE=Muscle;
RX Krishna R.G., Chin C.C.Q., Wolf F.;
RA MEDLINE=9222120; PubMed=1807161;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after
RT unblocking with N-acylaminoacyl-peptide hydrolase";
RL Anal. Biochem. 199:45-50(1991).

CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
CC + peptide.

CC -!- SUBUNIT: Homotetramer.

CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.

DR PIR; A49792; A49792.

DR MEROPS; S09.004; -.

DR InterPro; IPR002471; Prol_endopep_ser.

DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.

KW Hydrolase; Acetylation.

FT MOD_RES 1 1 ACETYLATION.

FT NON_TER 6 6

SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
Db 5 VL 6

RESULT 15

UH11_RAT UH11_RAT STANDARD; PRT; 7 AA.
ID UH11_RAT
AC P56576;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 20-page of heart tissue (Spot P11) (Fragment).
OS Rattus norvegicus [Rat].
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleisner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.5, ITS MW IS: 42 KDa.
FT UNSURE 2 2 OR A.
FT NON TER 7 7
SQ SEQUENCE 7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QS 3
Db 1 QS 2

RESULT 16

WWA1_ACHF UH11_RAT STANDARD; PRT; 7 AA.
ID WWA1_ACHF
AC P35919;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Wwamide-1.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RA Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.;
RL FEBS Lett. 323:104-108(1993).
CC -!- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
DR PIR; S33245; S33245.
KW Neuropeptide; Amidation.
FT MOD RES 7 7
SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4
Db 5 SV 6

RESULT 17

WWA2_ACHF UH11_RAT STANDARD; PRT; 7 AA.
ID WWA2_ACHF
AC P35920;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Wwamide-2.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RA Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.;
RL FEBS Lett. 323:104-108(1993).
DR PIR; S33246; S33246.
KW Neuropeptide; Amidation.
FT MOD RES 7 7
SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4
Db 5 SV 6

RESULT 18

WWA3_ACHF UH11_RAT STANDARD; PRT; 7 AA.
ID WWA3_ACHF
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Wwamide-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RA Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.;
RL FEBS Lett. 323:104-108(1993).
DR PIR; S33244; S33244.
KW Neuropeptide; Amidation.
FT MOD RES 7 7
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4
Db 5 SV 6

RESULT 19

CAD1_ENTFA UH11_RAT STANDARD; PRT; 8 AA.
ID CAD1_ENTFA
AC P13269;

DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CAD1.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85051899; PubMed=6437872;
 RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,
 RA Craig R.A., Clewell D.B., Suzuki A.;
 RT "Isolation and structure of the bacterial sex pheromone, CAD1, that
 RT induces plasmid transfer in Streptococcus faecalis.";
 RL FEBS Lett. 178:97-100(1984).
 CC -!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC HEMOLYSIN PLASMID PAD1.
 KW Pheromone.
 SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;
 Query Match 33.3%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VL 5
 ||
 Db 5 VL 6

RESULT 20
 COW2_CONFU
 ID COW2_CONFU STANDARD; PRT; 8 AA.
 AC P58785;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leu-contryphan-P.
 OS Conus purpurascens (Purple cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=41690;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC STRAIN=Clipperton Island; TISSUE=Venom;
 RX MEDLINE=9388839; PubMed=10461743;
 RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
 RA Olivera B.M.;
 RT "A novel D-leucine-containing Conus peptide: diverse conformational
 RT dynamics in the contryphan family.";
 RL J. Pept. Res. 54:93-99(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
 CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
 KW Toxin; Hydroxylation; D-amino acid.
 FT DISULFID 2
 FT MOD_RES 4 4 D-LEUCINE.
 FT MOD_RES 4 4
 SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;
 Query Match 33.3%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VL 5
 ||
 Db 3 VL 4

RESULT 21
 CPD1_ENTFA
 ID CPD1_ENTFA STANDARD; PRT; 8 AA.
 AC P13269;

DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CPD1.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85040388; PubMed=6436978;
 RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
 RA Craig R.A., Clewell D.B.;
 RT "Isolation and structure of bacterial sex pheromone, CPD1.";
 RL Science 226:849-850(1984).
 CC -!- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC BACTERIOCIN PLASMID PPD1.
 KW Pheromone.
 SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;
 Query Match 33.3%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 LS 6
 ||
 Db 6 LS 7

RESULT 22
 LCK6_LEUMA
 ID LCK6_LEUMA STANDARD; PRT; 8 AA.
 AC P19988;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leucokinin VI (I-VI).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blateroidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Head;
 RX MEDLINE=87052651; PubMed=2877794;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
 RT myotropic peptides of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:27-30(1987).
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTEDEUM (HINDGUT).
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND
 CC PIR; JS0316; JS0316.
 DR HELIOTHIS ZEA ADIPOKINETIC HORMONE.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 FT MOD_RES 8 8
 SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;
 Query Match 33.3%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QS 3
 ||
 Db 1 QS 2

RESULT 23
 NPB_BOVIN
 ID NPB_BOVIN STANDARD; PRT; 8 AA.
 AC P15507;
 DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuropeptide B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RN SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=86067985; PubMed=3865193;
 RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
 RT "Isolation, sequencing, synthesis, and pharmacological
 RT characterization of two brain neuropeptides that modulate the action
 RT of morphine."
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
 CC -1- FUNCTION: MODULATES THE ACTION OF MORPHINE.
 DR PIR; B24749; B24749.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8
 SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;
 Query Match 33.3%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PQ 2
 Db 5 PQ 6
 RESULT 24
 ID UH09 RAT STANDARD; PRT; 8 AA.
 AC P56575;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE Unknown protein from 2D-page of heart tissue (Spot p9) (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RN SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Heart;
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
 RA Jungblut P.R.;
 RL Submitted (SEP-1998) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;
 Query Match 33.3%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 QS 3
 Db 5 QS 6
 RESULT 25
 ID AL10 CARMA STANDARD; PRT; 9 AA.
 AC P81813;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Carcinostatatin 10.
 OS Carcinus maenas (Common shore crab) (Green crab).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Brachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RN SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 963 MW; 372D79CDCB4776C7 CRC64;
 Query Match 33.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PQ 2
 Db 2 PQ 3
 RESULT 26
 BS43 SERPL STANDARD; PRT; 9 AA.
 ID BS43 SERPL STANDARD; PRT; 9 AA.
 AC P83375;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bacteriocin serracin P 43 kDa subunit (fragment).
 OS Serratia plymuthica.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Serratia.
 OX NCBI_TaxID=82996;
 RN [1]
 RN SEQUENCE, AND FUNCTION.
 RP STRAIN=J7;
 RC MEDLINE=22293561; PubMed=12406768;
 RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenbergh I.,
 RA Van Beumen J., Thonart P.;
 RT "Characterization of serracin P, a phage-tail-like bacteriocin, and
 RT its activity against *Erwinia amylovora*, the fire blight pathogen.";
 RL Appl. Environ. Microbiol. 68:5704-5710(2002).
 CC -1- FUNCTION: Major component of a prophage tail sheath (Probable).
 CC -1- FUNCTION: Antibacterial activity against Gram-negative bacterium
 CC *E. amylovora*.
 DR InterPro; IPR008498; Tail tube.
 DR Pfam; PF04985; Phage tube; 1.
 KW Antibiotic; Bacteriocin.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1095 MW; 1E66D413C871E1FB CRC64;
 Query Match 33.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 VL 5
 Db 8 VL 9
 RESULT 27
 ID F41 CALVO STANDARD; PRT; 9 AA.
 AC F41856;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

```

DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CallifMRamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RN SEQUENCE.
RP TISSUE=Thoracic ganglion;
RC MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Refeld J.P., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated callifMRFamides) from the blowfly
RT Calliphora vomitoria";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: A41978; A41978.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;
SQ
Query Match 33.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PQ 2
Db 2 PQ 3
RESULT 28
ID FIBB_ERYPA STANDARD; PRT; 9 AA.
AC P19346;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Erythrocebus patas (Red guenon) (Husar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RN SEQUENCE.
RP MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocebus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons.";
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR: D24180; D24180.
DR InterPro: IPR002181; Fibrinogen_C.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9
FT NON_TER 9 9
FIBRINOPEPTIDE B.

```

```

SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;
Query Match 33.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 VL 5
Db 4 VL 5
RESULT 29
ID HUTU_KLEAE STANDARD; PRT; 9 AA.
AC P12381;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urocanate hydratase (EC 4.2.1.49) (Urocanase) (Imidazolonepropionate
DE hydrolase) (Fragment).
GN HUTU.
OS Klebsiella aerogenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=28451;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=88198018; PubMed=2834335;
RA Nieuwkoop A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;
RT "Bidirectional promoter in the hut(p) region of the histidine
RT utilization (hut) operons from Klebsiella aerogenes.";
RL J. Bacteriol. 172:5477-5481(1990).
CC -!- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3-H-imidazol-4-
CC yl)propanoate = urocanate + H(2)O.
CC -!- COFACTOR: Binds 1 NAD per subunit (By similarity).
CC -!- PATHWAY: Histidine degradation; second step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use, by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
DR EMBL: M19665; AAA25078.1; -.
DR EMBL: M34604; AAA25076.1; -.
DR HAWAP; MF 00577; -.
DR InterPro: IPR000193; Urocanase.
DR PROSITE: PS01233; UROCANASE; PARTIAL.
KW Histidine metabolism; Lyase; NAD.
FT NON_TER 9 9
FT SEQUENCE 9 AA; 1140 MW; 970FC41B5325A6C5 CRC64;
Query Match 33.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 QS 3
Db 3 QS 4
RESULT 30

```

```

OXYT_BUFRE
ID_OXYT_BUFRE STANDARD; PRT; 9 AA.
AC P42995;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Seritocin ((Ser5,Ile8)-oxytocin).
OS Bufo regularis (Leopard toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;
OC Bufo.
OX NCBI_TaxID=8390;
RN [1]
RP SEQUENCE
RX MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
RT "A new neurohypophysial peptide, seritocin ((Ser5,Ile8)-oxytocin),
RT identified in a dryness-resistant African toad, Bufo regularis.";
RL Int. J. Pept. Protein Res. 45:482-487(1995).
CC -!- FUNCTION: Devoid of oxytocic activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 983 MW; 17FF476EA5A6D04B CRC64;

Query Match 33.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QS 3
DB 4 QS 5

RESULT 31
OXYT_RAJCJL
ID_OXYT_RAJCJL STANDARD; PRT; 9 AA.
AC P42994;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Glumitocin.
OS Raja clavata (Thornback ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Hypnosqualea; Priestiorajae; Batoidae;
OC Rajiformes; Rajidae; Raja.
OX NCBI_TaxID=7781;
RN [1]
RP SEQUENCE.
RX MEDLINE=66123415; PubMed=5880565;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Phylogeny of neurohypophysal peptides: isolation of a new hormone,
RT glumitocin (Ser 4-Gln 8-oxytocin) present in a cartilaginous fish,
RT the ray (Raja clavata).";
RL Biochim. Biophys. Acta 107:393-396(1965).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 984 MW; 17E9C76EB455B04B CRC64;

Query Match 33.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QS 3
DB 4 QS 5

RESULT 32
BPP2_BOTIN
ID_BPP2_BOTIN STANDARD; PRT; 10 AA.
AC P30422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; B37196; B37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQ 2
DB 7 PQ 8

RESULT 33
BPP2_BOTJA
ID_BPP2_BOTJA STANDARD; PRT; 10 AA.
AC P01022;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme
DE inhibitor V-6-II).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.

```

CC It acts as an indirect hypotensive agent.
 DR PIR; A01255; XAVI6B.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1232 MW; 30C53546C741773 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQ 2
 ||
 Db 6 PQ 7

RESULT 34
 ESL_LACCA STANDARD; PRT; 10 AA.
 ID ESL_LACCA
 AC P81758;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Putative esterase/lipase (EC 3.1.-.-) (Fragment).
 OS Lactobacillus casei.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1582;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=IFPL731;
 RA Lopez de Felipe F.;
 RL Submitted (MAR-1999) to the SWISS-PROT data bank.
 KW Hydrolase; Serine esterase.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1070 MW; 1C6132D732CAB1A0 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
 ||
 Db 6 VL 7

RESULT 35
 FAR6_PANRE STANDARD; PRT; 10 AA.
 ID FAR6_PANRE
 AC P82660;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FMRFamide-like neuropeptide PF6 (NGAPQFFVRF-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE, FUNCTION, AND AMIDATION.
 RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
 RA Maule A.G.;
 RA "Isolation, characterization and pharmacology of FMRFamide-related
 RT peptides (FARs) from free-living nematode, Panagrellus redivivus."
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.
 CC -!- FUNCTION: MYOACTIVE.
 CC -!- SIMILARITY: BELONGS TO THE FAR6 (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PQ 2
 ||
 Db 4 PQ 5

RESULT 36
 GON1_CLUPA STANDARD; PRT; 10 AA.
 ID GON1_CLUPA
 AC P81749;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH)
 DE (mulliberin I).
 GN GNRH1.
 OS Clupea pallasii (Pacific herring).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
 OC Clupea.
 OX NCBI_TaxID=30724;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Brain, and Pituitary;
 RX MEDLINE=20114351; PubMed=10650929;
 RA Carlsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
 RA Chang J.P., Rivier J.E., Sherwood N.M.;
 RT "Primary structure and function of three gonadotropin-releasing
 RT hormones, including a novel form, from an ancient teleost, herring."
 RL Endocrinology 141:505-512(2000).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GNRH family.
 DR InterPro: IPR002012; GNRH.
 DR Pfam: PF00446; GNRH; 1.
 DR PROSITE: PS00473; GNRH; 1.
 KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA; 1105 MW; 284B20B72871F5A3 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6
 ||
 Db 7 LS 8

RESULT 37
 GS09_BACSU STANDARD; PRT; 10 AA.
 ID GS09_BACSU
 AC P80243;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE General stress protein 9 (GSP9) (Fragment).
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=168 / IS58;
 RX MEDLINE=94282319; PubMed=8012595;
 RA Voelker U., Engelmann S., Maul B., Riethdorf S., Voelker A.,
 RA Schmid R., Mach H., Hecker M.;
 RT "Analysis of the induction of general stress proteins of Bacillus
 RT subtilis."
 RL Microbiology 140:741-752(1994).
 CC -!- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, GLUCOSE
 CC LIMITATION AND OXYGEN LIMITATION.

CC -!- CAUTION: Could not be found in the genome of B.subtilis 168.
 KW Heat shock.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1168 MW; 99766442D5A2C05A CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SV 4
 Db 6 SV 7

RESULT 38

LSK2_LEUMA STANDARD; PRT; 10 AA.
 AC P09039;
 DT 01-NOV-1998 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leucosulfakinin-II (LSK-II).
 OS Leucophaea maderae (Madeira, cockroach), and
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988, 6978;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=L.maderae;
 RX MEDLINE=87048769; PubMed=3778455;
 RA Nachman R.J., Holman G.M., Cook B.J., Haddon W.F., Ling N.;
 RT "Leucosulfakinin-II, a blocked sulfated insect neuropeptide with
 RT homology to cholecystokinin and gastrin."
 RL Biochem. Biophys. Res. Commun. 140:357-364 (1986).
 RN [2]

SEQUENCE.
 RP SPECIES=P.americana; TISSUE=Corpora cardiaca;
 RC MEDLINE=90137190; PubMed=2615921;
 RX Venstra J.A.;
 RA "Isolation and structure of two gastrin/CKK-like neuropeptides from
 RT the American cockroach homologous to the leucosulfakinins."
 RL Neuropeptides 14:145-149 (1989).
 CC -!- FUNCTION: CHANGE THE FREQUENCY AND AMPLITUDE OF CONTRACTIONS OF
 CC THE COCKROACH HINGUT. STIMULATES MUSCLE CONTRACTION OF HINDGUT.
 CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.

DR PIR; A26335; GMR02.
 DR PIR; B60656; B60656.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; 1.
 KW Hormone; Amidation; Sulfation; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 5 5 SULEFATION (IN L.MADERAE, BUT NOT IN
 FT P.AMERICANA).
 FT MOD RES 10 10 AMIDATION.
 FT SEQUENCE 10 AA; 1255 MW; 9B4F5391E86B5AAA CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QS 3
 Db 1 QS 2

RESULT 39

MALE KLEPN STANDARD; PRT; 10 AA.
 AC Q05564;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Maltose-binding periplasmic protein (Maltodextrin-binding protein)
 DE (MWBp) (Fragment).
 GN MALE.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1033-SP14 / KAY2026;
 RX MEDLINE=93211295; PubMed=8459773;
 RA Bachellier S., Perrin D., Hofnung M., Gilson E.;
 RT "Bacterial interspersed mosaic elements (BIMEs) are present in the
 RT genome of Klebsiella."
 RL Mol. Microbiol. 7:537-544 (1993).
 CC -!- FUNCTION: MALE IS INVOLVED IN THE HIGH-AFFINITY MALTOSE MEMBRANE
 CC TRANSPORT SYSTEM. INITIAL RECEPTOR FOR THE ACTIVE TRANSPORT OF AND
 CC CHEMOTAXIS TOWARD MALTOOLIGOSACCHARIDES.
 CC -!- SUBCELLULAR LOCATION: Periplasmic.
 CC -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
 CC PROTEIN FAMILY 1.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; X68329; CAA48406.1; -.
 DR InterPro; IPR006061; SBP_dom1.
 DR PROSITE; PS01037; SBP_BACTERIAL_1; PARTIAL.
 KW Transport; Sugar transport; Periplasmic.
 FT NON TER 1 1
 FT SEQUENCE 10 AA; 1159 MW; 8F8DC4415A6DDDA CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QS 3
 Db 1 QS 6

RESULT 40

RRPL_PHODV STANDARD; PRT; 10 AA.
 AC P35946;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
 DE (L protein) (fragment).
 GN L.
 OS Phocine distemper virus (PDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
 OX NCBI_TaxID=11240;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=U1ster/88;
 RX MEDLINE=92268877; PubMed=1588321;
 RA Curran M.D., O'Loan D., Kennedy S., Rima B.K.;
 RT "Molecular characterization of phocine distemper virus: gene order
 RT and sequence of the gene encoding the attachment (H) protein."
 RL J. Gen. Virol. 73:1189-1194 (1992).
 CC -!- FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY
 CC FUNCTION IN RNA SYNTHESIS. CAPPING, METHYLATION AND POLY(A)
 CC SYNTHESIS OF NEWLY SYNTHESIZED VIRAL MRNAs, RNA EDITING OF THE P
 CC GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.

CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA} (N).
 CC -!- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D10371; BAA01208.1; -
 CC Transferase; RNA-directed RNA polymerase.
 CC NON TER 10 10
 CC SEQUENCE 10 AA; 1105 MW; 9C2B7FD452D5A2D5 CRC64;
 CC
 CC Query Match 33.3%; Score 2; DB 1; Length 10;
 CC Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 3 SV 4
 CC DB 3 SV 4
 CC
 CC RESULT 41
 CC TKL2_LOCMI
 CC ID TKL2_LOCMI STANDARD; PRT; 10 AA.
 CC AC P16224;
 CC DT 01-APR-1990 (Rel. 14, Created)
 CC DT 01-APR-1990 (Rel. 14, Last sequence update)
 CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
 CC DE Locustatachykinin II (TK-II).
 CC OS Locusta migratoria (Migratory locust).
 CC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 CC OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 CC ON NCBI_TaxID=7004;
 CC RN [1]_
 CC RP SEQUENCE.
 CC RC TISSUE=Brain;
 CC RX MEDLINE=90184489; PubMed=2311766;
 CC RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 CC RT "Locustatachykinin I and II, two novel insect neuro-peptides with
 CC RT homology to peptides of the vertebrate tachykinin family.";
 CC RL FEBS Lett. 261:397-401 (1990).
 CC CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
 CC CC OVIDUCT AND FOREGUT.
 CC CC -!- SUBCELLULAR LOCATION: Secreted.
 CC CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 CC KW Tachykinin; Neuropeptide; Amidation.
 CC FT MOD_RES 10 10
 CC SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;
 CC
 CC Query Match 33.3%; Score 2; DB 1; Length 10;
 CC Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 5 LS 6
 CC DB 3 LS 4
 CC
 CC RESULT 42
 CC TKL3_LOCMI
 CC ID TKL3_LOCMI STANDARD; PRT; 10 AA.
 CC AC P30249;
 CC DT 01-APR-1993 (Rel. 25, Created)
 CC DT 01-APR-1993 (Rel. 25, Last sequence update)
 CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
 CC DE Locustatachykinin III (TK-III).
 CC OS Locusta migratoria (Migratory locust).
 CC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 CC OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 CC ON NCBI_TaxID=7004;
 CC RN [1]_
 CC RP SEQUENCE.
 CC RC TISSUE=Brain;
 CC RX MEDLINE=90184489; PubMed=2311766;
 CC RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 CC RT "Locustatachykinin I and II, two novel insect neuro-peptides with
 CC RT homology to peptides of the vertebrate tachykinin family.";
 CC RL FEBS Lett. 261:397-401 (1990).
 CC CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
 CC CC OVIDUCT AND FOREGUT.
 CC CC -!- SUBCELLULAR LOCATION: Secreted.
 CC CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 CC KW Tachykinin; Neuropeptide; Amidation.
 CC FT MOD_RES 10 10
 CC SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;
 CC
 CC Query Match 33.3%; Score 2; DB 1; Length 10;
 CC Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 5 LS 6
 CC DB 3 LS 4
 CC
 CC RESULT 43
 CC TKUL_UREUN
 CC ID TKUL_UREUN STANDARD; PRT; 10 AA.
 CC AC P40751;
 CC DT 01-FEB-1995 (Rel. 31, Created)
 CC DT 01-FEB-1995 (Rel. 31, Last sequence update)
 CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
 CC DE Urechistachykinin I.
 CC OS Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.
 CC ON NCBI_TaxID=6432;
 CC RN [1]_
 CC RP SEQUENCE, AND SYNTHESIS.
 CC RC TISSUE=ventral nerve cord;
 CC RX MEDLINE=93236558; PubMed=8476410;
 CC RA Ikeda T., Minakata H., Nomoto K., Kubota I., Muneoka Y.;
 CC RT "Two novel tachykinin-related neuro-peptides in the echiuroid worm,
 CC RT Urechis unicinctus.";
 CC RL Biochem. Biophys. Res. Commun. 192:1-6 (1993).
 CC CC -!- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY-WALL
 CC CC MUSCLE OF THE ANIMAL.
 CC CC -!- SUBCELLULAR LOCATION: Secreted.
 CC CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 CC KW Tachykinin; Neuropeptide; Amidation.
 CC FT MOD_RES 10 10
 CC SEQUENCE 10 AA; 1177 MW; C6D1C462C9D6C5A6 CRC64;
 CC
 CC Query Match 33.3%; Score 2; DB 1; Length 10;
 CC Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 2 QS 3
 CC DB 3 QS 4
 CC
 CC RESULT 44
 CC UPA2_HUMAN
 CC ID UPA2_HUMAN STANDARD; PRT; 10 AA.
 CC AC P30088;
 CC DT 01-APR-1993 (Rel. 25, Created)
 CC DT 01-APR-1993 (Rel. 25, Last sequence update)

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 ON NCBI_TaxID=7004;
 RN [1]_
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=91219696; PubMed=2132575;
 RA Schoofs L., Holman G.M., Hayes T.K., Kochansky J.P., Nachman R.J.,
 RA de Loof A.;
 RT "Locustatachykinin III and IV: two additional insect neuro-peptides
 RT with homology to peptides of the vertebrate tachykinin family.";
 RL Regul. Pept. 31:199-212 (1990).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
 CC CC OVIDUCT AND FOREGUT.
 CC CC -!- SUBCELLULAR LOCATION: Secreted.
 CC CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 CC PIR; A60073; ECLQ3M.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 10 10
 SEQUENCE 10 AA; 1065 MW; C452CD6B59C87DC6 CRC64;
 CC
 CC Query Match 33.3%; Score 2; DB 1; Length 10;
 CC Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 PQ 2
 CC DB 2 PQ 3
 CC
 CC RESULT 43
 CC TKUL_UREUN
 CC ID TKUL_UREUN STANDARD; PRT; 10 AA.
 CC AC P40751;
 CC DT 01-FEB-1995 (Rel. 31, Created)
 CC DT 01-FEB-1995 (Rel. 31, Last sequence update)
 CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
 CC DE Urechistachykinin I.
 CC OS Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.
 CC ON NCBI_TaxID=6432;
 CC RN [1]_
 CC RP SEQUENCE, AND SYNTHESIS.
 CC RC TISSUE=ventral nerve cord;
 CC RX MEDLINE=93236558; PubMed=8476410;
 CC RA Ikeda T., Minakata H., Nomoto K., Kubota I., Muneoka Y.;
 CC RT "Two novel tachykinin-related neuro-peptides in the echiuroid worm,
 CC RT Urechis unicinctus.";
 CC RL Biochem. Biophys. Res. Commun. 192:1-6 (1993).
 CC CC -!- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY-WALL
 CC CC MUSCLE OF THE ANIMAL.
 CC CC -!- SUBCELLULAR LOCATION: Secreted.
 CC CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 CC KW Tachykinin; Neuropeptide; Amidation.
 CC FT MOD_RES 10 10
 CC SEQUENCE 10 AA; 1177 MW; C6D1C462C9D6C5A6 CRC64;
 CC
 CC Query Match 33.3%; Score 2; DB 1; Length 10;
 CC Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 2 QS 3
 CC DB 3 QS 4
 CC
 CC RESULT 44
 CC UPA2_HUMAN
 CC ID UPA2_HUMAN STANDARD; PRT; 10 AA.
 CC AC P30088;
 CC DT 01-APR-1993 (Rel. 25, Created)
 CC DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.4, ITS MW IS: 49 kDa.
DR SWISS-2DPAGE; P30088; HUMAN.
FT NON TER 1 1
FT UNSURE 6 6
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1079 MW; 51AC54AAB77775B7 CRC64;
Query Match 33.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 LS 6
DB 3 LS 4
RESULT 45
UPA5 HUMAN
ID UPA5 HUMAN STANDARD; PRT; 10 AA.
AC P30091;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.85, ITS MW IS: 40 kDa.
CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
CC PROTEIN.
DR SWISS-2DPAGE; P30091; HUMAN.
FT NON TER 1 1
FT VARIANT 9 9 G -> Y.
FT 10 /FTID=VAR_000002.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;
Query Match 33.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 VL 5
DB 6 VL 7

RESULT 46
BPP3 BOTIN
ID BPP3 BOTIN STANDARD; PRT; 11 AA.
AC P30423;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; C37196; C37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;
Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PQ 2
DB 7 PQ 8
RESULT 47
BPP4 BOTIN
ID BPP4 BOTIN STANDARD; PRT; 11 AA.
AC P30424;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; D37196; D37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1143 MW; 20BBF13C7741777 CRC64;
Query Match 33.3%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0;

Qy 1 PQ 2

Db 7 PQ 8

RESULT 48

CEP1_ACHFU
ID CEP1_ACHFU STANDARD; PRT; 11 AA.
AC P22790;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Cardio-excitatory peptide-1 (ACEP-1).
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylomatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC STRAIN=Ferussac; TISSUE=Heart atrium;
RX MEDLINE=90211261; PubMed=2322251;
RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
RT "A novel cardio-excitatory peptide isolated from the atria of the
RT African giant snail, Achatina fulica.";
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
CC -1- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO
CC EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL
CC MUSCLE AND THE IDENTIFIED NEURONS CONTROLLING THE BUCCAL MUSCLE
CC MOVEMENT OF ACHATINA.
CC -1- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
PR; A34662; A34662.
KW Hormone; Amidation.
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0;

Qy 2 QS 3

Db 3 QS 4

RESULT 49

FAR9_CALVO
ID FAR9_CALVO STANDARD; PRT; 11 AA.
AC P41864;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE CalliprPamide 9.
CS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliprPamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
CC FAMILY.
PR; I41978; I41978.

KW Neuropeptide; Amidation.
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1359 MW; 8160CE46CAA44321 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0;

Qy 3 SV 4

Db 1 SV 2

RESULT 50

PQQC_PSEFL
ID PQQC_PSEFL STANDARD; PRT; 11 AA.
AC P55173;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Coenzyme PQQ synthesis protein C (Fragment).
GN PQQC.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHAO;
RX MEDLINE=96064397; PubMed=8526497;
RA Schnider U., Keel C., Defago G., Haas D.;
RT "In3-directed cloning of pqq genes from Pseudomonas fluorescens CHAO:
RT mutational inactivation of the genes results in overproduction of the
RT antibiotic pyoluteorin.";
RL Appl. Environ. Microbiol. 61:3856-3864(1995).
CC -1- FUNCTION: REQUIRED FOR COENZYME PYROLO-QUINOLINE-QUINONE (PQQ)
CC BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER BACTERIAL PQQC.

THIS SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; X87299; CAA60734.1; -;
PIR; S58244; S58244.

FT NON_TER 11

SQ SEQUENCE 11 AA; 1182 MW; 89DF46E4C5B73771 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0;

Qy 5 LS 6

Db 6 LS 7

RESULT 51

RANC_RANPI
ID RANC_RANPI STANDARD; PRT; 11 AA.
AC P08951;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ranatensin-C.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.


```

OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=84131098; PubMed=6141890;
RA Nakajima T.;
RL Unpublished results, cited by:
RL Erspamer V., Erspamer G.F., Mazzanti G., Edean R.;
RL Comp. Biochem. Physiol. 77C:99-108(1984).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY
DR InterPro: IPR000874; Bombesin.
DR Pfam: PF02044; Bombesin; 1.
DR PROSITE: PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation.
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PQ 2
Db 3 PQ 4

RESULT 52
T2P1_PROVU
ID T2P1_PROVU STANDARD; PRT; 11 AA.
AC P31031;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)
DE (R.PvuI) (Fragment).
GN PVUIR.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=585;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 13315;
RX MEDLINE=93087186; PubMed=1454536;
RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
RT "Cloning and characterization of genes for the PvuI restriction and
RT modification system.";
RL Nucleic Acids Res. 20:5743-5747(1992).
CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
CC CLEAVES AFTER T-4.
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC specific double-stranded fragments with terminal 5'-phosphates.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L04163; AAA25660.1; -.
DR PIR; S35490; S35490.
DR REBASE; 1541; PvuI.
KW Restriction system; Hydrolase; Nuclease; Endonuclease.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;

```

```

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SV 4
Db 2 SV 3

RESULT 53
TKNA_CHICK
ID TKNA_CHICK STANDARD; PRT; 11 AA.
AC P19850;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=88204263; PubMed=2452461;
RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT "[Arg3]substance P and neurokinin A from chicken small intestine.";
RL Regul. Pept. 20:171-180(1988).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; JN0023; JN0023.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PQ 2
Db 4 PQ 5

RESULT 54
TKNA_GADMO
ID TKNA_GADMO STANDARD; PRT; 11 AA.
AC P28438;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OX NCBI_TaxID=8049;
RN [1]
RP SEQUENCE.
RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
RT "Substance-P-related and neurokinin-A-related peptides from the brain
RT of the cod and trout.";
RL Eur. J. Biochem. 206:659-664(1992).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND

```

CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES
CC -!- SUBCELLULAR LOCATION: Secreted.
CC PIR; S23306; S23306.
CC InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD RES 11 11
SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;
Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PQ 2
DB 4 PQ 5
RESULT 55
TKNA_HORSE
ID TKNA_HORSE STANDARD; PRT; 11 AA.
AC P01250;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Substance P.
GN TAC1 OR NKNA OR TAC2 OR NKA.
OS Equus caballus (Horse), and
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796, 10141;
RN [1]
RP SEQUENCE.
RC SPECIES=Horse;
RA Studer R.O., Trzeciak A., Lergier W.;
RT "Isolation and amino-acid sequence of substance P from horse
intestine.";
RL Helv. Chim. Acta 56:860-866(1973).
RN [2]
RP SEQUENCE.
RC SPECIES=C.porcellus;
RX MEDLINE=90044685; PubMed=2478925;
RA Murphy R.;
RT "Primary amino acid sequence of guinea-pig substance P.";
RL Neuropeptides 14:105-110(1989).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; A01558; SPHO.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD RES 11 11
SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;
Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PQ 2

DB 4 PQ 5
RESULT 56
FIFI_SARBU
ID FIFI_SARBU STANDARD; PRT; 12 AA.
AC P83349;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FIFamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
protein-coupled FMRFamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;
Query Match 33.3%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PQ 2
DB 3 PQ 4
RESULT 57
FRE1_LITIN
ID FRE1_LITIN STANDARD; PRT; 12 AA.
AC P82021;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Frenatin 1.
OS Litoria infraenata (Giant tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=61195;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=97368637; PubMed=9225251;
RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "The structures of the frenatin peptides from the skin secretion of
the giant tree frog Litoria infraenata.";
RL J. Pept. Sci. 2:117-124(1996).
CC -!- FUNCTION: Wide spectrum antimicrobial peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral
glands.
CC -!- MASS SPECTROMETRY: MW=1140; METHOD=FAB.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1141 MW; CG22550BC365B72D CRC64;

Query Match 33.3%; Score 2; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6
 DB 6 LS 7

RESULT 58

HCY1_CARMA
 ID HCY1_CARMA STANDARD; PRT; 12 AA.
 AC P83176;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hemocyanin subunit 1 (Fragment).
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubranchyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph; PubMed=2620501;
 RX MEDLINE=90151075; Sierdema S.J., Beintema J.J.;
 RA Neuteboom B., Sierdema S.J., Beintema J.J.;
 RT "The relationship between N-terminal sequences and immunological
 characterization of crustacean hemocyanins.";
 RL Comp. Biochem. Physiol. 94B:587-592(1989).
 CC -!- FUNCTION: Hemocyanins are copper-containing oxygen carriers
 occurring freely dissolved in the hemolymph of many mollusks and
 arthropods.
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: Hemolymph.
 CC -!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
 SUBFAMILY.
 CC PIR: C60529; C60529.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0016970; F:hemocyanin; IDA.
 DR GO: GO:0015671; P:oxygen transport; TAS.
 KW Transport; Oxygen transport; Copper; Hemolymph.
 FT NON TER 12 12
 SQ SEQUENCE 12 AA; 1237 MW; 89936F6E2B5A2D5 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4
 DB 5 SV 6

RESULT 59

PPK4_PERFU
 ID PPK4_PERFU STANDARD; PRT; 12 AA.
 AC P82630;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-4 (PEF-PK-4) (YXPKL-amide).
 OS Periplaneta fuliginosa (Smokybrown cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattellidae; Periplaneta.
 OX NCBI_TaxID=36977;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;

RT "Tagma-specific distribution of FXPRlamides in the nervous system of
 the American cockroach.";
 RT J. Comp. Neurol. 419:352-363(2000).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 (MYOTROPIC ACTIVITY).
 CC -!- MASS SPECTROMETRY: MW=1437.9; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; FALSE NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 12 12
 SQ SEQUENCE 12 AA; 1439 MW; F9B53049FF42CAA1 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6
 DB 3 LS 4

RESULT 60

TM2A_METMA
 ID TM2A_METMA STANDARD; PRT; 12 AA.
 AC P80652;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit
 (EC 2.1.1.86) (N5-methyltetrahydromethanopterin-coenzyme M
 methyltransferase 28 kDa subunit) (Fragment).
 DE Methanosarcina mazei (Methanosarcina frisia).
 OS Methanosarcina mazei (Methanosarcina frisia).
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2209;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
 RX MEDLINE=96370840; PubMed=8774736;
 RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;
 RT "Sodium ion translocation by N5-methyltetrahydromethanopterin:
 coenzyme M methyltransferase from Methanosarcina mazei Go1
 reconstituted in ether lipid liposomes.";
 RL Eur. J. Biochem. 239:857-864(1996).
 CC -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN
 METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND
 TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-
 TETRAHYDROMETHANOPTERIN.
 CC -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
 mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
 (methylthio)ethanesulfonate.
 CC -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 KW Transferase; Methyltransferase; Transmembrane; Methanogenesis.
 FT NON TER 12 12
 SQ SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D768 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
 DB 7 VL 8

RESULT 61

V25K_WSSV
 ID V25K_WSSV STANDARD; PRT; 12 AA.
 AC P82004;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

```

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 25 kDa structural polyprotein (Fragment).
OS White spot syndrome virus (WSNV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE.
RC STRAIN=South Carolina;
RX MEDLINE=20214217; PubMed=10752552;
RA Wang Q., Poulos B.T., Lightner D.V.;
RT "Protein analysis of geographic isolates of shrimp white spot syndrome virus.";
RL Arch. Virol. 145:263-274(2000).
CC -!- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1283 MW; C5409AD9ECB731A9 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LS 6
Db 3 LS 4

RESULT 62
ID BOML_PSEGU STANDARD; PRT; 13 AA.
AC P42991;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Bombesin-like peptide I (PG-L).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Saimaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erpamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
DR PIR; A60409.
DR InterPro; IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 13 13 AMIDATION.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1372 MW; D6DE0D24BD98C366 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQ 2
Db 5 PQ 6

RESULT 63
CHEP_PARID

```

```

ID CHEP_PARID STANDARD; PRT; 13 AA.
AC P42718;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Chemotactic peptide.
OS Parapolybia indica.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Vespoidea;
OC Vespidae; Polistinae; Parapolybia.
OX NCBI_TaxID=31921;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Toki T., Yasuhara T., Nakajima T.;
RT "Isolation and sequential analysis of peptides on the venom sac of
RT Parapolybia indica.";
RL Eisei Dobutsu 39:105-111(1988).
KW Chemotaxis; Amidation.
MOD_RES 13 13 AMIDATION.
FT SEQUENCE 13 AA; 1298 MW; 5C950CE8E39D5873 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LS 6
Db 12 LS 13

RESULT 64
CRBL_VESMA STANDARD; PRT; 13 AA.
ID CRBL_VESMA STANDARD; PRT; 13 AA.
AC P17232;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vespid chemotactic peptide M (VESCP-M).
OS Vespa mandarinia (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7446;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,
RA Fujino M.;
RL (in) Muneke E. (eds.);
RL Peptide chemistry 1983, pp.185-190, Protein Research Foundation,
RL Osaka (1984).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD_RES 13 13 AMIDATION.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1384 MW; 2650402B9DF92338 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LS 6
Db 9 LS 10

RESULT 65
FIBB_RABIT STANDARD; PRT; 13 AA.
ID FIBB_RABIT STANDARD; PRT; 13 AA.
AC P14478;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)

```

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
 GN FGB.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1789-1791(1965).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 DR InterPro: IPR002181; Fibrinogen C.
 DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
 KW Blood coagulation; Plasma; Sulfation.
 FT PEPTIDE 1 13 FIBRINOPEPTIDE B.
 FT MOD RES 4 4 SULFATION.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1493 MW; 9417F3B76337CB1A CRC64;

 Query Match 33.3%; Score 2; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 VL 5
 DB 8 VL 9

 RESULT 66
 HPAL RANES STANDARD; PRT; 13 AA.
 ID F32415;
 AC F32415;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hemolytic protein A1 (Fragment).
 OS Rana esculenta (Edible frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8401;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90198965; PubMed=2317508;
 RA Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,
 RA Barra D., Bossa F.;
 RT "Purification and characterization of bioactive peptides from skin
 RT extracts of Rana esculenta.";
 RL Biochim. Biophys. Acta 1033:318-323(1990).
 CC -!- FUNCTION: Shows hemolytic activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR; S09018.
 KW Amphibian defense peptide; Amidation; Hemolysis.
 FT MOD_RES 13 13
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1390 MW; C6BA76B9DFE587D CRC64;

 Query Match 33.3%; Score 2; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 5 LS 6

DB 9 LS 10

 RESULT 67
 IDHC_PIG STANDARD; PRT; 13 AA.
 ID P20304;
 AC P20304;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Isocitrate dehydrogenase [NADP] cytoplasmic (EC 1.1.1.42)
 DE (Oxalosuccinate decarboxylase) (IDH) (NADP+-specific IDH) (IDP)
 DE (Fragment).
 GN IDH1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=87308293; PubMed=2887570;
 RA Bailey J.M., Colman R.F.;
 RT "Isolation of the glutamyl peptide labeled by the nucleotide analogue
 RT 2-(4-bromo-2,3-dioxobutylthio)-1,N(6)-ethenoadenosine
 RT 2',5'-biphosphate in the active site of NADP+-specific isocitrate
 RT dehydrogenase.";
 RL J. Biol. Chem. 262:12614-12619(1987).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=87308292; PubMed=3624273;
 RA Ehrlich R.S., Colman R.F.;
 RT "Characterization of an active site peptide modified by the substrate
 RT analogue 3-bromo-2-ketoglutarate on a single chain of dimeric NADP+-
 RT dependent isocitrate dehydrogenase.";
 RL J. Biol. Chem. 262:12614-12619(1987).
 CC -!- CATALYTIC ACTIVITY: Isocitrate + NADP(+) = 2-oxoglutarate + CO(2)
 CC + NADPH.
 CC -!- SUBUNIT: Homodimer.
 DR InterPro: IPR001804; IsoDH.
 DR PROSITE; PS00470; IDH IMDH; PARTIAL.
 KW Oxidoreductase; NADP; Tricarboxylic acid cycle.
 FT NON_TER 1 1
 FT ACT_SITE 5 5 POTENTIAL.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1353 MW; 1B640F0B9F7C71E0 CRC64;

 Query Match 33.3%; Score 2; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 5 LS 6
 DB 9 LS 10

 RESULT 68
 LMAL LOCM1 STANDARD; PRT; 13 AA.
 ID P38436;
 AC P38436;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Lcm-AG-myotropin I (Accessory gland myotropin I).
 DE Locusta migratoria (Migratory locust).
 OS Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE AND SYNTHESIS.
 RC TISSUE=Male accessory gland;
 RX MEDLINE=91271087; PubMed=2052501;

```

RA Paemen L., Tips A., Schoofs L., Proost P., van Damme J., de Loof A.;
RT "Lcm-Ag-myotropin: a novel myotropic peptide from the male accessory
RL Glands of Locusta migratoria."
CC -!- FUNCTION: THE EXACT PHYSIOLOGICAL FUNCTION IS STILL UNKNOWN. THIS
CC MYOTROPIC PEPTIDE IS ACTIVE ON THE OVIDUCT AND, TO A LESSER
CC EXTENT, ON THE HINDGUT. TRANSFERRED FROM THE MALE TO THE FEMALE
CC DURING COPULATION.
CC -!- TISSUE SPECIFICITY: MALE ACCESSORY GLANDS.
KW Neuroptera; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1368 MW; DE1ACAF482EB72D CRC64;

Query Match 33.3%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.4e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

Qy 5 LS 6
Db 7 LS 8

RESULT 69
NEUT_RANTE STANDARD; PRT; 13 AA.
ID NEUT_RANTE
AC P41536;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurotensin (NT).
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.

RA MEDLINE=92245104; PubMed=1574601;
RX Shaw C., McKay D.M., Halton D.W., Thim L., Buchanan K.D.;
RT "Isolation and primary structure of an amphibian neurotensin."
RL Regul. Pept. 38:23-31(1992).
CC -!- FUNCTION: Smooth muscle-contracting peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: IDENTIFIED IN BRAIN, INTESTINE, AND RECTUM,
CC BUT NOT IN STOMACH OR SKIN.
CC -!- SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.
DR PIR; A61067; A61067.
KW Vasoactive; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1569 MW; 56A53D69EF410DD3 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.4e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

Qy 2 QS 3
Db 1 QS 2

RESULT 70
PEDI_HYDAT STANDARD; PRT; 13 AA.
ID PEDI_HYDAT
AC P80578;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pedin.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;
RN [1]
RP SEQUENCE.

```

```

RX MEDLINE=96232307; PubMed=8674432;
RA Hoffmeister S.A.H.;
RT "Isolation and characterization of two new morphogenetically active
RL peptides from Hydra vulgaris."
RL Development 122:1941-1948(1996).
CC -!- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT
CC DEVELOPMENT.
KW Morphogen.
SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

Query Match 33.3%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.4e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

Qy 4 VL 5
Db 7 VL 8

RESULT 71
SAZA_ONCMY STANDARD; PRT; 13 AA.
ID SAZA_ONCMY
AC P82238;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Salmocidin 2A (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Serum;
RA Henry M.A., Secombes C.J.;
RT "Purification and partial characterization of antibacterial peptides
RT from rainbow trout, Oncorhynchus mykiss."
RL Submitted (DEC-1999) to the SWISS-PROT data bank.
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE BACTERIA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma serum.
KW Antibiotic.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1416 MW; 5FFB792AFC645873 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.4e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

Qy 4 VL 5
Db 4 VL 5

RESULT 72
SAZB_ONCMY STANDARD; PRT; 13 AA.
ID SAZB_ONCMY
AC P82239;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Salmocidin 2B (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Serum;
RA Henry M.A., Secombes C.J.;
RT "Purification and partial characterization of antibacterial peptides

```

```

RT from rainbow trout, Oncorhynchus mykiss."
RL Submitted (DEC-1999) to the SWISS-PROT data bank.
CC -!- FUNCTION: Antibacterial activity against Gram-negative bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma serum.
KW Antibiotic.
FT NON TER 13
SQ SEQUENCE 13 AA; 1400 MW; 5FFB792AABE5873 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
Db 4 VL 5

RESULT 73
TIME RANTE STANDARD; PRT; 13 AA.
ID _VG16_BACSU STANDARD; PRT; 13 AA.
AC P56920;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin E.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria."
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1379 MW; 26503DFA79A92448 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
Db 1 VL 2

RESULT 74
UN12_CLOPA STANDARD; PRT; 13 AA.
ID _F81353;
AC P81353;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 12 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;

```

```

RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum WS."
RL Electrophoresis 19:802-806(1998).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.8, ITS MW IS: 42.7 kDa.
FT VARIANT 4 4 L->V.
FT VARIANT 5 5 Q->I.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1465 MW; 70AA9E98455D405B CRC64;

Query Match 33.3%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
Db 3 VL 4

RESULT 75
VG16_BACSU STANDARD; PRT; 13 AA.
ID _P80857;
AC P80857;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vegetative protein 16 (VEG16) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE.
RC STRAIN=168 / IS58;
RX MEDLINE=97443988; PubMed=9298659;
RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
RA Hecker M.;
RT "First steps from a two-dimensional protein index towards a response-
RT regulation map for Bacillus subtilis."
RL Electrophoresis 18:1451-1463(1997).
CC -!- CAUTION: Could not be found in the genome of B.subtilis 168.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1372 MW; 20FB27BDC9ECA2D7 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4
Db 8 SV 9

Search completed: November 25, 2003, 19:28:24
Job time : 3.19934 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 11.2674 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-26

Perfect score: 6

Sequence: 1 PQSVLS 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL.23.*

- 1: sp archae.*
- 2: sp bacteria.*
- 3: sp fungi.*
- 4: sp human.*
- 5: sp invertebrate.*
- 6: sp mammal.*
- 7: sp mhc.*
- 8: sp organelle.*
- 9: sp phase.*
- 10: sp plant.*
- 11: sp rodent.*
- 12: sp virus.*
- 13: sp vertebrate.*
- 14: sp unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	66.7	15	15 Q97090	Q97090 human immun
2	4	66.7	15	15 Q80362	Q80362 human immun
3	4	66.7	15	15 Q97098	Q97098 human immun
4	4	66.7	15	15 Q79359	Q79359 human immun
5	4	66.7	15	15 Q97092	Q97092 human immun
6	4	66.7	15	15 Q97094	Q97094 human immun
7	4	66.7	18	15 Q12692	Q12692 simian-huma
8	4	66.7	20	3 Q9UR76	Q9UR76 candida alb
9	3	50.0	8	4 Q9HCQ0	Q9HCQ0 homo sapien
10	3	50.0	8	12 Q83349	Q83349 murine coro
11	3	50.0	8	12 Q89498	Q89498 murine hepa
12	3	50.0	8	13 P87488	P87488 oncorhynch
13	3	50.0	9	4 Q9UCS8	Q9UCS8 homo sapien
14	3	50.0	9	6 Q8HZY2	Q8HZY2 canis famil
15	3	50.0	11	7 Q29831	Q29831 homo sapien
16	3	50.0	12	4 Q9NTR7	Q9NTR7 homo sapien

17	3	50.0	12	6 Q9TQY4	Q9TQY4 bos taurus
18	3	50.0	12	6 Q9MZS4	Q9MZS4 canis famil
19	3	50.0	13	2 Q8RS99	Q8RS99 uncultured
20	3	50.0	13	5 Q9U5J2	Q9U5J2 trypanosoma
21	3	50.0	13	12 Q9WMG5	Q9WMG5 sigma virus
22	3	50.0	14	4 P78359	P78359 homo sapien
23	3	50.0	14	11 Q9RI03	Q9RI03 rattus norv
24	3	50.0	15	7 Q9TNQ3	Q9TNQ3 homo sapien
25	3	50.0	15	11 Q05694	Q05694 mus musculu
26	3	50.0	15	16 Q9K8C3	Q9K8C3 bacillus ha
27	3	50.0	16	2 Q45663	Q45663 bacillus su
28	3	50.0	16	2 Q9P5C1	Q9P5C1 nitrosomona
29	3	50.0	16	2 P82597	P82597 bacillus sp
30	3	50.0	16	7 Q77922	Q77922 oreochromis
31	3	50.0	16	8 Q9T2Q6	Q9T2Q6 solanum tub
32	3	50.0	16	12 Q88250	Q88250 sendai viru
33	3	50.0	16	12 Q88249	Q88249 sendai viru
34	3	50.0	16	12 Q86966	Q86966 murine hepa
35	3	50.0	16	12 Q99154	Q99154 sendai viru
36	3	50.0	17	2 Q9R560	Q9R560 bacillus su
37	3	50.0	17	2 Q93UW3	Q93UW3 agrobacteri
38	3	50.0	17	5 Q9TWC6	Q9TWC6 dirofilaria
39	3	50.0	17	6 Q9TRW1	Q9TRW1 oryctolagus
40	3	50.0	17	10 Q8S8Y3	Q8S8Y3 lupinus arb
41	3	50.0	17	12 Q84098	Q84098 influenzavi
42	3	50.0	18	2 Q8L2T5	Q8L2T5 neisseria m
43	3	50.0	18	4 Q9POM3	Q9POM3 homo sapien
44	3	50.0	18	4 Q9UCF4	Q9UCF4 homo sapien
45	3	50.0	18	4 Q8N303	Q8N303 homo sapien
46	3	50.0	18	6 Q97773	Q97773 cercopithec
47	3	50.0	18	6 P79214	P79214 oryctolagus
48	3	50.0	18	6 Q9TR57	Q9TR57 sus scrofa
49	3	50.0	18	8 Q8HBE6	Q8HBE6 tectona gra
50	3	50.0	18	10 Q9S8I7	Q9S8I7 oryza sativ
51	3	50.0	18	10 Q9S8I8	Q9S8I8 oryza sativ
52	3	50.0	18	11 Q9WTF8	Q9WTF8 rattus norv
53	3	50.0	19	2 Q9RLU4	Q9RLU4 lactococcus
54	3	50.0	19	2 Q9R5M3	Q9R5M3 rhodococcus
55	3	50.0	19	4 Q9NP11	Q9NP11 homo sapien
56	3	50.0	19	11 Q62637	Q62637 rattus norv
57	3	50.0	19	12 Q69345	Q69345 human herpe
58	3	50.0	19	15 Q90RP8	Q90RP8 human immun
59	3	50.0	19	15 Q905G8	Q905G8 human immun
60	3	50.0	20	4 Q9NZ27	Q9NZ27 homo sapien
61	3	50.0	20	4 Q9NZ28	Q9NZ28 homo sapien
62	3	50.0	20	10 Q9S7J0	Q9S7J0 ananas como
63	3	50.0	20	10 Q41475	Q41475 solanum tub
64	3	50.0	20	10 Q9S965	Q9S965 ananas como
65	3	50.0	20	10 Q9S8M1	Q9S8M1 ananas como
66	3	50.0	20	10 Q9FPB8	Q9FPB8 arabidopsis
67	3	50.0	20	11 Q9QVH2	Q9QVH2 rattus sp.
68	3	50.0	20	16 Q8CYA3	Q8CYA3 streptococc
69	2	33.3	4	11 Q08433	Q08433 rattus sp.
70	2	33.3	7	8 Q9S945	Q9S945 saccharomyc
71	2	33.3	7	10 Q9CSB3	Q9CSB3 arabidopsis
72	2	33.3	7	13 Q8JJ20	Q8JJ20 gallus gall
73	2	33.3	7	13 Q42564	Q42564 fugu rubrip
74	2	33.3	7	15 Q8JB81	Q8JB81 human immun
75	2	33.3	8	2 Q45615	Q45615 bacillus su
76	2	33.3	8	2 Q9X3K1	Q9X3K1 prochloroco
77	2	33.3	8	2 Q56140	Q56140 streptococc
78	2	33.3	8	2 Q56246	Q56246 thermophili
79	2	33.3	8	2 Q56429	Q56429 thermus the
80	2	33.3	8	2 Q93SP2	Q93SP2 pseudomonas
81	2	33.3	8	2 Q45889	Q45889 clostridium
82	2	33.3	8	2 Q9R4M3	Q9R4M3 enterococcu
83	2	33.3	8	2 P87225	P87225 saccharomyc
84	2	33.3	8	3 Q9URB9	Q9URB9 saccharomyc
85	2	33.3	8	4 Q9UHK1	Q9UHK1 homo sapien
86	2	33.3	8	4 Q9Y4X6	Q9Y4X6 homo sapien
87	2	33.3	8	4 Q9H4D3	Q9H4D3 homo sapien
88	2	33.3	8	4 Q8IUB8	Q8IUB8 homo sapien
89	2	33.3	8	5 Q02032	Q02032 lytechinus

90 2 33.3 8 8 019957 019957 gossypium h
 91 2 33.3 8 8 0972Y3 0972Y3 begonia for
 92 2 33.3 8 8 019961 019961 gossypium d
 93 2 33.3 8 8 019958 019958 gossypium b
 94 2 33.3 8 8 094V82 094V82 varanus yuw
 95 2 33.3 8 8 0974Y2 0974Y2 asterina pe
 96 2 33.3 8 8 019960 019960 gossypium m
 97 2 33.3 8 8 097WN4 097WN4 begonia for
 98 2 33.3 8 8 094V82 094V82 varanus sal
 99 2 33.3 8 8 0972Y2 0972Y2 begonia tai
 100 2 33.3 8 8 019959 019959 gossypium t

ALIGNMENTS

RESULT 1
 Q97090 ID Q97090 PRELIMINARY; PRT; 15 AA.
 AC Q97090;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Gag polyprotein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LAI;
 RX MEDLINE=98184535; PubMed=9525623;
 RA Wei Q., Fultz P.N.;
 RT "Extensive diversification of human immunodeficiency virus type 1
 RT subtype B strains during dual infection of a chimpanzee that
 RT progressed to AIDS.";
 RL J. Virol. 72:3005-3017(1998).
 DR EMBL; U56889; AAC59299.1; -.
 DR InterPro; IPR000071; Retrovir_p17.
 DR Pfam; PF00540; Gag_p17; 1.
 KW AIDS; Core protein; Polyprotein.
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1577 MW; 5AC228686229C18E CRC64;
 Query Match 66.7%; Score 4; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
 ||||
 Db 6 SVLS 9

RESULT 2
 Q80362 ID Q80362 PRELIMINARY; PRT; 15 AA.
 AC Q80362;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Gag protein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UG266;
 RX MEDLINE=93371703; PubMed=8363755;
 RA Louwagie J.J., McCutchan F., Brennan T., Peeters M., Brennan T.,
 RA Sanders-Buell E., Eddy G., van der Groen G., Fransen K.,
 RA Gershy-Damet M., Deleys R., Burke D.;
 RT "Phylogenetic analysis of gag genes from seventy international HIV-1

RT isolates provides evidence for multiple genotypes.";
 RL AIDS 7:769-780(1993).
 DR EMBL; L11798; AAA45087.1; -.
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1533 MW; 43123AEAF229C18E CRC64;

Query Match 66.7%; Score 4; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
 ||||
 Db 6 SVLS 9

RESULT 3
 Q97098 ID Q97098 PRELIMINARY; PRT; 15 AA.
 AC Q97098;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Gag polyprotein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LAI;
 RX MEDLINE=98184535; PubMed=9525623;
 RA Wei Q., Fultz P.N.;
 RT "Extensive diversification of human immunodeficiency virus type 1
 RT subtype B strains during dual infection of a chimpanzee that
 RT progressed to AIDS.";
 RL J. Virol. 72:3005-3017(1998).
 DR EMBL; U56897; AAC59307.1; -.
 DR InterPro; IPR000071; Retrovir_p17.
 DR Pfam; PF00540; Gag_p17; 1.
 KW AIDS; Core protein; Polyprotein.
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1487 MW; 5AC22868622AA49A CRC64;

Query Match 66.7%; Score 4; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
 ||||
 Db 6 SVLS 9

RESULT 4
 Q79359 ID Q79359 PRELIMINARY; PRT; 15 AA.
 AC Q79359;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Gag protein (Gag polyprotein) (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K7;
 RX MEDLINE=93371703; PubMed=8363755;
 RA Louwagie J.J., McCutchan F., Brennan T., Peeters M., Brennan T.,
 RA Sanders-Buell E., Eddy G., van der Groen G., Fransen K.,
 RA Gershy-Damet M., Deleys R., Burke D.;
 RT "Phylogenetic analysis of gag genes from seventy international HIV-1
 RT isolates provides evidence for multiple genotypes.";

```
RL AIDS 7:769-780(1993).
DR EMBL: L11772; AAA44692.2; -.
DR InterPro: IPR000071; Retrovir_pl7.
DR Pfam: PF00540; Gag_pl7; 1.
KW AIDS; Core protein; Polyprotein.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1604 MW; 5AC22874122AA49A CRC64;

Query Match
Best Local Similarity 66.7%; Score 4; DB 15; Length 15;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db ||||
6 SVLS 9

RESULT 5
Q97092 ID Q97092 PRELIMINARY; PRT; 15 AA.
AC Q97092;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag polyprotein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LAI;
RX MEDLINE=98184535; PubMed=9525623;
RA Wei Q., Fultz P.N.;
RT "Extensive diversification of human immunodeficiency virus type 1
RT subtype B strains during dual infection of a chimpanzee that
RT progressed to AIDS";
RL J. Virol. 72:3005-3017(1998).
DR EMBL: U56891; AAC59301.1; -.
KW Polyprotein.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1616 MW; 5AC228686227909A CRC64;

Query Match
Best Local Similarity 66.7%; Score 4; DB 15; Length 15;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db ||||
6 SVLS 9

RESULT 6
Q97094 ID Q97094 PRELIMINARY; PRT; 15 AA.
AC Q97094;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag polyprotein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LAI;
RX MEDLINE=98184535; PubMed=9525623;
RA Wei Q., Fultz P.N.;
RT "Extensive diversification of human immunodeficiency virus type 1
RT subtype B strains during dual infection of a chimpanzee that
RT progressed to AIDS";
RL J. Virol. 72:3005-3017(1998).

RL AIDS 7:769-780(1993).
DR EMBL: L11772; AAA44692.2; -.
DR InterPro: IPR000071; Retrovir_pl7.
DR Pfam: PF00540; Gag_pl7; 1.
KW AIDS; Core protein; Polyprotein.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1604 MW; 5AC22874122AA49A CRC64;

Query Match
Best Local Similarity 66.7%; Score 4; DB 15; Length 15;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db ||||
6 SVLS 9

RESULT 7
Q12692 ID Q12692 PRELIMINARY; PRT; 18 AA.
AC Q12692;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag polyprotein (Fragment).
GN GAG.
OS Simian-Human immunodeficiency virus.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=57667;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SHIVku1;
RX MEDLINE=97312452; PubMed=9168893;
RA Stephens E.B., Mukherjee S., Sami M., Zhuge W., Raghavan R.,
RA Singh D.K., Leung K.K., Atkinson R.B., Li Z., Joag S.V., Liu Z.Q.,
RA Narayan O.;
RT "A cell-free stock of simian-human immunodeficiency virus that causes
RT AIDS in pig-tailed macaques has a limited number of amino acid
RT substitutions in both SIVmac and HIV-1 regions of the genome and has
RT offered cytopathism.";
RL Virology 231:313-321(1997).
DR EMBL: U89249; AAC57878.1; -.
DR InterPro: IPR000071; Retrovir_pl7.
DR Pfam: PF00540; Gag_pl7; 1.
KW AIDS; Core protein; Polyprotein.
FT NON_TER 18
SQ SEQUENCE 18 AA; 1961 MW; E0647725D22E62EB CRC64;

Query Match
Best Local Similarity 100.0%; Score 4; DB 15; Length 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db ||||
6 SVLS 9

RESULT 8
Q9UR76 ID Q9UR76 PRELIMINARY; PRT; 20 AA.
AC Q9UR76;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE N-acetylglucosaminidase A (Fragment).
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE.
RX MEDLINE=94356217; PubMed=8075797;
RA Molloy C., Cannon R.D., Sullivan P.A., Shepherd M.G.;
RT "Purification and characterization of two forms of N-
```

RT acetylglucosaminidase from *Candida albicans* showing widely different
 RT outer chain glycosylation."
 RL Microbiology 140:1543-1553(1994).
 SQ SEQUENCE 20 AA; 2178 MW; DA602087EDDB4D47 CRC64;

Query Match 66.7%; Score 4; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POSV 4
 ||||
 DB 9 POSV 12

RESULT 9

Q9HCQ0 PRELIMINARY; PRT; 8 AA.
 ID Q9HCQ0;
 AC Q9HCQ0;
 DT 01-NOV-2001 (TrEMBLrel. 16, Created)
 DT 01-NOV-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Phosphodiesterase 10A7 (PDE10A7) (Fragment).
 GN HSPDE10A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20453115; PubMed=10998054;
 RA Fujishige K., Kozera J., Yuasa K., Omori K.;
 RT "The human phosphodiesterase PDE10A gene. Genomic organization and
 RT evolutionary relatedness with other PDEs containing GAP domains."
 RL Eur. J. Biochem. 267:5943-5951(2000).
 DR EMBL; AB041779; BAB16368.1; -.
 FT NON TER
 SQ SEQUENCE 8 AA; 966 MW; FD4B19D5A6C76446 CRC64;

Query Match 50.0%; Score 3; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POS 3
 ||||
 DB 3 POS 5

RESULT 10

Q83349 PRELIMINARY; PRT; 8 AA.
 ID Q83349;
 AC Q83349;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 0.8 kDa protein.
 OS Murine coronavirus MHV (strain A59).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus.
 OX NCBI_TaxID=11142;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A59;
 RX MEDLINE=89299451; PubMed=2545027;
 RA Pachuk C.J., Bredenbeek P.J., Zoltick P.W., Spaan W.J., Weiss S.R.;
 RT "Molecular cloning of the gene encoding the putative polymerase of
 RT mouse hepatitis coronavirus, strain A59."
 RL Virology 171:141-148(1989).
 DR EMBL; M27198; AAA74010.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 8 AA; 787 MW; ECB732C7287DC766 CRC64;

Query Match 50.0%; Score 3; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POS 3
 ||||
 DB 3 POS 5

RESULT 11

Q89498 PRELIMINARY; PRT; 8 AA.
 ID Q89498;
 AC Q89498;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE CORONAVIRUS proviral defective INTERFERING PARTICLE (DLSE) OBTAINED
 DE AFTER SERIAL PASSAGE 17, with 2 recombination sites and ORFs (DLSE).
 OS Murine hepatitis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus.
 OX NCBI_TaxID=11138;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89020822; PubMed=2845661;
 RA Makino S., Shieh C.K., Soe L.H., Baker S.C., Lai M.M.;
 RT "Primary structure and translation of a defective interfering RNA of
 RT murine coronavirus."
 RL Virology 166:550-560(1988).
 DR EMBL; M23258; AAA91862.1; -.
 FT NON TER
 SQ SEQUENCE 8 AA; 815 MW; ECB732C72862D766 CRC64;

Query Match 50.0%; Score 3; DB 12; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
 ||||
 DB 6 VLS 8

RESULT 12

P87488 PRELIMINARY; PRT; 8 AA.
 ID P87488;
 AC P87488;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Growth hormone 2 (Fragment).
 GN GH-2-A OR GH-2-B.
 OS Oncorhynchus kisutch (Coho salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8019;
 RN [1]
 RP SEQUENCE OF 41-48 FROM N.A.
 RX MEDLINE=94173883; PubMed=8127856;
 RA Forbes S.H., Knudsen K.L., North T.W., Allendorf F.W.;
 RT "One of two growth hormone genes in coho salmon is sex-linked."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:1628-1631(1994).
 DR EMBL; U04930; AAD13472.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE FROM N.A.
 RA Forbes S.H., Knudsen K.L., North T.W., Allendorf F.W.;
 RL Proc. Natl. Acad. Sci. U.S.A. 91:0-0(0).
 DR EMBL; U04930; AAD13472.1; -.
 DR EMBL; U04931; AAD13476.1; -.

```

FT  NON_TER      1      1
FT  NON_TER      8      8
SQ  SEQUENCE      8 AA;  902 MW;  92233732D5A5B326 CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 13; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 SVL 5
Db  4 SVL 6

RESULT 13
Q9UCS8
ID  Q9UCS8      PRELIMINARY;      PRT;      9 AA.
AC  Q9UCS8;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Apolipoprotein A-I (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]_TaxID=9606;
RP  SEQUENCE.
RX  MEDLINE=92075698; PubMed=1742316;
RA  Ehnholm C., Bozas S.E., Tenkanen H., Kirszbaum L., Metso J.,
RA  Murphy B., Walker I.D.;
RT  "The apolipoprotein A-I binding protein of placenta and the SP-40,40
RT  protein of human blood are different proteins which both bind to
RT  apolipoprotein A-I.";
RL  Biochim. Biophys. Acta 1086:255-260(1991).
FT  NON_TER      1
FT  NON_TER      9
SQ  SEQUENCE      9 AA;  981 MW;  7FE37775A6C7776B CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 4; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 POS 3
Db  4 POS 6

RESULT 14
Q8HZY2
ID  Q8HZY2      PRELIMINARY;      PRT;      9 AA.
AC  Q8HZY2;
DT  01-MAR-2003 (TrEMBLrel. 23, Created)
DT  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Leptin (Fragment).
GN  LEP.
OS  Canis familiaris (Dog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX  NCBI_TaxID=9615;
RN  [1]_TaxID=9615;
RP  SEQUENCE FROM N.A.
RA  Kansaku N., Toda M.;
RT  "PCR cloning of the dog leptin gene.";
RL  Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AB097078; BAC41247.1; -.
FT  NON_TER      1
FT  NON_TER      9
SQ  SEQUENCE      9 AA;  945 MW;  8088A2D5A6C1A1F5 CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 6; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FT  NON_TER      1
FT  NON_TER      8
SQ  SEQUENCE      8 AA;  902 MW;  92233732D5A5B326 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 SVL 5
Db  4 SVL 6

RESULT 15
Q29831
ID  Q29831      PRELIMINARY;      PRT;      11 AA.
AC  Q29831;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  Gene fragment encoding human histocompatibility antigen HLA-DR alpha
DE  (exon 2).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]_TaxID=9606;
RP  SEQUENCE FROM N.A.
RX  MEDLINE=83169718; PubMed=6403940;
RA  Das H.K., Biro P.A., Cohen S.N., Erlich H.A., von Gabain A.,
RA  Lawrence S.K., Lemaux P.G., McDevitt H.O., Peterlin B.M., Schulz M.P.,
RA  Sood A.K., Weissman S.M.;
RT  "Use of synthetic oligonucleotide probes complementary to genes for
RT  human HLA-DR alpha and beta as extension primers for the isolation of
RT  5' specific clones.";
RL  Proc. Natl. Acad. Sci. U.S.A. 80:1531-1535(1983).
DR  EMBL; V00525; CAA23784.1; -.
SQ  SEQUENCE      11 AA;  1230 MW;  9378714E0865B1EA CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 7; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 VLS 6
Db  9 VLS 11

RESULT 16
Q9NTR7
ID  Q9NTR7      PRELIMINARY;      PRT;      12 AA.
AC  Q9NTR7;
DT  01-OCT-2000 (TrEMBLrel. 15, Created)
DT  01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT  01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE  DJ78N10.1 (Eyes absent (Drosophila) homolog 4) (Fragment).
GN  EYA4.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]_TaxID=9606;
RP  SEQUENCE FROM N.A.
RA  Dunn M.;
RT  Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AL121959; CAB92069.1; -.
FT  NON_TER      12
FT  NON_TER      12
SQ  SEQUENCE      12 AA;  1394 MW;  C15EA7952D472AB6 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 QSV 4
Db  10 QSV 12

RESULT 17
Q9TQY4

```

ID Q9TQV4 PRELIMINARY; PRT; 12 AA.
AC Q9TQV4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Glycoprotein H-8 N-TERMINAL, GPH-B N-TERMINAL=KEX2/subtilisin-related protease (Fragment).
DE Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SQ MEDLINE=91340701; PubMed=1874725;
RP Christie D.L., Batchelor D.C., Palmer D.J.;
RA "Identification of kex2-related proteases in chromaffin granules by partial amino acid sequence analysis."
RL J. Biol. Chem. 266:15679-15683(1991).
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1303 MW; 9F2FF9E2782DC5BA CRC64;

Query Match 50.0%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
Db 1 SVL 3

RESULT 18

Q9WZS4
ID Q9WZS4 PRELIMINARY; PRT; 12 AA.
AC Q9WZS4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
SQ SEQUENCE FROM N.A.
RA Lantinga-van Leeuwen I.S., Mol J.A.;
RP "Cloning and characterization of the 5'-flanking region of the canine growth hormone gene."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF166119; AAF89582.1; -.
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1229 MW; 2B597268ECB45417 CRC64;

Query Match 50.0%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
Db 8 SVL 10

RESULT 19

Q8RSQ9
ID Q8RSQ9 PRELIMINARY; PRT; 13 AA.
AC Q8RSQ9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 1.4 kDa protein.
OS uncultured bacterium.

OG Plasmid pB4.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP SEQUENCE FROM N.A.
RA Tauch A.;
RT "The IncP beta plasmid pB4 encodes a tripartite antibiotic efflux system of the RND-MFP-OEP type conferring erythromycin and roxithromycin resistance in Pseudomonas sp. B13."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ431260; CAD24397.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 13 AA; 1359 MW; D1535C038748A33D CRC64;

Query Match 50.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
Db 2 SVL 4

RESULT 20

Q9U5J2
ID Q9U5J2 PRELIMINARY; PRT; 13 AA.
AC Q9U5J2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE GPI-phospholipase C (Fragment).
GN GPI-PLC.
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STEAIN=ILTarl;
RA Webb H.D., Gaud A.F., Carrington M.;
RT "The trypanosoma brucei GPI-PLC gene is not linked to functionally related genes or to genes showing the same developmentally regulated expression."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250727; CAB60093.1; -.
DR InterPro; IPR003633; Varsurf_glyc_PPLC.
DR Pfam; PF03490; Varsurf_PPLC; 1.
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1541 MW; 535AA96B464CA373 CRC64;

Query Match 50.0%; Score 3; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQS 3
Db 9 PQS 11

RESULT 21

Q9MMG5
ID Q9MMG5 PRELIMINARY; PRT; 13 AA.
AC Q9MMG5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE 3 protein (Fragment).
GN GENE 3.
OS Sigma virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; unclassified Rhabdoviridae.
OX NCBI_TaxID=11301;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=93212481; PubMed=8384742;
 RA Teninges D., Bras F., Dzeleee S.;
 RT "Genome organization of the sigma rhabdovirus: six genes and a gene
 RT overlapp.";
 RL Virology 193:1018-1023(1993).
 DR EMBL; S57850; AAD40700.1; -.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1456 MW; 9AF4F3FDE75E32D5 CRC64;

Query Match 50.0%; Score 3; DB 12; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVL 5
 Db 6 SVL 8

RESULT 22
 P78359 PRELIMINARY; PRT; 14 AA.
 ID F78359
 AC F78359;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE NF-kappa-B transcription factor p85 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Umbilical vein;
 RA Remacle J.E., Brys R., Pye S., Nelles L., Huylebroeck D.;
 RT "5' cDNA sequence RelA isolated from Human umbilical vein endothelial
 RT cells.";
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U88316; AAB48487.1; -.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1662 MW; 5E30458F8262F957 CRC64;

Query Match 50.0%; Score 3; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 POS 3
 Db 10 POS 12

RESULT 23
 Q9RIU3 PRELIMINARY; PRT; 14 AA.
 ID Q9RIU3
 AC Q9RIU3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE R-ras GTPase activating protein (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Iwashita S.;
 RT "5'-flanking region of R-ras GTPase activating protein.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021982; BAA01903.1; -.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1594 MW; 3C91E28A0C8E3E28 CRC64;

Query Match 50.0%; Score 3; DB 11; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 QSV 4
 Db 12 QSV 14

RESULT 24

Q9TNQ3 PRELIMINARY; PRT; 15 AA.
 ID Q9TNQ3;
 AC Q9TNQ3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Class II HLA DR5 ligand.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94164692; PubMed=8119729;
 RA Falk K., Rotzschke O., Stevanovic S., Jung G., Rammensee H.G.;
 RT "Pool sequencing of natural HLA-DR, DQ, and DP ligands reveals
 RT detailed peptide motifs, constraints of processing, and general
 RT rules.";
 RL Immunogenetics 39:230-242(1994).
 KW MHC.
 SQ SEQUENCE 15 AA; 1738 MW; 5C8F3CB934481042 CRC64;

Query Match 50.0%; Score 3; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
 Db 13 VLS 15

RESULT 25

Q05694 PRELIMINARY; PRT; 15 AA.
 ID Q05694
 AC Q05694;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Proline-rich protein (Fragment).
 GN MP6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=92020206; PubMed=1747160;
 RA Roberts S.G.E., Layfield R., McDonald C.J.;
 RT "The mouse proline-rich protein MP6 promoter binds isoprenaline-
 RT inducible parotid nuclear proteins via a highly conserved NFkB/rel-
 RT like site.";
 RL Nucleic Acids Res. 19:5205-5211(1991).
 DR EMBL; X61126; CAA43438.1; -.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1557 MW; C0FF9514A8F70BE4 CRC64;

Query Match 50.0%; Score 3; DB 11; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
 Db 12 VLS 14

```
RESULT 26
Q9K8C3
ID Q9K8C3 PRELIMINARY; PRT; 15 AA.
AC Q9K8C3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein BH3083.
GN BH3083.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=96665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hiram C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL: AP001517; BAB06802.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 15 AA; 1816 MW; 9044F141ED577A58 CRC64;

Query Match 50.0%; Score 3; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
DB 10 VLS 12

RESULT 27
Q45663
ID Q45663 PRELIMINARY; PRT; 16 AA.
AC Q45663;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE SacB levansucrase.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Marburg;
RX MEDLINE=8529507; PubMed=2993818;
RA Steinmetz M., Le Coq D., Aymerich S., Gonzy-Trebol G., Gay P.;
RT "The DNA sequence of the gene for the secreted Bacillus subtilis
RT enzyme levansucrase and its genetic control sites.";
RL Mol. Gen. Genet. 200:220-228(1985).
DR EMBL: X02730; CAA26512.1; -.
SQ SEQUENCE 16 AA; 1840 MW; E8CF83DC73713DA9 CRC64;

Query Match 50.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4
DB 5 QSV 7

RESULT 28
Q9R5C1
ID Q9R5C1 PRELIMINARY; PRT; 16 AA.
AC Q9R5C1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
```

```
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cytochrome C554 (Fragment).
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE.
RX MEDLINE=93224468; PubMed=8385668;
RA McTavish H., LaQuier F., Arciero D., Logan M., Mundfrom G.,
RA Fuchs J.A., Hooper A.B.;
RT "Multiple copies of genes coding for electron transport proteins in
RT the bacterium Nitrosomonas europaea.";
RL J. Bacteriol. 175:2445-2447(1993).
DR HSP; P02185; 111M.
SQ SEQUENCE 16 AA; 1895 MW; 8A4F5D240FB0B3F9 CRC64;

Query Match 50.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
DB 1 VLS 3

RESULT 29
P82597
ID P82597 PRELIMINARY; PRT; 16 AA.
AC P82597;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Thermostable monoacylglycerol lipase (MGLP) (24 kDa) (BC 3.1.1.23)
DE (Fragment).
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE.
RC STRAIN=H-257; PubMed=10731713;
RX MEDLINE=20198254; PubMed=10731713;
RA Inamura S., Kitaura S.;
RT "Purification and characterization of a monoacylglycerol lipase from
RT the moderately thermophilic Bacillus sp. H-257.";
RL J. Biochem. 127:419-425(2000).
CC -!- FUNCTION: HYDROLYZES MONOACYLGLYCEROLS, WITH THE HIGHEST ACTIVITY
CC OCCURRING WITH 1-MONOLAURYLGLYCEROL.
CC -!- ENZYME REGULATION: NOT INHIBITED BY CHOLATE, BUT SLIGHTLY
CC INHIBITED BY TRITON X-100 AND DEOXYCHOLATE.
CC -!- SUBUNIT: MONOMER.
CC -!- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 4.66. OPTIMUM
CC TEMPERATURE IS 75 DEGREES CELSIUS AND MAXIMUM ACTIVITY AT PH 6-8.
CC -!- MISCELLANEOUS: THIS LIPASE IS NOT SECRETED EXTRACELLULARLY AS
CC OTHER BACTERIAL LIPASES.
KW Hydrolase.
FT NON TER
SQ SEQUENCE 16 AA; 1787 MW; 900CF59289521D8F CRC64;

Query Match 50.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
DB 6 VLS 8

RESULT 30
O77922
ID O77922 PRELIMINARY; PRT; 16 AA.
AC O77922;
```

DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 16 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
 CC Cichlidae; Oreochromis.
 CX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sullmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050035; AAC41374.1; -.
 FT NON TER 1
 SQ SEQUENCE 16 AA; 1893 MW; A56619E46BAB5F2D CRC64;

 Query Match 50.0%; Score 3; DB 7; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 VLS 6
 DB |||||
 6 VLS 8

 RESULT 31
 Q9T2Q6 PRELIMINARY; PRT; 16 AA.
 AC Q9T2Q6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Cytochrome-C reductase 11 kDa subunit (BC 1.10.2.2) (Fragment).
 OS Solanum tuberosum (Potato).
 OG Mitochondrion.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; lamids; Solanales; Solanaceae; Solanum.
 CX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94198758; PubMed=7764624;
 RA Braun H.P., Kruff V., Schmitz U.K.;
 RL Planta 193:99-106(1994).
 SQ SEQUENCE 16 AA; 1904 MW; AFC237AE7549E2B5 CRC64;

 Query Match 50.0%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 SVL 5
 DB |||||
 7 SVL 9

 RESULT 32
 Q88250 PRELIMINARY; PRT; 16 AA.
 AC Q88250;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE F protein (Fragment).
 OS Sendai virus.
 CC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 CC Paramyxoviridae; Paramyxovirinae; Respirovirus.
 CX NCBI_TaxID=11191;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91012818; PubMed=2170692;
 RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;
 RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,
 RT TCs, which is sensitive to trypsin and chymotrypsin.";
 RL J. Virol. 64:5660-5664(1990).
 DR EMBL; M60152; AAA47808.1; -.
 FT NON TER 1
 FT NON TER 16
 SQ SEQUENCE 16 AA; 1648 MW; 049B529F01B29066 CRC64;

 Query Match 50.0%; Score 3; DB 12; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 PQS 3
 DB |||||
 6 PQS 8

 RESULT 33
 Q88249 PRELIMINARY; PRT; 16 AA.
 AC Q88249;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE F protein (Fragment).
 OS Sendai virus.
 CC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 CC Paramyxoviridae; Paramyxovirinae; Respirovirus.
 CX NCBI_TaxID=11191;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91012818; PubMed=2170692;
 RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;
 RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,
 RT TCs, which is sensitive to trypsin and chymotrypsin.";
 RL J. Virol. 64:5660-5664(1990).
 DR EMBL; M60154; AAA47807.1; -.
 FT NON TER 1
 FT NON TER 16
 SQ SEQUENCE 16 AA; 1649 MW; 049B529F01B298C4 CRC64;

 Query Match 50.0%; Score 3; DB 12; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 PQS 3
 DB |||||
 6 PQS 8

 RESULT 34
 Q86966 PRELIMINARY; PRT; 16 AA.
 AC Q86966;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE P28 (Fragment).
 GN ORF 1A.
 OS Murine hepatitis virus.
 CC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 CC Coronaviridae; Coronavirus.
 CX NCBI_TaxID=11138;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96078996; PubMed=7494259;
 RA Chen W., Batic R.S.;
 RT "Function of a 5'-end genomic RNA mutation that evolves during
 RT persistent mouse hepatitis virus infection in vitro.";


```

RL J. Virol. 69:7529-7540(1995).
DR EMBL; S80452; AAB35657.1; -.
FT NON TER 16
SQ SEQUENCE 16 AA; 1567 MW; 8B1AE80EB72E00CF CRC64;

Query Match 50.0%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
Db 14 VLS 16

RESULT 35
Q99154 ID Q99154 PRELIMINARY; PRT; 16 AA.
AC Q99154;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE F protein (Fragment).
OS Sendai virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Respirivirus.
OX NCBI_TaxID=11191;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91012818; PubMed=2170692;
RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,
RT TCs, which is sensitive to trypsin and chymotrypsin.";
RL J. Virol. 64:5660-5664(1990).
DR EMBL; M60153; AAA47806.1; -.
FT NON TER 1
FT NON TER 16
SQ SEQUENCE 16 AA; 1606 MW; 739B529F01B298D0 CRC64;

Query Match 50.0%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POS 3
Db 6 POS 8

RESULT 36
Q9R560 ID Q9R560 PRELIMINARY; PRT; 17 AA.
AC Q9R560;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE Menagiolin oxidase (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE.
RX MEDLINE=93356600; PubMed=8394685;
RA Lemna E., Schagger H., Kroger A.;
RT "The menagiolin oxidase of Bacillus subtilis W23.";
RL Arch. Microbiol. 159:574-578(1993).
SQ SEQUENCE 17 AA; 1750 MW; 87A251230A5831C3 CRC64;

Query Match 50.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
Db 5 SVL 7

RESULT 37
Q93UW3 ID Q93UW3 PRELIMINARY; PRT; 17 AA.
AC Q93UW3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RepA protein (Fragment).
OS Agrobacterium tumefaciens.
OG Plasmid pRiA4b.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=358;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A4;
RA Liang Y., Aoyama T., Oka A.;
RT "Organization of the conjugal transfer genes of the hairy-root-
RT inducing plasmid A4.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB050904; BAB47270.1; -.
FT NON TER 17
FT NON TER 17
SQ SEQUENCE 17 AA; 1655 MW; 4455CAD15C1A5520 CRC64;

Query Match 50.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
Db 4 SVL 6

RESULT 38
Q9TWC6 ID Q9TWC6 PRELIMINARY; PRT; 17 AA.
AC Q9TWC6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE 22L kDa excretory-secretory protein (Fragment).
OS Dirofilaria immitis (Canine heartworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Dirofilaria.
OX NCBI_TaxID=6287;
RN [1]
RP SEQUENCE.
RX MEDLINE=96258562; PubMed=8992320;
RA Frank G.R., Griewe R.B.;
RT "Purification and characterization of three larval excretory-secretory
RT proteins of Dirofilaria immitis.";
RL Mol. Biochem. Parasitol. 75:221-229(1996).
FT NON TER 1
FT NON TER 17
SQ SEQUENCE 17 AA; 2048 MW; 478557C5392B4AE7 CRC64;

Query Match 50.0%; Score 3; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POS 3
Db 2 POS 4

RESULT 39
Q9TRW1 ID Q9TRW1 PRELIMINARY; PRT; 17 AA.
AC Q9TRW1;

```

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
 DE CALDESMON=PHOSPHORYLATION site (fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91378498; PubMed=1898046;
 RA Ikebe M., Hornick T.;
 RT "Determination of the phosphorylation sites of smooth muscle caldesmon
 by protein kinase C";
 RL Arch. Biochem. Biophys. 288:538-542(1991).
 DR InterPro: IPR006018; Caldesmon_LSP.
 DR Pfam: PF02029; Caldesmon; 1.
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1889 MW; 77EACD3EB02F95F6 CRC64;
 Query Match 50.0%; Score 3; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QSV 4
 Db 6 QSV 8
 RESULT 40
 Q9S8Y3
 ID Q9S8Y3 PRELIMINARY; PRT; 17 AA.
 AC Q9S8Y3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
 DE L-asparaginase isoform A (EC 3.5.1.1) (Fragment).
 OS Lupinus arboreus (Tree lupine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
 OX NCBI_TaxID=3872;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=92344803; PubMed=1368361;
 RA Lough T.J., Chang K.S., Carne A., Monk B.C., Reynolds P.H.,
 RA Farnden K.J.;
 RL Phytochemistry 31:1519-1527(1992).
 SQ SEQUENCE 17 AA; 1703 MW; 9AEDD9691F7F0807 CRC64;
 Query Match 50.0%; Score 3; DB 10; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SVL 5
 Db 8 SVL 10
 RESULT 41
 Q84098
 ID Q84098 PRELIMINARY; PRT; 17 AA.
 AC Q84098;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Influenza A/fv/tosstock/34 (H7n1), matrix protein (Seg 7), 3' end of
 DE vrna (Initiator region for protein coding) (fragment).
 OS Influenzavirus A.
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses.
 OX NCBI_TaxID=197911;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80034428; PubMed=493121;
 RA Robertson J.S.;
 RT "5' and 3' terminal nucleotide sequences of the rna genome segments of
 RT influenza virus."; 6:3745-3757(1979).
 RL Nucleic Acids Res.
 DR EMBL; J02112; AAA43305.1; -.
 DR InterPro: IPR001561; Flu_M1.
 DR Pfam: PF00598; Flu_M1; 1.
 KW Matrix protein.
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1795 MW; COD59B0984ED10E1 CRC64;
 Query Match 50.0%; Score 3; DB 12; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VLS 6
 Db 11 VLS 13
 RESULT 42
 Q8L2T5
 ID Q8L2T5 PRELIMINARY; PRT; 18 AA.
 AC Q8L2T5;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Tryptophan transporter (Fragment).
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=128E;
 RX MEDLINE=22051050; PubMed=12055303;
 RA Zhu P., Klutch M.J., Bash M.C., Tsang R.S.W., Ng L.K., Tsai C.M.;
 RT "Genetic Diversity of Three Lgt Loci for Biosynthesis of
 RT Lipooligosaccharide (LOS) in Neisseria Species.";
 RL Microbiology 148:1833-1844(2002).
 DR EMBL; AF470685; AAM33537.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 18 AA; 1944 MW; 08DE06F3E9B8C27E CRC64;
 Query Match 50.0%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VLS 6
 Db 6 VLS 8
 RESULT 43
 Q9POM3
 ID Q9POM3 PRELIMINARY; PRT; 18 AA.
 AC Q9POM3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Polymyositis/scleroderma autoantigen 2 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bliskovsky V., Miller M., Mock B.;
 RT "Structure and localization of mouse PM-Scl genes.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF152839; AAF73199.1; -;
FT NON TER 18
SQ SEQUENCE 18 AA; 2025 MW; A1F292BC77872D67 CRC64;

Query Match 50.0%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
|||
Db 11 VLS 13

RESULT 44

Q9UCF4 PRELIMINARY; PRT; 18 AA.

AC Q9UCF4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE Chymotrypsinogen homolog (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93285747; PubMed=8509158;
RA Kim Y.J., Zhou Z., Hurtado J., Wood D.L., Choi A.S., Pescovitz M.D.,
RA Warfel K.A., Vandagriff J., Davis J.K., Kwon B.S.;
RT "IDDM patients' sera recognize a novel 30-kD pancreatic autoantigen
RT related to chymotrypsinogen.";
RL Immunol. Invest. 22:219-227(1993).
SQ SEQUENCE 18 AA; 1826 MW; 38105D1037CA6837 CRC64;

Query Match 50.0%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
|||
Db 9 VLS 11

RESULT 45

Q8N303 PRELIMINARY; PRT; 18 AA.

AC Q8N303;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029372; AAH29372.1; -;
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 18 AA; 2043 MW; 3D94B543DBE8825F CRC64;

Query Match 50.0%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
|||
Db 3 VLS 5

RESULT 46

O97773 PRELIMINARY; PRT; 18 AA.

AC O97773;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE Mibp protein (Fragment).
GN MIBP.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.

RA Bliskovsky V., Zajac K.M.;
RT "Evolutionary conservation of a 2 kilobase intronic sequence flanking
RT a tissue specific alternative exon in the mibp gene.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U89970; AAD00667.1; -;
FT NON TER 1
FT NON TER 18
SQ SEQUENCE 18 AA; 2069 MW; CA377C765ABEE28A CRC64;

Query Match 50.0%; Score 3; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 POS 3
|||
Db 11 POS 13

RESULT 47

P79214 PRELIMINARY; PRT; 18 AA.

AC P79214;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE CFTR protein.
GN CFTR.

OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97254985; PubMed=9100367;
RA Vuillaume S., Kaltenboeck B., Lecointre G., Lehn P., Denamur E.;
RT "Phylogenetic analysis of cystic fibrosis transmembrane conductance
RT regulator gene in mammalian species argues for the development of a
RT rabbit model for cystic fibrosis.";
RL Mol. Biol. Evol. 14:372-380(1997).
DR EMBL; X95931; CAA65172.1; -;
SQ SEQUENCE 18 AA; 2080 MW; 4D1C55056C1CE1B5 CRC64;

Query Match 50.0%; Score 3; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
|||
Db 11 VLS 13

RESULT 48

Q9TR57 PRELIMINARY; PRT; 18 AA.

ID Q9TR57
AC Q9TR57;

```

DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (T-EMBLrel. 14, Last annotation update)
DE Epoxide hydrolase (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=95377322; PubMed=7649186;
RA Arava Z., Hellman U., Hansson R.;
RT "Characterisation of taurochenodeoxycholic acid 6 alpha-hydroxylase
from pig liver microsomes.";
RL Eur. J. Biochem. 231:855-861(1995).
SQ SEQUENCE 18 AA; 2111 MW; 13A2F3440B64B187 CRC64;

Query Match 50.0%; Score 3; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
DB 8 SVL 10

RESULT 49
QHBE6 PRELIMINARY; PRT; 18 AA.
AC QHBE6;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 23, Last sequence update)
DE Putative NADH enzyme subunit (Fragment).
GN NDHA.
OS Tectona grandis.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Lamiales; Lamiaceae; Lamiaceae incertae sedis;
OC Tectona.
OX NCBI_TaxID=41396;
RN [1]
RP SEQUENCE FROM N.A.
RA Volkert H.A.;
RT "Range wide diversity in teak, Tectona grandis.";
RL Submitted (Oct-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ514411; CAD5822.1; -.
DR EMBL; AJ514412; CAD5823.1; -.
KW NAD; Chloroplast.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1873 MW; A18E687A89661B6F CRC64;

Query Match 50.0%; Score 3; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
DB 7 VLS 9

RESULT 50
QHS17 PRELIMINARY; PRT; 18 AA.
AC QHS17;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE 40 kDa PI 8.5 ABCISSIC acid-induced histidine rich protein
(Fragment).
OS Oryza sativa (Rice).

```

```

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RX MEDLINE=95175599; PubMed=7870812;
RA Moons A., Bauw G., Prinsen E., Van Montagu M., Van der Straeten D.;
RT "Molecular and physiological responses to abscisic acid and salts in
RT roots of salt-sensitive and salt-tolerant Indica rice varieties.";
RL Plant Physiol. 107:177-186(1995).
DR Gramene; Q9S817; -.
SQ SEQUENCE 18 AA; 2094 MW; 0CD245DB237E7520 CRC64;

Query Match 50.0%; Score 3; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
DB 12 SVL 14

RESULT 51
Q9S18 PRELIMINARY; PRT; 18 AA.
AC Q9S18;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE 40 kDa PI 8.5 ABCISSIC acid-induced protein (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RX MEDLINE=95175599; PubMed=7870812;
RA Moons A., Bauw G., Prinsen E., Van Montagu M., Van der Straeten D.;
RT "Molecular and physiological responses to abscisic acid and salts in
RT roots of salt-sensitive and salt-tolerant Indica rice varieties.";
RL Plant Physiol. 107:177-186(1995).
DR Gramene; Q9S818; -.
SQ SEQUENCE 18 AA; 2097 MW; 146450D9A97E6D83 CRC64;

Query Match 50.0%; Score 3; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
DB 12 SVL 14

RESULT 52
Q9WTP8 PRELIMINARY; PRT; 18 AA.
AC Q9WTP8;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (T-EMBLrel. 12, Last annotation update)
DE R-ras GTPase activating protein (Fragment).
GN R-RAS GAP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Iwashita S., Kobayashi M.;
RT "NGF-mediated downregulation of R-ras GAP expression.";

```

RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB020479; BAA78368.1; -;
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 2104 MW; 6BC3355FDC91E28A CRC64;

Query Match 50.0%; Score 3; DB 11; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4
 Db 12 QSV 14

RESULT 53
 Q9RLU4 PRELIMINARY; PRT; 19 AA.
 ID Q9RLU4
 AC Q9RLU4
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 15, Last annotation update)
 DE NISG protein (Fragment).
 DE NISG.
 GN Lactococcus lactis.
 OS Lactococcus lactis.
 OG Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1358;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N8; TRANSPOSON=Tn5481;
 RX MEDLINE=99452384; PubMed=10524753;
 RA Immonen T., Wahlstrom G., Takala T., Saris P.E.J.;
 FT "Evidence for a mosaic structure of the Tn5481 in Lactococcus lactis N8.";
 RT DNA Seq. 9:245-261 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N8; TRANSPOSON=Tn5481;
 RX MEDLINE=99452385; PubMed=10524754;
 RA Immonen T., Saris P.E.J.;
 FT "Characterization of the nisFEG operon of the nisin Z producing Lactococcus lactis subsp. lactis N8 strain.";
 RT DNA Seq. 9:263-274 (1998).
 RL EMBL; AJ000993; CAA04441.1; -;
 KW Plasmid.
 FT NON_TER 1
 SQ SEQUENCE 19 AA; 2139 MW; 6A429DC80E673613 CRC64;

Query Match 50.0%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
 Db 4 VLS 6

RESULT 54
 Q9R5M3 PRELIMINARY; PRT; 19 AA.
 ID Q9R5M3
 AC Q9R5M3
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Quinolone oxidoreductase 82 kDa subunit (Fragment).
 DE Rhodococcus.
 OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Nocardiaceae.
 OX NCBI_TaxID=1827;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92162192; PubMed=1789933;
 RA Peschke B., Lingens F.;

RT "Microbial metabolism of quinoline and related compounds. XII. Isolation and characterization of the quinoline oxidoreductase from Rhodococcus spec. B1 compared with the quinoline oxidoreductase from Pseudomonas putida 86.";
 RT Biol. Chem. Hoppe-Seyler 372:1081-1088 (1991).
 RL NON_TER 19
 SQ SEQUENCE 19 AA; 2057 MW; C21C630CDFB128E0 CRC64;

Query Match 50.0%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
 Db 17 SVL 19

RESULT 55
 Q9NP11 PRELIMINARY; PRT; 19 AA.
 ID Q9NP11
 AC Q9NP11
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Pyruvate dehydrogenase E1-alpha subunit (EC 1.2.4.1) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=89132585; PubMed=2537010;
 RA Endo H., Tomura H., Kagawa Y., Ohta S.;
 RT "Defective gene in lactic acidosis: abnormal pyruvate dehydrogenase E1 alpha-subunit caused by a frame shift.";
 RT Am. J. Hum. Genet. 44:358-364 (1989).
 RL EMBL; M2147; AAA31853.2; -;
 KW Oxidoreductase.
 FT NON_TER 19
 SQ SEQUENCE 19 AA; 2030 MW; 02984909538D3E94 CRC64;

Query Match 50.0%; Score 3; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
 Db 11 VLS 13

RESULT 56
 Q62637 PRELIMINARY; PRT; 19 AA.
 ID Q62637
 AC Q62637
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Xanthine dehydrogenase (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague Dawley;
 RX MEDLINE=94268906; PubMed=8208609;
 RA Chow C.-W., Clark M., Rinaldo J., Chalkley R.;
 RT "Identification of the Rat Xanthine Dehydrogenase/Oxidase Promoter.";
 RL Nucleic Acids Res. 22:1846-1854 (1994).
 DR EMBL; U08123; AAB60444.1; -;
 FT NON_TER 1
 FT VARIANT 19 H -> Q.

```

FT  NON TER      19      19
SQ  SEQUENCE 19 AA; 2128 MW; A02841D686P50139 CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 11; Length 19;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 QSV 4
Db  8 QSV 10

RESULT 57
Q69345
ID  Q69345 PRELIMINARY; PRT; 19 AA.
AC  Q69345;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  57 k protein (Fragment).
OS  Human herpesvirus 1.
OC  Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC  Alphaherpesvirinae; Simplexvirus.
OX  NCBI_TaxID=10298;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=86232558; PubMed=3012465;
RA  McGeoch D.J., Davison A.J.;
RT  "DNA sequence of the herpes simplex virus type 1 gene encoding
RT  glycoprotein gH, and identification of homologues in the genomes of
RT  varicella-zoster virus and Epstein-Barr virus.";
RL  Nucleic Acids Res. 14:4281-4292(1986).
DR  EMBL; X03896; CAA2735.1; -.
DR  InterPro; IPR004936; Herpes_UL21.
PF  Pfam; PF03252; UL21; 1.
FT  NON TER      1
SQ  SEQUENCE 19 AA; 2155 MW; D960532B4FACE79A CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 12; Length 19;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 QSV 4
Db  17 QSV 19

RESULT 58
Q90RF8
ID  Q90RF8 PRELIMINARY; PRT; 19 AA.
AC  Q90RF8;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE  Tat protein (Fragment).
GN  TAT.
OS  Human immunodeficiency virus 1.
OC  Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX  NCBI_TaxID=11676;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  STRAIN=97CG276;
RA  Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA  N'Doundou-N'Kodia M.-Y., Obengui, M'Pele P., Harada Y.,
RA  Hayami M., Ichimura H., Parra J.H.;
RT  "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT  Republic of Congo-Brazzaville.";
RL  Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF127550; AAK84913.1; -.
FT  NON TER      1
FT  NON TER      19
SQ  SEQUENCE 19 AA; 2304 MW; 2727D4B66ABE69237 CRC64;

FT  NON TER      19      19
SQ  SEQUENCE 19 AA; 2128 MW; A02841D686P50139 CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 11; Length 19;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 QSV 4
Db  8 QSV 10

RESULT 57
Q69345
ID  Q69345 PRELIMINARY; PRT; 19 AA.
AC  Q69345;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  57 k protein (Fragment).
OS  Human herpesvirus 1.
OC  Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC  Alphaherpesvirinae; Simplexvirus.
OX  NCBI_TaxID=10298;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=86232558; PubMed=3012465;
RA  McGeoch D.J., Davison A.J.;
RT  "DNA sequence of the herpes simplex virus type 1 gene encoding
RT  glycoprotein gH, and identification of homologues in the genomes of
RT  varicella-zoster virus and Epstein-Barr virus.";
RL  Nucleic Acids Res. 14:4281-4292(1986).
DR  EMBL; X03896; CAA2735.1; -.
DR  InterPro; IPR004936; Herpes_UL21.
PF  Pfam; PF03252; UL21; 1.
FT  NON TER      1
SQ  SEQUENCE 19 AA; 2155 MW; D960532B4FACE79A CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 12; Length 19;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 QSV 4
Db  17 QSV 19

RESULT 58
Q90RF8
ID  Q90RF8 PRELIMINARY; PRT; 19 AA.
AC  Q90RF8;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE  Tat protein (Fragment).
GN  TAT.
OS  Human immunodeficiency virus 1.
OC  Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX  NCBI_TaxID=11676;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  STRAIN=97CG276;
RA  Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA  N'Doundou-N'Kodia M.-Y., Obengui, M'Pele P., Harada Y.,
RA  Hayami M., Ichimura H., Parra J.H.;
RT  "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT  Republic of Congo-Brazzaville.";
RL  Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF127550; AAK84913.1; -.
FT  NON TER      1
FT  NON TER      19
SQ  SEQUENCE 19 AA; 2304 MW; 2727D4B66ABE69237 CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 15; Length 19;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 PQS 3
Db  7 PQS 9

RESULT 59
Q905G8
ID  Q905G8 PRELIMINARY; PRT; 19 AA.
AC  Q905G8;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE  Tat protein (Fragment).
OS  Human immunodeficiency virus 1.
OC  Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX  NCBI_TaxID=11676;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  STRAIN=97CG281;
RA  Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA  N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA  Ichimura H., Parra J.H.;
RT  "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT  Republic of Congo-Brazzaville.";
RL  Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF10447; AAL10254.1; -.
FT  NON TER      1
FT  NON TER      19
SQ  SEQUENCE 19 AA; 2366 MW; 367B64E194069237 CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 15; Length 19;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 PQS 3
Db  7 PQS 9

RESULT 60
Q9NZ27
ID  Q9NZ27 PRELIMINARY; PRT; 20 AA.
AC  Q9NZ27;
DT  01-OCT-2000 (TrEMBLrel. 15, Created)
DT  01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT  01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE  ATP7B (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  Wu Z.Y., Wang N., MuRong S.X., Lin M.T., Fang L.;
RA  Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RL  EMBL; AF220213; AAF67659.1; -.
FT  NON TER      1
FT  VARIANT      3
FT  NON TER      20
FT  NON TER      20
SQ  SEQUENCE 20 AA; 2365 MW; AAB07911D719FBF2 CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 4; Length 20;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  3 SVL 5
Db  6 SVL 8

```

09N728

Qy	3	SVL	5
Db	6	SVL	8

09S7J0

Query Match	50.0%;	Score 3;	DB 10;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 6.9e+03;		
Matches 3;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

RESULT 65

RESULT 63

Qy 3 SVL 5
|||
Db 6 SVL 8

596560
095965

Qy 1 PS 3
Db 2 PS 4

Q9S8M1
 ID Q9S8M1 PRELIMINARY; PRT; 20 AA.
 AC Q9S8M1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE COMOSAIN (Fragment).
 OS Ananas comosus (Pineapple).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Commelinidae incertae sedis;
 OC Bromeliaceae; Ananas.
 OC NCBI_TaxID=4615;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94330946; PubMed=8053898;
 RA Napper A.D., Bennett S.P., Borowski M., Holdridge M.B., Leonard M.J.,
 RA Rogers E.E., Duan Y., Laursen R.A., Reinhold B., Shames S.D.;
 RL Biochem. J. 301:727-735(1994).
 DR InterPro; IPR000668; Peptidase_C1.
 DR Pfam; PF00112; Peptidase_C1; 1.
 SQ SEQUENCE 20 AA; 2219 MW; 83A84A16232C3EBC CRC64;
 Query Match 50.0%; Score 3; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 POS 3
 Db |||
 2 POS 4
 RESULT 66
 Q9FPF8
 ID Q9FPF8 PRELIMINARY; PRT; 20 AA.
 AC Q9FPF8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Fl6G20.160.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chao Q., Brooks S., Chen H., Johnson-Hopson C., Khan S., Shinn P.,
 RA Ecker J.;
 RT "Full length cDNA sequence of Arabidopsis thaliana."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF325021; AAG40373.1; -
 SQ SEQUENCE 20 AA; 2231 MW; 5E30B3448A415CA4 CRC64;
 Query Match 50.0%; Score 3; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VLS 6
 Db |||
 3 VLS 5
 RESULT 67
 Q9QVH2
 ID Q9QVH2 PRELIMINARY; PRT; 20 AA.
 AC Q9QVH2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Chromogranin-B, CG8-GLUCAGONOMA peptide (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92063871; PubMed=1954895;
 RA Nielsen E., Welinder B.S., Madsen O.D.;
 RT "Chromogranin-B, a putative precursor of eight novel rat glucagonoma
 peptide through processing at mono-, di-, or tribasic residues.";
 RL Endocrinology 129:3147-3156(1991).
 DR InterPro; IPR001990; Granin.
 DR Pfam; PF01271; Granin; 1.
 FT NON_TER 1 1
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2549 MW; 9AA9A230D0FJ51A8 CRC64;
 Query Match 50.0%; Score 3; DB 11; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 POS 3
 Db |||
 2 POS 4
 RESULT 68
 Q8CYA3
 ID Q8CYA3 PRELIMINARY; PRT; 20 AA.
 AC Q8CYA3;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN SPRI755.
 OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=171101;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21429245; PubMed=11544234;
 RA Hoskins J., Aborn W.E. Jr., Arnold J., Blaszcak L.C., Burgatt S.,
 RA DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
 RA Gilmore R., Glass J.S., Khaja H., Kraft A.R., Lagace R.E.,
 RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
 RA McAhren S.M., McHenry M., McLeaster K., Mundy C.W., Nicas T.I.,
 RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
 RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
 RA Zook C.A., Baitz R.H., Jaskunas S.R., Rostek P.R. Jr., Skatrud P.L.,
 RA Glass J.I.;
 RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
 RL J. Bacteriol. 183:5709-5717(2001).
 DR EMBL; AE008540; AAL00558.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 20 AA; 2386 MW; 22FE65701CB2D21F CRC64;
 Query Match 50.0%; Score 3; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VLS 6
 Db |||
 5 VLS 7
 RESULT 69
 Q08433
 ID Q08433 PRELIMINARY; PRT; 4 AA.
 AC Q08433;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Bilirubin UDP-glucuronosyltransferase (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCB1_TaxID=10116;
RP SEQUENCE FROM N.A.

RC STRAIN=Gunn;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
DR EMBL; S38636; AAB19259.1; -.
KW Transferase.
FT NON TER 1
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 33.3%; Score 2; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
Db 2 VL 3

RESULT 70

Q95945 ID Q95945 PRELIMINARY; PRT; 7 AA.
AC Q95945;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Inside intron 5 (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
OX NCB1_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D273-110B;
RX MEDLINE=81069885; PubMed=6254986;
RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
RT "Assembly of the mitochondrial membrane system: Structure and
nucleotide sequence of the gene coding for subunit 1 of yeast
cytochrome oxidase.";
RL J. Biol. Chem. 255:11927-11941(1980).
DR EMBL; V00694; CAA24066.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 7 AA; 359 MW; 75B7232362CDC460 CRC64;

Query Match 33.3%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6
Db 6 LS 7

RESULT 71

Q9CSB3 ID Q9CSB3 PRELIMINARY; PRT; 7 AA.
AC Q9CSB3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 0.7 kDa protein (Fragment).
GN DIDI 10A-2B.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.

OX NCB1_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root;
RX MEDLINE=21171025; PubMed=11277426;
RA Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;
RT "Arabidopsis thaliana genes expressed in the early compatible
interaction with root-knot nematodes.";
RL Mol. Plant Microbe Interact. 14:288-299(2001).
DR EMBL; AJ286350; CAB71014.2; -.
KW Hypothetical protein.
FT NON TER 1
FT NON TER 7
SQ SEQUENCE 7 AA; 719 MW; 6732C7287EB325D0 CRC64;

Query Match 33.3%; Score 2; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
Db 6 VL 7

RESULT 72

Q8JU20 ID Q8JU20 PRELIMINARY; PRT; 7 AA.
AC Q8JU20;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Extracellular fatty acid binding protein (Fragment).
GN EXPABP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCB1_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Wang Q., Li N., Li H.;
RT "Cloning and sequencing of 3' UTR of EXPABP gene in chicken.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF487519; AAL96665.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 780 MW; 72CB1AB2D5BEBB70 CRC64;

Query Match 33.3%; Score 2; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4
Db 3 SV 4

RESULT 73

O42564 ID O42564 PRELIMINARY; PRT; 7 AA.
AC O42564;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN SCN8A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCB1_TaxID=31033;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=97424276; PubMed=9295353;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RL two-domain protein in fetal brain and non-neuronal cells.";
J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -.
KW Ionic channel.
FT NON TER
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 33.3%; Score 2; DB 13; Length 7;
Best Local Similarity 100.0%; Pred.No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LS 6
Db ||
6 LS 7

RESULT 74
Q8JE81
ID Q8JE81 PRELIMINARY; PRT; 7 AA.
AC Q8JE81;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Truncated pol protein (Fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4874;
RX MEDLINE=22056123; PubMed=12060770;
RA Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
Hoffmann D., Korn K., Selbig J.;
RT "Diversity and complexity of HIV-1 drug resistance: A bioinformatics
RL approach to predicting phenotype from genotype.";
Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
DR EMBL; AF347267; AAK32344.1; -.
FT NON TER
SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;

Query Match 33.3%; Score 2; DB 15; Length 7;
Best Local Similarity 100.0%; Pred.No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQ 2
Db ||
1 PQ 2

RESULT 75
Q45615
ID Q45615 PRELIMINARY; PRT; 8 AA.
AC Q45615;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GutB protein (Fragment).
GN GUTB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=94253000; PubMed=8195086;
RA Ye R., Wong S.L.;
RT "Transcriptional regulation of the Bacillus subtilis glucitol
dehydrogenase gene.";

RL J. Bacteriol. 176:3314-3320(1994).
DR EMBL; L16626; AAA20875.1; -.
FT NON TER
SQ SEQUENCE 8 AA; 927 MW; FD56C772D1A1F1A6 CRC64;

Query Match 33.3%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred.No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQ 2
Db ||
6 PQ 7

Search completed: November 25, 2003, 19:34:05
Job time : 12.2674 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 15.314 Seconds
(without alignments)
62.189 Million cell updates/sec

Title: US-09-641-801-26

Perfect score: 6

Sequence: 1 PQSVLS 6

Scoring table: OLIGO
Gapop 60.0 , Capext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	100.0	6	22	Colostrinin derive
2	6	100.0	6	22	Colostrinin peptid
3	6	100.0	6	22	Colostrinin peptid
4	6	100.0	6	22	Ewe colostrinin pe
5	6	100.0	6	23	Colostrinin consti
6	6	100.0	6	23	Colostrinin consti
7	6	100.0	6	23	Neural cell regula
8	6	100.0	18	15	Hypotensive polype
9	4	66.7	4	16	Ubiquitin peptide

10	4	66.7	4	20	AAW92324	E2A/pbx1 immunogen
11	4	66.7	5	20	AAW92323	E2A/pbx1 immunogen
12	4	66.7	5	23	AAU75881	SREBP2 SIP proteas
13	4	66.7	6	20	AAW92315	E2A/pbx1 immunogen
14	4	66.7	6	20	AAW82302	Transport peptide
15	4	66.7	8	15	AAW48270	Plasma membrane lo
16	4	66.7	8	20	AAW96368	Plasma membrane lo
17	4	66.7	8	21	AAU15693	HIV gag myristolat
18	4	66.7	8	21	AAW22848	HIV gag plasma mem
19	4	66.7	8	22	ABP12530	HIV A02 super moti
20	4	66.7	8	22	ABP12531	HIV A03 super moti
21	4	66.7	8	22	ABP14440	HIV A03 super moti
22	4	66.7	8	22	ABP15515	HIV A03 super moti
23	4	66.7	8	22	ABP15516	HIV A03 super moti
24	4	66.7	8	22	ABP20717	HIV A03 super moti
25	4	66.7	8	22	ABP22864	HIV A03 motif gag
26	4	66.7	8	23	ABG93003	Myristoylation org
27	4	66.7	8	24	ABP56598	HIV gag amino-term
28	4	66.7	9	15	AAW73717	Antigen fragment 3
29	4	66.7	9	20	AAW5463	HLA binding plu-1
30	4	66.7	9	20	AAW92321	E2A immunogenic pe
31	4	66.7	9	22	ABP14476	HIV A03 super moti
32	4	66.7	9	22	ABP17821	HIV B58 super moti
33	4	66.7	9	22	ABP17918	HIV B58 super moti
34	4	66.7	9	22	ABP20722	HIV B58 super moti
35	4	66.7	9	22	ABP22869	HIV A03 motif gag
36	4	66.7	9	22	AAW73123	HIV A11 motif gag
37	4	66.7	9	22	AAW73124	Tumour antigen pep
38	4	66.7	9	22	AAW73125	Tumour antigen pep
39	4	66.7	9	23	ABJ03400	Hepatitis B virus
40	4	66.7	9	23	AAU03453	Chlamydia pneumoniae
41	4	66.7	10	17	AAW90649	S. acidocaldarius
42	4	66.7	10	20	AAW82304	Transport peptide
43	4	66.7	10	22	AAW82304	HIV A01 super moti
44	4	66.7	10	22	ABP11686	HIV A02 super moti
45	4	66.7	10	22	ABP12769	HIV A02 super moti
46	4	66.7	10	22	ABP12770	HIV A02 super moti
47	4	66.7	10	22	ABP12771	HIV A02 super moti
48	4	66.7	10	22	ABP15694	HIV A02 super moti
49	4	66.7	10	22	ABP17825	HIV B58 super moti
50	4	66.7	10	22	ABP17919	HIV B58 super moti
51	4	66.7	10	22	ABP20530	HIV A03 motif gag
52	4	66.7	10	22	ABP20539	HIV A03 motif gag
53	4	66.7	10	22	ABP22863	HIV A03 motif gag
54	4	66.7	10	22	AAW99453	PRAME derived HLA-
55	4	66.7	10	22	AAW95614	Human complementar
56	4	66.7	10	22	AAW95616	Human complementar
57	4	66.7	10	22	AAW85693	Saccharomyces cere
58	4	66.7	10	24	ABJ19987	MHC binding peptid
59	4	66.7	10	24	ABJ19627	Neuronal nitric ox
60	4	66.7	11	16	AAW67271	Ubiquitin peptide
61	4	66.7	11	16	AAW67272	Ubiquitin peptide
62	4	66.7	11	21	AAW56247	Human secreted pro
63	4	66.7	11	22	ABP14552	HIV A03 super moti
64	4	66.7	11	22	ABP17201	HIV B27 super moti
65	4	66.7	11	22	ABP17202	HIV B27 super moti
66	4	66.7	11	22	ABP18788	HIV B62 super moti
67	4	66.7	12	20	AAW80388	Peptide eluted aft
68	4	66.7	12	21	AAW06328	Sterol-regulatory
69	4	66.7	12	23	ABG78536	Multiple sclerosis
70	4	66.7	13	6	AAW50842	Sequence (b) of a
71	4	66.7	13	20	AAW92320	E2A/pbx1 immunogen
72	4	66.7	13	22	AAW68083	Antitumour peptide
73	4	66.7	13	22	AAW68084	Antitumour peptide
74	4	66.7	13	22	AAW31919	Amino acid sequenc
75	4	66.7	13	22	AAW73149	Tumour antigen pep
76	4	66.7	13	22	AAW73150	Tumour antigen pep
77	4	66.7	13	22	AAW73151	Tumour antigen pep
78	4	66.7	13	23	AAU91248	Nucleic acid selec
79	4	66.7	13	23	AAU75880	SREBP2 SIP proteas
80	4	66.7	14	20	AAW36491	Fragment of human
81	4	66.7	14	20	AAW92316	E2A/pbx1 immunogen
82	4	66.7	14	20	AAW95267	Anti-progesterone

83 4 66.7 14 20 AAW95269 Anti-progesterone
84 4 66.7 14 21 AAY84226 Amino acid sequenc
85 4 66.7 14 22 AAM97129 Human peptide #404
86 4 66.7 14 23 ABP62326 Human immunopeptid
87 4 66.7 15 10 AAP90191 Antigenic peptide
88 4 66.7 15 14 AAR39526 Calmodulin inhibit
89 4 66.7 15 15 AAR48962 Truncated GAG. Sy
90 4 66.7 15 16 AAR80352 Protein polymeric
91 4 66.7 15 16 AAR80353 Protein polymeric
92 4 66.7 15 16 AAR80355 Protein polymeric
93 4 66.7 15 18 AAW25036 Ubiquitous nuclear
94 4 66.7 15 19 AAW49740 Glutamine donor pe
95 4 66.7 15 19 AAW54714 Peptide from HIV p
96 4 66.7 15 20 AAW95144 Phage peptide K5 b
97 4 66.7 15 20 AAW95125 Peptide K5 express
98 4 66.7 15 21 AAB07637 A human alpha-heli
99 4 66.7 15 22 ABP24574 HIV DR super motif
100 4 66.7 15 22 ABB56064 Vascular dementia-

ALIGNMENTS

RESULT 1

AAB72271
ID AAB72271 standard; peptide; 6 AA.

XX AC AAB72271;

XX DT 14-MAY-2001 (first entry)

XX DE Colostrinin derived cytokine inducing peptide SEQ ID 26.

XX KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.

XX OS Synthetic.

XX FN WO20011937-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 200OWO-US22818.

XX PR 17-AUG-1999; 99US-0149311.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PA (REGE-) REGEN THERAPEUTICS PLC.

XX PI Stanton GU, Hughes TK, Boldogh I, Georgiades J;

XX DR WPI; 2001-202804/20.

XX PT Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator -

XX PS Claim 1; Page 34; 50pp; English.

XX CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The
CC peptides have immune response modulatory activity, and are capable of
CC inducing cytokines. Colostrinin and its derived peptides are useful for
CC inducing cytokine production, for modulating an immunological response
CC and for inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 6; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQSVLS 6

Db 1 PQSVLS 6

RESULT 2

AAB72524
ID AAB72524 standard; Peptide; 6 AA.

XX AC AAB72524;

XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #25.

XX KW Dermatalogical; oxidative stress regulator; colostrinin.

XX OS Unidentified.

XX FN WO200112650-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 200OWO-US22665.

XX PR 17-AUG-1999; 99US-0149310.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Stanton GU, Hughes TK, Boldogh I;

XX DR WPI; 2001-218342/22.

XX PT Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -

XX PS Claim 6; Page 26; 48pp; English.

XX CC The present invention relates to a method for modulating the oxidative
XX stress level in a cell or a patient, comprising contacting the cell with,
XX or administering to the patient, an oxidative stress regulator selected
XX from colostrinin, or its constituent peptide (e.g. the present peptide),
XX to change the level of an oxidising species in the cell. The method can
XX be used to treat oxidative damage to skin, by decreasing or preventing an
XX increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 6; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQSVLS 6

Db 1 PQSVLS 6

RESULT 3

AAB72556
ID AAB72556 standard; Peptide; 6 AA.

XX AC AAB72556;

XX DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #25.
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrinum.
 XX Unidentified.
 OS
 XX WO200112651-A2.
 PN
 XX
 XX 22-FEB-2001.
 PD
 XX
 XX 17-AUG-2000; 2000WO-US22774.
 PF
 XX
 XX 17-AUG-1999; 99US-0149633.
 PR
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX
 XX Boldogh I;
 PI
 XX
 XX WPI; 2001-226545/23.
 DR
 XX
 XX Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating
 PT damaged neural cells in a patient -
 PT
 XX
 XX Claim 6; Page 21; 35pp; English.
 PS
 XX
 XX The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
 CC
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 6; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PQSVLS 6
 Db |||||
 1 PQSVLS 6
 RESULT 4
 AAE59335
 ID AAE59335 standard; Peptide; 6 AA.
 XX
 AC AAE59335;
 XX
 XX 21-MAR-2001 (first entry)
 DT
 XX
 DE Ewe colostrinin peptide fragment C-10.
 XX
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX
 XX Ovis sp.
 OS
 XX WO200075173-A2.
 PN
 XX
 XX 14-DEC-2000.
 PD
 XX
 XX 02-JUN-2000; 2000WO-GS02128.
 PF
 XX
 XX 02-JUN-1999; 99GB-0012852.
 PR
 XX
 XX (REGG-) REGEN THERAPEUTICS PLC.
 PA
 XX
 XX Georgiades JA;
 PI
 XX
 XX WPI; 2001-071058/08.
 DR
 XX
 XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX
 PS Claim 7; Page 27; 63pp; English.
 XX
 XX The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 6; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PQSVLS 6
 Db |||||
 1 PQSVLS 6
 RESULT 5
 AAE20253
 ID AAE20253 standard; peptide; 6 AA.
 XX
 AC AAE20253;
 XX
 XX 19-JUN-2002 (first entry)
 DT
 XX
 XX Colostrinin constituent peptide #25.
 DE
 XX
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnery.
 XX
 XX Unidentified.
 OS
 XX
 XX Key Location/Qualifiers
 FH Modified-site 6
 FT /note= "Optionally C-terminal amide"
 FT
 XX
 XX WO200213850-A1.
 PN
 XX
 XX 21-FEB-2002.
 PD
 XX
 XX 17-AUG-2000; 2000WO-US22776.
 PF
 XX
 XX 17-AUG-2000; 2000WO-US22776.
 PR
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX
 XX Stanton GJ, Hughes TK, Boldogh I;
 PI
 XX
 XX WPI; 2002-269151/31.
 DR
 XX
 XX Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog -
 PT
 XX
 XX Claim 6; Page 26; 51pp; English.
 PS
 XX
 XX The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 6; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQSVLS 6
 |||||
 Db 1 PQSVLS 6

RESULT 6
 AAM51060
 ID AAM51060 standard; Peptide; 6 AA.

XX AC AAM51060;

XX DT 30-MAY-2002 (first entry)

XX DE Colostrinin constituent peptide (casein amino acids 174-179).

XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;

XX KW blood cell regulator; cytokine inducer; beta-casein; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 6 /note= "optional C-terminal amidation"

XX PN WO200213849-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22775.

XX PR 17-AUG-2000; 2000WO-US22775.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PA (REGE-) REGEN THERAPEUTICS PLC.

XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX DR WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -

XX PS Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified
 CC as having a beta-casein homologue precursor, and corresponds to
 CC casein amino acids 174-179. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ
 CC or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 6; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQSVLS 6
 |||||
 Db 1 PQSVLS 6

RESULT 7

AAO14602

XX ID AAO14602 standard; peptide; 6 AA.

XX AC AAO14602;

XX DT 27-MAY-2002 (first entry)

XX DE Neural cell regulatory colostrinin peptide 25.

XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;

XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

XX KW neural cell treatment.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Modified-site 6 /note= "Optional C-terminal amide"

XX PN WO200213851-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22777.

XX PR 17-AUG-2000; 2000WO-US22777.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Boldogh I, Stanton JG, Hughes TK;

XX DR WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -

XX PS Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 6; DB 23; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POSVLS 6

Db 1 POSVLS 6

RESULT 8

AAR58332
ID AAR58332 standard; peptide; 18 AA.

XX AC AAR58332;

XX AC AAR58332;

DT 22-SEP-1994 (first entry)

XX DE Hypotensive polypeptide.

XX KW Hypotensive; antioxidative; calcium absorption; salt; food;

XX KW pharmaceuticals; physiologically active agents.

XX OS Lactobacillus helveticus.

XX PN JP06041191-A.

XX PD 15-FEB-1994.

XX PF 03-MAR-1993; 93JP-0043047.

XX PR 04-MAR-1992; 92JP-0047340.

XX PA (CALV) CALPIS SHOKUHIN KOGYO KK.

XX DR WPI; 1994-089332/11.

XX PT New polypeptide - used in physiologically active agents having
PT e.g. hypotensive antioxidative and calcium absorption promoting
PT activity

XX PS Claim 1-2; Page 8; 10pp; Japanese.

XX CC Sequences (AAR58319-341) are used in conjunction with
CC physiologically active agents showing a property such as
CC hypotensive activity, calcium absorption promoting activity and
CC antioxidative activity. The peptides are non-toxic and can be
CC used in physiologically active agents.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 6; DB 15; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POSVLS 6

Db 2 POSVLS 7

RESULT 9

AAR67270
ID AAR67270 standard; peptide; 4 AA.

XX AC AAR67270;

XX AC AAR67270;

XX DT 27-JUL-1995 (first entry)

XX DE Ubiquitin peptide extension, cRAS.

XX

KW Ubiquitin; peptide extension; assay; protein kinase; C-terminal;
KW Ha-RAS protein; farnesyl-protein transferase;
KW carboxy methyl transferase.

XX Synthetic.

XX PN US5366871-A.

XX PD 22-NOV-1994.

XX PF 13-NOV-1991; 91US-0791935.

XX PR 13-NOV-1991; 91US-0791935.

XX PA (UTAH) UNIV UTAH.

XX PI Rechsteiner MC, Yoo YJ;

XX DR WPI; 1995-005826/01.

XX PT Assay for enzymes that modify peptide chains - using a substrate
PT comprising a ubiquitin-peptide extension contg. a sequence
PT modified by the enzyme

XX PS Disclosure; Column 7; 14pp; English.

XX CC The sequences given in AAR67262-70 represent ubiquitin-peptide
CC extensions which are used in the method of the invention for
CC assaying enzymes that modify peptide chains. These sequences
CC represent extensions which are known to be modified in the presence
CC of an enzyme being assayed for, and the reaction mixture formed is
CC then analysed. This method may be used for assaying protein kinases
CC or enzymes which modify the C-terminal end of Ha-RAS protein, such
CC as farnesyl-protein transferase, or carboxy methyl transferase.

CC These peptides are less expensive to synthesise than standard
CC peptides used in these methods and they may be purified from
CC bacterial extracts by simple acid extraction.

XX SQ Sequence 4 AA;

Query Match 66.7%; Score 4; DB 16; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6

Db 1 SVLS 4

RESULT 10

AAW92324

ID AAW92324 standard; peptide; 4 AA.

XX AC AAW92324;

XX DT 09-APR-1999 (first entry)

XX DE E2A/pbx1 immunogenic fusion peptide #7.

XX KW E2A; pbx1; fusion protein; antigen; monoclonal antibody; diagnosis;
KW epitope; acute lymphoblastic leukemia.

XX OS Synthetic.

XX PN US5858682-A.

XX PD 12-JAN-1999.

XX PF 02-AUG-1996; 96US-0691997.

XX PR 02-AUG-1996; 96US-0691997.

XX PA (PHAR-) PHARMINGEN.

```

XX Gruenwald S, Monell C, Sang B;
XX WPI; 1999-119870/10.
XX Monoclonal antibody specific for E2A/pbx1 fusion protein - useful
XX for diagnosis of acute lymphoblastic leukemia
XX Claim 6; Column 27-28; 21pp; English.
XX This sequence represents a peptide used in a method for constructing
XX antigenic E2A/pbx1 fusion proteins used for raising monoclonal
XX antibodies which specifically bind with an E2A/pbx1 fusion epitope. This
XX peptide can be used for the diagnosis of acute lymphoblastic leukemia.
XX
SQ Sequence 4 AA;
    Query Match      66.7%; Score 4; DB 20; Length 4;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db |||||
   1 SVLS 4

RESULT 11
AAW92323
ID AAW92323 standard; peptide; 5 AA.
XX
AC AAW92323;
XX
DT 09-APR-1999 (first entry)
XX
DE E2A/pbx1 immunogenic fusion peptide #6.
XX
KW E2A; pbx1; fusion protein; antigen; monoclonal antibody; diagnosis;
KW epitope; acute lymphoblastic leukemia.
XX
OS Synthetic.
XX
PN US5858682-A.
XX
PD 12-JAN-1999.
XX
PF 02-AUG-1996; 96US-0691997.
XX
PR 02-AUG-1996; 96US-0691997.
XX
PA (PHAR-) PHARMINGEN.
XX
PI Gruenwald S, Monell C, Sang B;
XX
DR WPI; 1999-119870/10.
XX
PT Monoclonal antibody specific for E2A/pbx1 fusion protein - useful
PT for diagnosis of acute lymphoblastic leukemia
XX
XX Claim 5; Column 27-28; 21pp; English.
XX This sequence represents a peptide used in a method for constructing
XX antigenic E2A/pbx1 fusion proteins used for raising monoclonal
XX antibodies which specifically bind with an E2A/pbx1 fusion epitope. This
XX peptide can be used for the diagnosis of acute lymphoblastic leukemia.
XX
SQ Sequence 5 AA;
    Query Match      66.7%; Score 4; DB 20; Length 5;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db |||||
   1 SVLS 4

```

```

Db 2 SVLS 5

RESULT 12
AAU75881
ID AAU75881 standard; Protein; 5 AA.
XX
AC AAU75881;
XX
DT 08-MAY-2002 (first entry)
XX
DE SREBP2 S1P protease recognition sequence #2.
XX
KW Amyloid precursor protein; SREBP2-LacI fusion protein;
KW nontropic; neuroprotective; cardiant; antidiabetic; vasotropic;
KW proteolysis inhibition; transcription repressor; reporter gene;
KW transcriptional regulator; Notch-1; SREBP; neurological disease;
KW sterol regulatory element-binding protein; cardiac disease;
KW metabolic disease; Alzheimer's disease; diabetes; cardiovascular disease;
KW S1P protease recognition sequence.
XX
OS Cricetulus griseus.
OS Homo sapiens.
XX
PN US6333167-B1.
XX
PD 25-DEC-2001.
XX
PF 10-MAR-2000; 2000US-0522666.
XX
PR 10-MAR-2000; 2000US-0522666.
XX
PA (AMHP ) AMERICAN HOME PROD CORP.
XX
PI Quinet EM, Shuey DU;
XX
DR WPI, 2002-163178/21.
XX
PT Screening compounds for inhibition of proteolysis, useful for
PT identifying agents for treating e.g. Alzheimer's disease, comprises
PT using cells that express a transcription repressor in the presence of a
PT protease -
XX
PS Disclosure; Column 8; 48pp; English.
XX
XX The invention relates to screening compounds for the ability to inhibit
XX proteolysis of a substrate by using a recombinant eukaryotic cell
XX that expresses: (i) a chimaeric protein consisting of a transcription
XX repressor part and a protease recognition part; and (ii) a
XX reporter gene, linked to a transcriptional regulator sequence,
XX responsive to the transcription regulator. The method is used to identify
XX inhibitors of the proteolysis of membrane-associated polypeptides,
XX specifically amyloid precursor protein (APP), Notch-1 and sterol
XX regulatory element-binding proteins (SREBP). The inhibitors are
XX potentially useful in treatment of neurological, cardiac or metabolic
XX diseases, e.g. Alzheimer's disease, diabetes and cardiovascular disease.
XX The method is suitable for large scale screening and does not require
XX preliminary cloning of the target protease. The present sequence
XX represents an S1P protease recognition sequence as found in the
XX SREBP2-LacI (lac repressor) chimaeric fusion protein used
XX to demonstrate the method of the invention.
XX
SQ Sequence 5 AA;
    Query Match      66.7%; Score 4; DB 23; Length 5;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db |||||
   2 SVLS 5

```


RESULT 13
AAW92315
ID AAW92315 standard; peptide; 6 AA.
XX
AC AAW92315;
XX
DT 09-APR-1999 (first entry)
XX
XX E2A/pbx1 immunogenic fusion peptide #1.
DE
XX E2A; pbx1; fusion protein; antigen; monoclonal antibody; diagnosis;
KW epitope; acute lymphoblastic leukemia.
KW
XX Synthetic.
OS
XX US5858682-A.
PN
XX 12-JAN-1999.
PD
XX 02-AUG-1996; 96US-0691997.
PF
XX 02-AUG-1996; 96US-0691997.
PR
XX (PHAR-) PHARMINGEN.
PA
XX Gruenwald S, Monell C, Sang B;
PI
XX WPI; 1999-119870/10.
DR
XX Monoclonal antibody specific for E2A/pbx1 fusion protein - useful
PT for diagnosis of acute lymphoblastic leukemia
PT
XX Claim 1; Column 23-24; 21pp; English.
PS
XX This sequence represents a peptide used in a method for constructing
CC antigenic E2A/pbx1 fusion proteins used for raising monoclonal
CC antibodies which specifically bind with an E2A/pbx1 fusion epitope. This
CC peptide can be used for the diagnosis of acute lymphoblastic leukemia.
XX
SQ Sequence 6 AA;
Query Match 66.7%; Score 4; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SVLS 6
Db 3 SVLS 6

RESULT 14
AAW82302
ID AAW82302 standard; Peptide; 6 AA.
XX
AC AAW82302;
XX
DT 15-MAR-1999 (first entry)
XX
DE Transport peptide fragment.
XX
KW Targetting agent; Gastrointestinal tract; brain; drug delivery;
KW drug targetting; phage display; transport peptide.
KW
XX Synthetic.
OS
XX WO9851825-A1.
PN
XX 19-NOV-1998.
PD
XX 15-MAY-1998; 98WO-US10079.
PF
XX 15-MAY-1997; 97US-0857046.
PR
XX

PA (CYTO-) CYTOGEN CORP.
PA (ELAN-) ELAN CORP PLC.
XX
PI Alvarez VL, O'Mahony DJ, Seveso M;
XX
XX WPI; 1999-009778/01.
DR
XX New targetting agents enabling transport of active agents through
PT human/animal tissue, or their uptake - useful in the treatment and
PT prevention of diseases, especially of the gastro-intestinal tract
PT (GIT)
XX
XX Claim 7; Page 65; 83pp; English.
PS
XX This is a fragment of peptide 28.1 (see AAW82290), a peptide isolated
CC from a phage display library on the basis of its ability to enhance
CC transport of phage from the rat gastrointestinal tract (GIT) to
CC brain. Claimed transport or uptake targetting agents can include
CC this, or other, claimed peptide fragments (see AAW82300-10). Such
CC transport or targetting agents permit or facilitate the transport
CC of an active agent through a human or animal tissue such as GIT
CC lumen, or uptake of the active agent into the human or animal
CC tissue. The active agent is preferably a drug or drug-containing
CC nanoparticle or microparticle. Therapeutic methods of
CC administration, pharmaceutical compositions and formulations based
CC of the targetting peptides are also provided.
XX
SQ Sequence 6 AA;
Query Match 66.7%; Score 4; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 QSVL 5
Db 2 QSVL 5

RESULT 15
AAR48270
ID AAR48270 standard; peptide; 8 AA.
XX
AC AAR48270;
XX
DT 25-MAR-2003 (updated)
DT 29-JUL-1994 (first entry)
XX
XX Plasma membrane localised protein HIV gag N-terminal sequence.
XX
XX Single chain antibody; sFv; heavy chain; light chain; kappa;
KW variable domain; hydrophilic linker; antibodies; HIV; gag;
KW HTLV-III; subcellular localisation signal; plasma membrane;
KW retention signal.
XX
XX Human Immunodeficiency Virus.
OS
XX WO9402610-A1.
PN
XX 03-FEB-1994.
PD
XX 16-JUL-1993; 93WO-US06735.
PF
XX 17-JUL-1992; 92US-0916939.
PR
XX 17-MAR-1993; 93US-0045274.
PR
XX (DAND) DANA FARBER CANCER INST INC.
PA
XX Haseltine WA, Marasco WA;
PI
XX WPI; 1994-048868/06.
DR
XX Intracellular binding of antigens - by using antibody targetting
PT with vector system, for e.g. tumour suppression

XX Claim 34; Page 42; 155pp; English.

XX New vector systems comprise a sequence adapted for intracellular

CC delivery and expression contg. a promoter operably linked to an

CC antibody gene encoding an antibody which binds to a specific target

CC antigen. The antibody is esp. a single chain antibody in which the

CC heavy and light chain variable regions are joined via a hydrophilic

CC linker peptide. Localisation sequences are pref. included in the

CC constructs. The sequence AAR48270 is the known N-terminal sequence of

CC plasma membrane localised HIV gag protein and is a pref.

CC localisation sequence for the novel constructs.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 8 AA;

Query Match 66.7%; Score 4; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6

Db 5 SVLS 8

RESULT 16

AAW96368

ID AAW96368 standard; Peptide; 8 AA.

AC AAW96368;

XX

DT 19-JUL-1999 (first entry)

XX

DE Plasma membrane localisation signal peptide.

XX

KW Antibody; immune response; modulation; MHC; IRM; receptor;

KW intrabody; major histocompatibility complex; graft rejection;

KW immunomodulatory response molecule; regulation; transplantation;

KW retention signal; localisation signal; golgi apparatus; ER;

KW endoplasmic reticulum.

XX

OS Synthetic.

XX

PN WO9914353-A2.

XX

PD 25-MAR-1999.

XX

PF 18-SEP-1998; 98WO-US19563.

XX

PR 19-SEP-1997; 97US-0059339.

XX

PA (DAND) DANA FARBER CANCER INST INC.

XX

PI Marasco W, Mhashikar A;

XX

DR WPI; 1999-229546/19.

XX

PT Altering the regulation of the immune system

XX

PS Disclosure; Page 29; 56pp; English.

XX

CC Intracellular binding to a desired target by an intracellularly

CC expressed antibody (i.e. an intrabody) can be used to knock out

CC multiple locuses of immunomodulatory receptor molecules (IRMs),

CC so that the expression of multiple major histocompatibility (MHC)

CC molecules is blocked. This selective targeting of IRMs, their

CC pathways or components, can be used to selectively regulate the

CC immune system by controlling expression of these molecules and

CC preventing an undesired immune response in a cell. Any component

CC of the MHC pathway or the MHC assembly line or antigen presentation

CC can be targeted. Intrabodies can be used to knock out the immune

CC response in a particular tissue or portion of the body to prepare

CC it for cell or tissue transplantation. Alternatively, an organ for

CC transplantation can be perfused with the intrabody ex vivo. The

CC intrabodies can comprise whole antibodies, heavy chains, Fab'

CC fragments, single-chain antibodies and diabodies. The intrabodies

CC also comprise an intracellular localisation signal to facilitate

CC interception of expressed proteins. For example, if the target was

CC a cell surface receptor, the antibody would comprise a leader

CC sequence and an endoplasmic reticulum (ER) or Golgi apparatus

CC retention signal. This peptide is a localisation sequence for the

CC plasma membrane and is found in the HIV gag protein. For

CC other localisation sequences see AAW96345-W96377.

XX

SQ Sequence 8 AA;

Query Match 66.7%; Score 4; DB 20; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6

Db 5 SVLS 8

RESULT 17

AAB15693

ID AAB15693 standard; Peptide; 8 AA.

AC AAB15693;

XX

DT 08-JAN-2001 (first entry)

XX

DE HIV gag myristolation sequence.

XX

KW Human immunodeficiency virus; HIV; gag; myristolation sequence;

KW single-chain antibody; stabilon; stabilising fusion peptide; vaccine;

KW gene therapy; protein degradation modulation; protein stability;

KW Alzheimer's disease.

XX

OS Human immunodeficiency virus.

XX

PN WO200042185-A1.

XX

PD 20-JUL-2000.

XX

PF 11-JAN-2000; 2000WO-US00558.

XX

PR 11-JAN-1999; 99US-0115505.

XX

PA (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.

PA (MCIN/) MCINNIS P A.

XX

PI Chain DG;

XX

DR WPI; 2000-476059/41.

XX

PT Modulating degradability of protein or peptide useful for gene therapy

PT involving antibodies, comprises altering a gene at the N terminus to

PT render protein or peptide metabolically stable -

XX

PS Disclosure; Page 51; 76pp; English.

XX

CC The present sequence is the amino terminal myristolation sequence of

CC HIV gag. It may be used to direct stabilised single-chain antibodies

CC to the plasma membrane. The N-terminus of the single-chain antibody is

CC linked to a stabilising fusion peptide, referred to as a stabilon, which

CC increases stability of the antibody against proteolysis in vivo.

CC Degradation of the antibody may be modulated by linking the stabilon to

CC the antibody through a protease-sensitive linker region. The stabilon is

CC removed upon induction of expression of a specific restriction protease

CC by means of an inducible promoter, and this renders the antibody

CC susceptible to proteolysis by the N-end rule pathway. This method for

CC regulating protein stability allows removal of the antibody after it has

CC bound to its target antigen. Stabilised recombinant proteins may be used

CC in gene therapy for the treatment of disorders such as Alzheimer's

CC disease.
 XX Sequence 8 AA;
 SQ

Query Match 66.7%; Score 4; DB 21; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
 Db 5 SVLS 8
 |||||
 |||||

RESULT 18
 AAB22848
 ID AAB22848 standard; peptide; 8 AA.
 XX
 AC AAB22848;
 XX
 DT 10-JAN-2001 (first entry)
 XX
 DE HIV gag plasma membrane-targeting myristoylation sequence.
 XX
 KW Controlled release delivery system; drug targeting;
 KW drug-specific antibody; intracellular half-life; gene therapy;
 KW diabetes; autoimmune disease; inflammatory disease; infectious disease;
 KW cancer; side effect; subcellular localisation sequence.
 XX
 OS Human immunodeficiency virus.
 XX
 PN WO2000050089-A2.
 XX
 PD 31-AUG-2000.
 XX
 PF 25-FEB-2000; 2000WO-US04749.
 XX
 PR 26-FEB-1999; 99US-0122103.
 XX
 PA (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.
 XX
 PI Chain DG;
 XX
 DR WPI; 2000-572044/53.
 XX
 PT Delivering a drug, to a patient suffering from cancer or diabetes, at a
 PT predetermined site, comprises altering a target cell to express a drug
 PT specific antibody by gene therapy and administering the drug -
 XX
 XX Disclosure; Page 45; 69pp; English.
 XX
 CC The invention relates to a controlled release drug delivery system.
 CC Target cells in a patient are transformed with an expression construct
 CC encoding an antibody (particularly a single chain antibody) to the drug
 CC to be delivered. The antibody contains a modulator of intracellular
 CC half-life; this can either be a stabilising or destabilising residue
 CC located in the N-terminus after the initial methionine, or a peptide
 CC ("stabilon") containing a stabilising residue linked to the antibody
 CC N-terminus via a protease cleavage site. On administration of the drug,
 CC the antibody binds the drug, localising it at the target cells but
 CC maintaining it in an inactive state. As the antibody is degraded (the
 CC timescale for which is dependent upon the N-terminal or stabilon amino
 CC acids), the drug is released at its site of action where it can exert
 CC its effects. The antibody encoded by the expression construct (and
 CC therefore the therapeutic agent) can be targeted to particular
 CC subcellular locations (e.g., the nucleus) by including the appropriate
 CC cellular localisation signals. The novel method may be used to deliver
 CC therapeutic agents to patients with a variety of conditions such as
 CC diabetes, autoimmune diseases, inflammatory diseases, infectious
 CC diseases and especially cancer. The delivery method of the invention
 CC causes a drug to become almost immediately localised at its site of
 CC action in an inactive form where it accumulates. Once released by
 CC antibody degradation, the drug is at an effective concentration only at
 CC the target site, with very little free drug being available in the rest

CC of the body. The system of the invention therefore reduces the side
 CC effects caused by therapeutic agents, and also provides economic benefits
 CC as a smaller amount can be administered to the patient. Sequences
 CC AAB22835- AAB22837 and AAB22839-B22857 represent subcellular localisation
 CC sequences which can be incorporated into a drug-specific antibody used in
 CC the method of the invention.
 XX
 SQ Sequence 8 AA;
 Query Match 66.7%; Score 4; DB 21; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
 Db 5 SVLS 8
 |||||
 |||||

RESULT 19
 ABP12530
 ID ABP12530 standard; Peptide; 8 AA.
 XX
 AC ABP12530;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV A02 super motif gag peptide #1.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US27766.
 XX
 PR 05-OCT-1999; 99US-0412863.
 XX
 XX (EPIM-) EPIMMUNE INC.
 PA
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cellis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-354887/37.
 XX
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 PT
 PS Claim 32; Page 125; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABP125347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL) , and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.

XX SQ Sequence 8 AA;
 Query Match 66.7%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
 Db 1 SVLS 4

RESULT 20
 ABP12531
 ID ABP12531 standard; Peptide; 8 AA.
 XX AC ABP12531;
 XX DT 15-JUL-2002 (first entry)
 XX DE HIV A02 super motif gag peptide #2.
 XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX OS Human immunodeficiency virus type 1.
 XX PN WO200124810-A1.
 XX PD 12-APR-2001.
 XX PF 05-OCT-2000; 2000WO-US27766.
 XX PR 05-OCT-1999; 99US-0412863.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-354887/37.
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 PS Claim 32; Page 125; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.

XX SQ Sequence 8 AA;
 Query Match 66.7%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
 Db 1 SVLS 4

RESULT 21
 ABP14440
 ID ABP14440 standard; Peptide; 8 AA.
 XX AC ABP14440;
 XX DT 15-JUL-2002 (first entry)
 XX DE HIV A03 super motif gag peptide #2.
 XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX OS Human immunodeficiency virus type 1.
 XX PN WO200124810-A1.
 XX PD 12-APR-2001.
 XX PF 05-OCT-2000; 2000WO-US27766.
 XX PR 05-OCT-1999; 99US-0412863.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-354887/37.
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 PS Claim 32; Page 164; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.

XX SQ Sequence 8 AA;

Query Match 66.7%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
 Db 2 SVLS 5
 ||||

RESULT 22
 ABP15515
 ID ABP15515 standard; Peptide; 8 AA.

XX AC ABP15515;

XX DT 15-JUL-2002 (first entry)

XX DE HIV A24 super motif gag peptide #1.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -

XX PS Claim 32; Page 186; 448pp; English.

XX CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.

XX SQ Sequence 8 AA;

Query Match 66.7%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
 Db 1 SVLS 4
 ||||

RESULT 23

ABP15516
 ID ABP15516 standard; Peptide; 8 AA.

XX AC ABP15516;

XX DT 15-JUL-2002 (first entry)

XX DE HIV A24 super motif gag peptide #2.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -

XX PS Claim 32; Page 186; 448pp; English.

XX CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.

XX SQ Sequence 8 AA;

Query Match 66.7%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
 ||||

```

Db          1 SVLS 4

RESULT 24
ABP20717
ID ABP20717 standard; Peptide; 8 AA.
XX
AC
XX
DT
XX
DE
XX
DE HIV A03 motif gag peptide #380.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PD 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 294; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 8 AA;

Query Match 66.7%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
DB 2 SVLS 5

RESULT 26
ABG93003
ID ABG93003 standard; Peptide; 8 AA.

```

```

RESULT 25
ABP22864
ID ABP22864 standard; Peptide; 8 AA.
XX
AC ABP22864;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A11 motif gag peptide #243.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PD 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 337; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 8 AA;

Query Match 66.7%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
DB 2 SVLS 5

RESULT 26
ABG93003
ID ABG93003 standard; Peptide; 8 AA.

```


CC immunoglobulin molecules that regulate LDL and HDL metabolism; in skin
 CC biology applications; and in regulating or inhibiting keloid formation.
 CC AB222379 to AB222449 and ABP56536 to ABP56618 represent sequences used in
 CC the exemplification of the present invention.

XX Sequence 8 AA;

Query Match 66.7%; Score 4; DB 24; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
 Db 5 SVLS 8
 ||||
 ||||

RESULT 28
 AAR73717
 ID AAR73717 standard; peptide; 9 AA.

XX AAR73717;

DT 25-MAR-2003 (updated)

DT 15-JUN-1995 (first entry)

XX Antigen fragment 33, from HBV (a) has binding affinity for HLA-A2.1.
 XX antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
 KW MA6E-1; melanoma antigen-1; core antigen; surface antigen;
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
 KW diagnostic; MHC class I molecule; major histocompatibility complex;
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PIP; 8mer;
 KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
 KW herpes simplex virus; influenza A; M1.

XX Hepatitis B virus.

XX WO9420127-A1.

XX 15-SEP-1994.

XX 04-MAR-1994; 94WO-US02353.

XX 05-MAR-1993; 93US-0027146.

XX 04-JUN-1993; 93US-0073205.

XX 29-NOV-1993; 93US-0159184.

XX (CYTE-) CYTEL CORP.

XX Grey HM, Kast WM, Sette A, Sidney J;

XX WPI; 1994-302678/37.

XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
 PT for treatment or prophylaxis of cancer, virus infection or
 PT autoimmune diseases.

XX Disclosure; Page 81; 138pp; English.

XX AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using
 CC motifs disclosed in the invention, these peptides were screened for
 CC further motifs. Only peptides with binding affinity of at least 1%
 CC (binding affinity is expressed as an IC50 value) as compared to the
 CC standard peptide (AAR71293) in assays. This peptide from the HBV ENV(a)
 CC molecule has a binding value of 0.0580. The peptides of the
 CC invention can induce cytotoxic T lymphocytes which can react with
 CC target cells. They can be used for the treatment or prophylaxis of
 CC cancer, eg. prostate cancer or lymphoma, etc.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 9 AA;

Query Match 66.7%; Score 4; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQSV 4
 Db 6 PQSV 9
 ||||
 ||||

RESULT 29

AAV55463

ID AAV55463 standard; peptide; 9 AA.

XX AAV55463;

DT 17-JAN-2000 (first entry)

XX HLA binding plu-1 peptide.

XX Human; cancer-associated polypeptide; plu-1; ovarian cancer; vaccine;
 KW breast cancer; immune response; cytotoxic T lymphocyte; imaging agent;
 KW therapeutic; plu-1 antigen; breast tumor; tumor antigen; epitope.

XX Synthetic.

XX Homo sapiens.

XX WO9949034-A1.

XX 30-SEP-1999.

XX 19-MAR-1999; 99WO-GB00866.

XX 20-MAR-1998; 98GB-0005877.

XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.

XX Taylor-papadimitriou J;

XX WPI; 1999-591090/50.

XX New nucleic acid encoding the cancer-associated polypeptide plu-1, for
 PT diagnosis, treatment and prevention of cancer, especially of breast and
 PT ovary -

XX Example 2; Fig 12; 173pp; English.

XX The invention relates to a human cancer-associated polypeptide plu-1.
 CC The plu-1 polypeptide can be recombinantly expressed by standard
 CC recombinant methodology. Detection of the plu-1 nucleic acid or the
 CC polypeptide is used for the following: (i) diagnosis (including imaging)
 CC and prognosis of, and determination of susceptibility to, cancer,
 CC specifically ovarian or breast cancer; and (ii) treating cancer (by
 CC inducing an immune response against cancer cells, e.g. as a vaccine, or
 CC by antisense inhibition). Antigens derived from the polypeptide are used
 CC to generate activated cytotoxic T lymphocytes, or dendritic cells, for
 CC subsequent return to the patient for treatment of cancer. The polypeptide
 CC may also be used to identify inhibitors of plu-1 activity. Fragments of
 CC the polypeptide, and antibodies raised against plu-1, are useful as assay
 CC and imaging agents, also therapeutically (to induce an anti-idiotype
 CC response or where conjugated to cytotoxic agents). The plu-1 antigen is
 CC expressed more commonly in breast tumors than some known tumor antigens.
 CC Sequences AAV55320-629 represent predicted peptides from the plu-1
 CC polypeptide which may bind to the human class I alleles B27, A2, A3 and
 CC A11.

XX Sequence 9 AA;

Query Match 66.7%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSVL 5


```

Db          |||||
            4 QSVL 7

RESULT 30
AAW92321
ID AAW92321 standard; peptide; 9 AA.
XX AC AAW92321;
XX
XX
DT 09-APR-1999 (first entry)
XX
DE E2A immunogenic peptide.
XX
XX E2A; pbx1; fusion protein; antigen; monoclonal antibody; diagnosis;
KW epitope; acute lymphoblastic leukemia.
XX
OS Synthetic.
XX
PN US5858682-A.
XX
XX 12-JAN-1999.
PD
XX
XX 02-AUG-1996; 96US-0691997.
XX
XX 02-AUG-1996; 96US-0691997.
XX
XX (PHAR-) PHARMINGEN.
XX
XX Gruenwald S, Monell C, Sang B;
XX
XX WPI; 1999-119870/10.
DR
XX
XX Monoclonal antibody specific for E2A/pbx1 fusion protein - useful
PT for diagnosis of acute lymphoblastic leukemia
PT
XX
XX Example 2; Column 25-26; 21pp; English.
PS
XX
XX This sequence represents a peptide used in a method for constructing
CC antigenic E2A/pbx1 fusion proteins used for raising monoclonal
CC antibodies which specifically bind with an E2A/pbx1 fusion epitope. This
CC peptide can be used for the diagnosis of acute lymphoblastic leukemia.
XX
XX
SQ Sequence 9 AA;
Query Match 66.7%; Score 4; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db |||||
4 SVLS 7

RESULT 31
ABP14476
ID ABP14476 standard; Peptide; 9 AA.
XX
XX AC ABP14476;
XX
XX 15-JUL-2002 (first entry)
XX
DE HIV A03 super motif gag peptide #38.
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
XX Human immunodeficiency virus type 1.
OS
XX WO200124810-A1.
XX
XX 12-APR-2001.
PD

```

```

XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
XX (EPIW-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HW;
XX
XX WPI; 2001-354887/37.
XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
PT
PS Claim 32; Page 165; 448pp; English.
XX
XX The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 9 AA;
Query Match 66.7%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db |||||
3 SVLS 6

RESULT 32
ABP17821
ID ABP17821 standard; Peptide; 9 AA.
XX
XX AC ABP17821;
XX
XX 15-JUL-2002 (first entry)
XX
XX HIV B58 super motif gag peptide #40.
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
XX Human immunodeficiency virus type 1.
OS
XX WO200124810-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US27766.
XX

```

```

PR 05-OCT-1999; 99US-0412863.
XX (EPIM-) EPIMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX WPI; 2001-354887/37.
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1 -
XX
XX Claim 32; Page 234; 448pp; English.
XX
XX The present invention describes a composition (I) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (ABL25347 to
XX ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX may be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumour-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines.
XX An additional advantage of an group-based vaccine approach is the ability
XX to combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP1501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention.
XX
XX Query Match 66.7%; Score 4; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db ||||
2 SVLS 5

RESULT 33
ABP17918
XX ABP17918 standard; Peptide; 9 AA.
XX
XX ABP17918;
XX
XX 15-JUL-2002 (first entry)
XX
XX HIV B58 super motif gag peptide #137.
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; virucide.
XX
XX Human immunodeficiency virus type 1.
XX
XX WO200124810-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US27766.
XX
XX 05-OCT-1999; 99US-0412863.
XX (EPIM-) EPIMUNE INC.
XX

```

```

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX WPI; 2001-354887/37.
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1 -
XX
XX Claim 32; Page 236; 448pp; English.
XX
XX The present invention describes a composition (I) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (ABL25347 to
XX ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX may be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumour-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines.
XX An additional advantage of an group-based vaccine approach is the ability
XX to combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP1501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention.
XX
XX Query Match 66.7%; Score 4; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db ||||
2 SVLS 5

RESULT 34
ABP20722
XX ABP20722 standard; Peptide; 9 AA.
XX
XX ABP20722;
XX
XX 15-JUL-2002 (first entry)
XX
XX HIV A03 motif gag peptide #385.
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; virucide.
XX
XX Human immunodeficiency virus type 1.
XX
XX WO200124810-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US27766.
XX
XX 05-OCT-1999; 99US-0412863.
XX (EPIM-) EPIMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Celis E, Kubo RT, Grey HM;
XX

```

XX WPI; 2001-354887/37.
 XX
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 PT
 XX
 XX Claim 32; Page 294; 448pp; English.
 XX
 XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTI), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 66.7%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SVLS 6
 DB |||||
 3 SVLS 6
 RESULT 35
 ABP22869
 ID ABP22869 standard; Peptide; 9 AA.
 XX
 AC ABP22869;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV All motif gag peptide #248.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 FN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US27766.
 XX
 PR 05-OCT-1999; 99US-0412863.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cellis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-354887/37.
 XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 XX
 XX Claim 32; Page 337; 448pp; English.
 XX
 XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTI), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 66.7%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SVLS 6
 DB |||||
 3 SVLS 6
 RESULT 36
 AAB73123
 ID AAB73123 standard; Peptide; 9 AA.
 XX
 AC AAB73123;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Tumour antigen peptide #7.
 XX
 KW Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
 XX
 OS Homo sapiens.
 XX
 FN WO200111044-A1.
 XX
 PD 15-FEB-2001.
 XX
 PF 03-AUG-2000; 2000WO-JP05220.
 XX
 PR 05-AUG-1999; 99JP-0222101.
 XX
 PA (ITOH/) ITOH K.
 XX
 FI Itoh K;
 XX
 DR WPI; 2001-191541/19.
 XX
 PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells
 PT and polynucleotides encoding them for treatment of cancer -
 XX
 PS Claim 1; Page 67; 75pp; Japanese.
 XX
 CC The present invention relates to peptides which are partial sequences of

CC src/lck family proteins. The present sequence is one such peptide. The
 CC peptides are useful for producing vaccines for the treatment of cancer,
 CC including colon cancer and small-cell lung cancer.

XX
 XX Sequence 9 AA;

Query Match 66.7%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 QSVL 5
 |||||
 Db 6 QSVL 9

RESULT 37
 AAB73124
 ID AAB73124 standard; Peptide; 9 AA.
 XX
 AC AAB73124;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Tumour antigen peptide #8.
 XX
 KW Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200111044-A1.
 XX
 PD 15-FEB-2001.
 XX
 PF 03-AUG-2000; 2000WO-JP05220.
 XX
 PR 05-AUG-1999; 99JP-0222101.
 XX
 PA (ITOH/) ITOH K.
 XX
 PI Itoh K;
 XX
 DR WPI; 2001-191541/19.
 XX
 PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells
 PT and polynucleotides encoding them for treatment of cancer -
 XX
 PS Claim 1; Page 67; 75pp; Japanese.
 XX
 CC The present invention relates to peptides which are partial sequences of
 CC src/lck family proteins. The present sequence is one such peptide. The
 CC peptides are useful for producing vaccines for the treatment of cancer,
 CC including colon cancer and small-cell lung cancer.

XX
 SQ Sequence 9 AA;

Query Match 66.7%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 QSVL 5
 |||||
 Db 6 QSVL 9

RESULT 38
 AAB73125
 ID AAB73125 standard; Peptide; 9 AA.
 XX
 AC AAB73125;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Tumour antigen peptide #9.

XX Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
 KW Homo sapiens.
 OS WO200111044-A1.
 PN 15-FEB-2001.
 XX
 PD 03-AUG-2000; 2000WO-JP05220.
 XX
 PF 05-AUG-1999; 99JP-0222101.
 XX
 PR (ITOH/) ITOH K.
 XX
 PI Itoh K;
 XX
 DR WPI; 2001-191541/19.
 XX
 PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells
 PT and polynucleotides encoding them for treatment of cancer -
 XX
 PS Claim 1; Page 68; 75pp; Japanese.
 XX
 CC The present invention relates to peptides which are partial sequences of
 CC src/lck family proteins. The present sequence is one such peptide. The
 CC peptides are useful for producing vaccines for the treatment of cancer,
 CC including colon cancer and small-cell lung cancer.

XX
 SQ Sequence 9 AA;

Query Match 66.7%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 QSVL 5
 |||||
 Db 6 QSVL 9

RESULT 39
 ABJ09400
 ID ABJ09400 standard; Peptide; 9 AA.
 XX
 AC ABJ09400;
 XX
 DT 14-NOV-2002 (first entry)
 XX
 DE Hepatitis B virus analogue #12.
 XX
 KW Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 KW virucide; hepatotropic; antiinflammatory.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200219986-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 08-SEP-2000; 2000WO-US24802.
 XX
 PR 08-SEP-2000; 2000WO-US24802.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI (SETT/) SETTE A.
 XX
 PI Sette A, Sidney J, Southwood S, Vitello MA, Livingstone BD;
 PI Celis E, Kubo RT, Grey HM, Chesnut RW;
 XX
 DR WPI; 2002-643192/69.
 XX
 PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises

PT a HBV peptide epitope -
 XX Disclosure; Page 188; 228pp; English.
 XX
 CC The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention.
 XX
 SQ Sequence 9 AA;
 Query Match 66.7%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PQSV 4
 Db 6 PQSV 9
 RESULT 40
 AAU09453
 ID AAU09453 standard; peptide; 9 AA.
 XX
 AC AAU09453;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Chlamydomydia pneumoniae T-cell epitope #6 useful as Chlamydia antigen.
 XX
 KW ATP binding cassette; secretory locus open reading frame; endopeptidase;
 KW secretory locus ORF; protease; metalloprotease; CLP protease ATPase;
 KW CLP protease subunit; transglycolase/transpeptidase; CLPc protease;
 KW thioredoxin; Chlamydia infection; antibacterial; immunogen.
 XX
 OS Chlamydomydia pneumoniae CWL029.
 XX
 PN W0200185972-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 08-MAY-2001; 2001WO-CA00653.
 XX
 PR 08-MAY-2000; 2000US-202672P.
 PR 30-MAY-2000; 2000US-207852P.
 PR 16-JUN-2000; 2000US-211796P.
 PR 16-JUN-2000; 2000US-211797P.
 PR 16-JUN-2000; 2000US-211798P.
 PR 16-JUN-2000; 2000US-211801P.
 PR 16-JUN-2000; 2000US-212044P.
 PR 26-SEP-2000; 2000US-235335P.
 PR 26-SEP-2000; 2000US-235361P.
 PR 26-SEP-2000; 2000US-235398P.
 XX
 PA (AVET) AVENTIS PASTEUR LTD.
 XX
 PI Murdin AD, Oomen RP, Wang J, Dunn P;
 XX
 DR WPI; 2002-049447/06.
 XX
 PT Vaccine useful for immunising mammals against chlamydia infections,
 PT comprises vectors having sequences of ATP binding cassette gene,
 PT secretory locus open reading frame gene of chlamydia -
 XX
 XX Example 4; Page 81; 355pp; English.
 PS
 SS The present invention relates to the isolation of Chlamydomyphila
 CC pneumoniae strain CWL029 genes and their encoded proteins. The genes of
 CC the invention encode an ATP binding cassette gene, a secretory locus
 CC open reading frame (ORF), an endopeptidase, a protease, a
 CC metalloprotease, CLP protease ATPase, a CLP protease subunit, a
 CC transglycolase/transpeptidase, a CLPc protease, or thioredoxin. The

CC genes of the invention can be used in a vector as a vaccine for the
 CC prevention and treatment of Chlamydia infections. AAU09440-AAU09473
 CC represent B- or T-cell epitopes from the C. pneumoniae proteins
 CC (AAU09430-AAU09439) of the invention. These epitopes can be used as
 CC Chlamydia antigens.
 XX
 SQ Sequence 9 AA;
 Query Match 66.7%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SVLS 6
 Db 1 SVLS 4
 RESULT 41
 AAR90649
 ID AAR90649 standard; Peptide; 10 AA.
 XX
 AC AAR90649;
 XX
 DT 25-MAR-2003 (updated)
 DT 13-JUL-1996 (first entry)
 XX
 DE S. acidocaldarius transferase peptide fragment AP-20.
 XX
 KW transferase; amylase; Sulfolobus; production; alpha, alpha-trehalose;
 KW malto-oligosaccharide; hydrolysis; Achromobacter; protease; digestion.
 XX
 OS Sulfolobus acidocaldarius.
 XX
 PN W09534642-A1.
 XX
 PD 21-DEC-1995.
 XX
 PF 14-JUN-1995; 95WO-JF01189.
 XX
 PR 21-APR-1995; 95JP-0120673.
 PR 15-JUN-1994; 94JP-0133354.
 PR 18-AUG-1994; 94JP-0194223.
 PR 31-OCT-1994; 94JP-0290394.
 PR 21-NOV-1994; 94JP-0286917.
 PR 21-NOV-1994; 94JP-0311185.
 XX
 PA {KIRI } KIRIN BEER KK.
 XX
 PI Kato M, Miura Y, Kettoku M, Iwamatsu A, Kobayashi K, Komeda T;
 XX
 DR WPI; 1996-049671/05.
 XX
 PT Sulfolobus spp. derived transferase and amylase - for production of
 PT alpha, alpha-trehalose from malto-oligosaccharide(s)
 XX
 PS Example I-15; Page 179; 357pp; Japanese.
 XX
 CC AAR90640-51 are peptide fragments of a transferase isolated from
 CC Sulfolobus acidocaldarius, derived by digestion with Achromobacter
 CC protease (AP). The transferase (AAR90618) acts on a saccharide having at
 CC least three sugar units, in which at least three glucose units at the
 CC reducing end are alpha-1,4 linked, to transform the alpha-1,4 linkages to
 CC alpha-1, alpha-1 linkages. The transferase has a mol. wt. of 74 to 76
 CC kDa. It is characterised by working at pH 4.5-6.0 and at 60-80 deg.C.
 CC It has an isoelectric point of 5.3-6.3 and retains at least 90 percent
 CC activity after 6 hrs. at 80 deg.C. It is completely inhibited by 5 mM
 CC copper sulphate. Use of the transferase and an amylase in succession on
 CC suitable substrates such a malto-oligosaccharides, is useful for the
 CC production of alpha, alpha-trehalose.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 10 AA;

Query Match 66.7%; Score 4; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 2 SVLS 5

RESULT 42
AAW82304
ID AAW82304 standard; Peptide; 10 AA.

AC AAW82304;

DT 15-MAR-1999 (first entry)

DE Transport peptide fragment.

KW Targetting agent; gastrointestinal tract; brain; drug delivery;
KW drug targetting; phage display; transport peptide.

OS Synthetic.

PN WO9851825-A1.

PD 19-NOV-1998.

PF 15-MAY-1998; 98WO-US10079.

PR 15-MAY-1997; 97US-0857046.

PA (CYTO-) CYTOGEN CORP.

PA (ELAN-) ELAN CORP PLC.

PI Alvarez VL, O'Mahony DJ, Seveso M;

DR WPI; 1999-009778/01.

PT New targetting agents enabling transport of active agents through
PT human/animal tissue, or their uptake - useful in the treatment and
PT prevention of diseases, especially of the gastro-intestinal tract
(GIT)

PS Claim 7; Page 66; 83pp; English.

XX This is a fragment of peptide 28.1 (see AAW82290), a peptide isolated
CC from a phage display library on the basis of its ability to enhance
CC transport of phage from the rat gastrointestinal tract (GIT) to
CC brain. Claimed transport or uptake targetting agents can include
CC this, or other, claimed peptide fragments (see AAW82300-10). Such
CC transport or targetting agents permit or facilitate the transport
CC of an active agent through a human or animal tissue such as GIT
CC lumen, or uptake of the active agent into the human or animal
CC tissue. The active agent is preferably a drug or drug-containing
CC nanoparticle or microparticle. Therapeutic methods of
CC administration, pharmaceutical compositions and formulations based
CC of the targetting peptides are also provided.

SQ Sequence 10 AA;

Query Match 66.7%; Score 4; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSVL 5
Db 2 QSVL 5

RESULT 43
ABP11686

ID ABP11686 standard; Peptide; 10 AA.

AC ABP11686;

DT 15-JUL-2002 (first entry)

DE HIV A01 super motif gag peptide #58.

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.

OS Human immunodeficiency virus type 1.

PN WO200124810-A1.

PD 12-APR-2001.

PF 05-OCT-2000; 2000WO-US27766.

PR 05-OCT-1999; 99US-0412863.

PA (EPIM-) EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;

DR WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -

PS Claim 32; Page 108; 449pp; English.

XX The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (AB25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.

SQ Sequence 10 AA;

Query Match 66.7%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 1 SVLS 4

RESULT 44

ABP12769
ID ABP12769 standard; Peptide; 10 AA.

AC ABP12769;

```

XX DT 15-JUL-2002 (first entry)
XX KW HIV A02 super motif gag peptide #240.
XX DE HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX KW antigen; vaccine; HIV infection; immunisation; virucide.
XX OS Human immunodeficiency virus type 1.
XX PN WO200124810-A1.
XX PD 12-APR-2001.
XX PF 05-OCT-2000; 2000WO-US27766.
XX PR 05-OCT-1999; 99US-0412863.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Cells E, Kubo RT, Grey HM;
XX DR WPI; 2001-354887/37.
XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV-1 -
XX PS Claim 32; Page 130; 448pp; English.
XX CC The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (ABU25347 to
XX CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines,
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group-based vaccine approach is the ability
XX CC to combine selected groups (CTL and HTL), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be modulated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. ABP11501 to ABP25412
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 10 AA;
XX Query Match 66.7%; Score 4; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 2.6e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 3 SVLS 6
XX Db |||||
XX 3 SVLS 6
XX RESULT 45
XX ABP12770
XX ID ABP12770 standard; Peptide; 10 AA.
XX AC ABP12770;
XX XX
XX DT 15-JUL-2002 (first entry)
XX DE HIV A02 super motif gag peptide #242.
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;

```

```

DE XX HIV A02 super motif gag peptide #241.
KW XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
OS Human immunodeficiency virus type 1.
XX PN WO200124810-A1.
XX PD 12-APR-2001.
XX PF 05-OCT-2000; 2000WO-US27766.
XX PR 05-OCT-1999; 99US-0412863.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Cells E, Kubo RT, Grey HM;
XX DR WPI; 2001-354887/37.
XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV-1 -
XX PS Claim 32; Page 130; 448pp; English.
XX CC The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (ABU25347 to
XX CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines,
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group-based vaccine approach is the ability
XX CC to combine selected groups (CTL and HTL), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be modulated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. ABP11501 to ABP25412
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 10 AA;
XX Query Match 66.7%; Score 4; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 2.6e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 3 SVLS 6
XX Db |||||
XX 3 SVLS 6
XX RESULT 46
XX ABP12771
XX ID ABP12771 standard; Peptide; 10 AA.
XX AC ABP12771;
XX XX
XX DT 15-JUL-2002 (first entry)
XX DE HIV A02 super motif gag peptide #242.
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;

```

KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 XX antigen; vaccine; HIV infection; immunisation; virucide.
 OS Human immunodeficiency virus type 1.
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US27766.
 XX
 PR 05-OCT-1999; 99US-0412863.
 XX
 PA (EPTM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 PS Claim 32; Page 130; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 10 AA;
 Query Match 66.7%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SVLS 6
 Db |||||
 1 SVLS 4
 RESULT 47
 ABP15694
 ID ABP15694 standard; Peptide; 10 AA.
 XX
 AC ABP15694;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV A24 super motif gag peptide #180.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX

OS Human immunodeficiency virus type 1.
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US27766.
 XX
 PR 05-OCT-1999; 99US-0412863.
 XX
 PA (EPTM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 PS Claim 32; Page 190; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 10 AA;
 Query Match 66.7%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SVLS 6
 Db |||||
 1 SVLS 4
 RESULT 48
 ABP17825
 ID ABP17825 standard; Peptide; 10 AA.
 XX
 AC ABP17825;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV B58 super motif gag peptide #44.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 OS Human immunodeficiency virus type 1.
 PN WO200124810-A1.


```

XX PD 12-APR-2001.
XX PF 05-OCT-2000; 2000WO-US27766.
XX PF 05-OCT-1999; 99US-0412863.
XX XX 05-OCT-1999; 99US-0412863.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX DR WPI; 2001-354887/37.
XX XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV-1 -
XX PT Claim 32; Page 234; 448pp; English.
XX PS The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (ABL25347 to
XX CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines,
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group-based vaccine approach is the ability
XX CC to combine selected groups (CTL and HTL), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be modulated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. ABP1501 to ABP25412
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 10 AA;
XX
XX Query Match 66.7%; Score 4; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 2.6e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 3 SVLS 6
XX Db 3 SVLS 6
XX
XX RESULT 49
XX ABP17919
XX ID ABP17919 standard; Peptide; 10 AA.
XX AC ABP17919;
XX XX 15-JUL-2002 (first entry)
XX DT HIV B58 super motif gag peptide #138.
XX DE HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX XX vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX KW antigen; vaccine; HIV infection; immunisation; virucide.
XX OS Human immunodeficiency virus type 1.
XX XX WO200124810-A1.
XX PN 12-APR-2001.
XX PD 05-OCT-2000; 2000WO-US27766.
XX PF 05-OCT-1999; 99US-0412863.
XX PR

```

```

PF 05-OCT-2000; 2000WO-US27766.
XX 05-OCT-1999; 99US-0412863.
XX (EPIM-) EPIMMUNE INC.
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX DR WPI; 2001-354887/37.
XX XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV-1 -
XX PT Claim 32; Page 236; 448pp; English.
XX PS The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (ABL25347 to
XX CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines,
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group-based vaccine approach is the ability
XX CC to combine selected groups (CTL and HTL), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be modulated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. ABP1501 to ABP25412
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 10 AA;
XX
XX Query Match 66.7%; Score 4; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 2.6e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 3 SVLS 6
XX Db 3 SVLS 6
XX
XX RESULT 50
XX ABP20530
XX ID ABP20530 standard; Peptide; 10 AA.
XX AC ABP20530;
XX XX 15-JUL-2002 (first entry)
XX DT HIV A03 motif gag peptide #193.
XX DE HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX KW antigen; vaccine; HIV infection; immunisation; virucide.
XX OS Human immunodeficiency virus type 1.
XX XX WO200124810-A1.
XX PN 12-APR-2001.
XX PD 05-OCT-2000; 2000WO-US27766.
XX PF 05-OCT-1999; 99US-0412863.
XX PR

```

XX (EPIM-) EPIMMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 XX Baker DM, Cellis E, Kubo RT, Grey HM;
 PI WPI; 2001-354887/37.
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 PT Claim 32; Page 290; 448pp; English.
 XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX Sequence 10 AA;
 SQ Query Match 66.7%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SVLS 6
 DB 1 SVLS 4
 RESULT 51
 ABP20539
 ID ABP20539 standard; Peptide; 10 AA.
 XX AC ABP20539;
 XX 15-JUL-2002 (first entry)
 XX HIV A03 motif gag peptide #202.
 DE HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 XX vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX Human immunodeficiency virus type 1.
 OS WO200124810-A1.
 XX PN 12-APR-2001.
 XX PD 05-OCT-2000; 2000WO-US27766.
 XX PF 05-OCT-1999; 99US-0412863.
 XX PR 05-OCT-1999; 99US-0412863.
 XX PA (EPIM-) EPIMMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cellis E, Kubo RT, Grey HM;

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cellis E, Kubo RT, Grey HM;
 XX WPI; 2001-354887/37.
 DR Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 XX peptide groups, useful for vaccinating against HIV-1 -
 PT Claim 32; Page 290; 448pp; English.
 XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX Sequence 10 AA;
 SQ Query Match 66.7%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SVLS 6
 DB 2 SVLS 5
 RESULT 52
 ABP20716
 ID ABP20716 standard; Peptide; 10 AA.
 XX AC ABP20716;
 XX 15-JUL-2002 (first entry)
 XX HIV A03 motif gag peptide #379.
 DE HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 XX antigen; vaccine; HIV infection; immunisation; virucide.
 XX Human immunodeficiency virus type 1.
 OS WO200124810-A1.
 XX PN 12-APR-2001.
 XX PD 05-OCT-2000; 2000WO-US27766.
 XX PF 05-OCT-1999; 99US-0412863.
 XX PR (EPIM-) EPIMMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cellis E, Kubo RT, Grey HM;

DR WPI; 2001-354887/37.
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 XX Claim 32; Page 294; 448pp; English.
 XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CII and HII), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX SQ Sequence 10 AA;
 Query Match 66.7%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 SVLS 6
 Db 5 SVLS 8
 RESULT 53
 ABP22863
 ID ABP22863 standard; Peptide; 10 AA.
 AC
 AC ABP22863;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV A11 motif gag peptide #242.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US27766.
 XX
 PR 05-OCT-1999; 99US-0412863.
 XX
 XX (EPIM-) EPIMMUNE INC.
 PA Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-354887/37.
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -

PT peptide groups, useful for vaccinating against HIV-1 -
 XX Claim 32; Page 337; 448pp; English.
 XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CII and HII), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX SQ Sequence 10 AA;
 Query Match 66.7%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 SVLS 6
 Db 5 SVLS 8
 RESULT 54
 AAG99453
 ID AAG99453 standard; Peptide; 10 AA.
 XX
 AC AAG99453;
 XX
 DT 01-OCT-2001 (first entry)
 XX
 DE PRAME derived HLA-A*0201 binding peptide SEQ ID NO: 95.
 XX
 KW Vaccine; immune response; T cell response; epitope; proteasome;
 KW cancer; infection.
 XX
 OS Unidentified.
 XX
 PN EP1118860-A1.
 XX
 PD 25-JUL-2001.
 XX
 PF 21-JAN-2000; 2000EP-0200242.
 XX
 PR 21-JAN-2000; 2000EP-0200242.
 XX
 XX (UYLB-) RIKSUNIV LEIDEN.
 PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
 XX
 PI Ossendorp F, Offringa R, Melief CJM, Kessler JH;
 XX
 DR WPI; 2001-427158/46.
 XX Selecting and/or producing a T cell epitope useful in a vaccine
 PT comprises subjecting a precursor peptide or polypeptide to the action
 PT of a 20S proteasome to determine the location of the C-terminus -
 XX
 PS Disclosure; Page 53; 102pp; English.

```
XX The present invention describes a method of producing T cell epitopes,  
CC involving subjecting a precursor peptide to the action of a 20S  
CC proteasome, in order to locate the C-terminus of said epitope. This can  
CC be used in the production of vaccines, which can then be used to provoke  
CC a T cell response in the treatment of diseases such as cancer and  
CC infections. The present sequence is a peptide described in the  
CC exemplification of the invention.  
XX  
SQ Sequence 10 AA;  
  
Query Match 66.7%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 SVLS 6  
Db 3 SVLS 6  
|||||  
  
RESULT 55  
AAG95614  
ID AAG95614 standard; Peptide; 10 AA.  
XX  
AC AAG95614;  
XX  
DT 18-SEP-2001 (first entry)  
XX  
DE Human complementary peptide; ligand; drug discovery; drug design.  
XX  
KW Human; complementary peptide; ligand; drug discovery; drug design.  
XX  
OS Homo sapiens.  
XX  
PN WO200142277-A2.  
XX  
PD 14-JUN-2001.  
XX  
PF 13-DEC-2000; 2000WO-GB04776.  
XX  
PR 13-DEC-1999; 99GB-0029464.  
XX  
PA (PROT-) PROTEOM LTD.  
XX  
PI Roberts GW, Heal JR;  
XX  
DR WPI; 2001-408419/43.  
XX  
PT A set of peptide ligands consisting of specific complementary peptides  
DE Human complementary peptide, SEQ ID NO: 1808.  
XX  
KW Human; complementary peptide; ligand; drug discovery; drug design.  
XX  
OS Homo sapiens.  
XX  
PN WO200142277-A2.  
XX  
PD 14-JUN-2001.  
XX  
PF 13-DEC-2000; 2000WO-GB04776.  
XX  
PR 13-DEC-1999; 99GB-0029464.  
XX  
PA (PROT-) PROTEOM LTD.  
XX  
PI Roberts GW, Heal JR;  
XX  
DR WPI; 2001-408419/43.  
XX  
PT A set of peptide ligands consisting of specific complementary peptides  
PT to proteins encoded by genes of the human genome, useful in an assay  
PT for screening and identifying of one or more novel peptides which are  
PT drug candidates or pro-drugs -  
XX  
PS Example 4; Page 301; 646pp; English.  
XX  
CC The invention relates to a set of complementary peptide ligands  
CC generated from the human genome. The complementary peptides  
CC interact with their relevant target proteins encoded in the human  
CC genome. They can be used as reagents in drug discovery and as lead  
CC ligands to facilitate drug design and development. The present  
CC sequence is a complementary peptide provided in the specification.  
XX  
SQ Sequence 10 AA;  
  
Query Match 66.7%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 SVLS 6  
Db 4 SVLS 7  
|||||  
|||||  
  
RESULT 57  
AAG85693  
ID AAG85693 standard; Peptide; 10 AA.  
XX  
AC AAG85693;  
XX  
DT 11-SEP-2001 (first entry)  
XX  
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 642.  
XX  
KW Saccharomyces cerevisiae; complementary peptide; peptide identification;  
XX drug discovery; drug design.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200142276-A1.  
XX  
PD 14-JUN-2001.  
XX  
PF 13-DEC-2000; 2000WO-GB04773.
```

```
RESULT 56  
AAG95616  
ID AAG95616 standard; Peptide; 10 AA.  
XX  
AC AAG95616;  
XX  
DT 18-SEP-2001 (first entry)  
XX  
DE Human complementary peptide, SEQ ID NO: 1810.  
XX  
KW Human; complementary peptide; ligand; drug discovery; drug design.  
XX  
OS Homo sapiens.  
XX  
PN WO200142277-A2.  
XX  
PD 14-JUN-2001.  
XX  
PF 13-DEC-2000; 2000WO-GB04776.  
XX  
PR 13-DEC-1999; 99GB-0029464.  
XX  
PA (PROT-) PROTEOM LTD.  
XX  
PI Roberts GW, Heal JR;  
XX  
DR WPI; 2001-408419/43.  
XX  
PT A set of peptide ligands consisting of specific complementary peptides  
PT to proteins encoded by genes of the human genome, useful in an assay  
PT for screening and identifying of one or more novel peptides which are  
PT drug candidates or pro-drugs -  
XX  
PS Example 4; Page 301; 646pp; English.  
XX  
CC The invention relates to a set of complementary peptide ligands  
CC generated from the human genome. The complementary peptides  
CC interact with their relevant target proteins encoded in the human  
CC genome. They can be used as reagents in drug discovery and as lead  
CC ligands to facilitate drug design and development. The present  
CC sequence is a complementary peptide provided in the specification.  
XX  
SQ Sequence 10 AA;  
  
Query Match 66.7%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 SVLS 6  
Db 5 SVLS 8  
|||||  
|||||  
  
RESULT 57  
AAG85693  
ID AAG85693 standard; Peptide; 10 AA.  
XX  
AC AAG85693;  
XX  
DT 11-SEP-2001 (first entry)  
XX  
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 642.  
XX  
KW Saccharomyces cerevisiae; complementary peptide; peptide identification;  
XX drug discovery; drug design.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200142276-A1.  
XX  
PD 14-JUN-2001.  
XX  
PF 13-DEC-2000; 2000WO-GB04773.
```

```

XX PR 13-DEC-1999; 99GB-0029471.
XX PA (PROT-) PROTEOM LTD.
XX PI Roberts GW, Heal JR;
XX PI WPI; 2001-367863/38.
XX DR
XX PT Identifying complementary peptides by analysis of protein and
XX PT nucleotide sequence databases, useful in drug design -
XX PS Example 3; Page 118; 489pp; English.
XX CC The invention relates to the identification of complementary peptides
XX CC by analysis of protein and nucleotide sequence databases from higher
XX CC eukaryotic genomes, excluding human and plants. The specific
XX CC complementary peptides interact with their relevant target proteins
XX CC encoded in the eukaryote genome. The peptides may be used as reagents
XX CC and drugs for drug discovery and as lead ligands for drug design and
XX CC development. The present sequence is a complementary peptide from
XX CC Saccharomyces cerevisiae.
XX SQ Sequence 10 AA;

Query Match 66.7%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
DB 1 SVLS 4
|||||

RESULT 58
ABJ19987
ID ABJ19987 standard; Peptide; 10 AA.
XX AC ABJ19987;
XX DT 10-APR-2003 (first entry)
XX DE MHC binding peptide SEQ ID No 152.
XX KW Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;
XX KW antiinflammatory; major histocompatibility complex; MHC;
XX KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;
XX KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;
XX KW inflammation; gene therapy; MHC binding peptide.
XX OS Synthetic.
XX PN WO200294981-A2.
XX PD 28-NOV-2002.
XX PF 16-MAY-2002; 2002WO-IL00383.
XX PR 16-MAY-2001; 2001US-290958P.
XX PR 29-MAY-2001; 2001US-0865548.
XX PA (TECR ) TECHNION RES & DEV FOUND LTD.
XX PI Barnea E, Beer I, Ziv T, Admon A, Dassau L, Buchsbaum S;
XX DR WPI; 2003-210043/20.
XX PT Identifying peptides that are capable of binding to major
XX PT histocompatibility complex (MHC) molecules of a particular haplotype by
XX PT analyzing peptides bound to the soluble and secreted form of the MHC
XX PT molecules of the particular haplotype -
XX PS Claim 37; Page 183; 238pp; English.

```

```

XX CC The invention relates to a novel method for identifying peptides
XX CC originating from a particular cell type, which are capable of binding to
XX CC major histocompatibility complex (MHC) molecules of a particular
XX CC haplotype. The method comprises analysing peptides bound to the soluble
XX CC and secreted form of the MHC molecules of the particular haplotype. The
XX CC method is useful for identifying peptides for treating an autoimmune
XX CC disease, such as T or B cell and/or allergic disease or condition,
XX CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,
XX CC e.g. Alzheimer's disease, or diseases associated with inflammation. The
XX CC sequences of the invention may be used in a gene therapy application.
XX CC This sequence represents a peptide relating to the method for identifying
XX CC MHC binding peptides of the invention.
XX SQ Sequence 10 AA;

Query Match 66.7%; Score 4; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
DB 5 SVLS 8
|||||

RESULT 59
ABJ19627
ID ABJ19627 standard; Peptide; 10 AA.
XX AC ABJ19627;
XX DT 03-APR-2003 (first entry)
XX DE Neuronal nitric oxide synthase related peptide fragment SEQ ID No 85.
XX KW Antidiabetic; neuronal nitric oxide synthase; nNOS; enzyme; PIN;
XX KW inhibitor; insulin response; prediabetic; hyperinsulinic;
XX KW type 2 diabetes; rat.
XX OS Synthetic.
XX PN WO200283936-A2.
XX PD 24-OCT-2002.
XX PF 17-APR-2002; 2002WO-FR01327.
XX PR 18-APR-2001; 2001PR-0005248.
XX PA (INNO-) INNODIA.
XX PI Gross R, Lajoix A, Ribes G;
XX DR WPI; 2003-111816/10.
XX PT Identifying compounds that modulate interaction of neuronal nitric
XX PT oxide synthase and its inhibitor, useful e.g. for treating prediabetic
XX PT states -
XX PS Claim 10; Page 43; 89pp; French.
XX CC The invention relates to a novel method for detecting compounds that
XX CC modulate the complexation between neuronal nitric oxide synthase (nNOS)
XX CC and the inhibitor of nNOS (PIN). The nNOS protein comprises a 1429 amino
XX CC acid sequence, fully defined in the specification, or its variants. The
XX CC nNOS protein, its peptide fragments identified by the new method, and the
XX CC compound 1-(4-ethoxyphenyl)-5-(5-(benzimidazol-2-ylthio)-fur-2-
XX CC ylmethylidene)-hexahydropyrimidin-2,4,6-trione are used to treat altered
XX CC insulin responses in prediabetic and hyperinsulinic states, and in
XX CC subjects with type 2 diabetes. This sequence represents an nNOS peptide
XX CC fragment relating to the invention.
XX SQ Sequence 10 AA;

```

```

Query Match      66.7%; Score 4; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 4 SVLS 7

RESULT 60
AAR67271
ID AAR67271 standard; peptide; 11 AA.
XX
AC AAR67271;
XX
DT 27-JUL-1995 (first entry)
XX
DE Ubiquitin peptide extension, cRAS.
XX
KW Ubiquitin; peptide extension; assay; protein kinase; C-terminal;
KW Ha-RAS protein; farnesyl-protein transferase;
KW carboxy methyl transferase.
XX
OS Synthetic.
XX
FN US5366871-A.
XX
PD 22-NOV-1994.
XX
PF 13-NOV-1991; 91US-0791935.
XX
FR 13-NOV-1991; 91US-0791935.
XX
PA (UTAH ) UNIV UTAH.
XX
PI Rechsteiner MC, Yoo YJ;
XX
DR WPI; 1995-005826/01.
XX
N-PSDB; AAQ75292.
XX
Assay for enzymes that modify peptide chains - using a substrate
comprising a ubiquitin-peptide extension contg. a sequence
modified by the enzyme
XX
Example 1; Column 8; 14pp; English.
XX
This sequence represents a ubiquitin-peptide extension which is used
in the method of the invention for assaying enzymes that modify peptide
chains. This peptide sequence represents an extension which is known
to be modified in the presence of an enzyme being assayed for, and the
reaction mixture formed is then analysed. This method may be used for
assaying protein kinases or enzymes which modify the C-terminal end of
Ha-RAS protein, such as farnesyl-protein transferase, or carboxy methyl
transferase. Peptides such as this are less expensive to synthesise
than standard peptides used in these methods and they may be purified
from bacterial extracts by simple acid extraction.
XX
Query Match      66.7%; Score 4; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 8 SVLS 11

RESULT 61
AAR67272
ID AAR67272 standard; peptide; 11 AA.
XX

```

```

AC AAR67272;
XX
DT 27-JUL-1995 (first entry)
XX
DE Ubiquitin peptide extension, Ha-RAS.
XX
KW Ubiquitin; peptide extension; assay; protein kinase; C-terminal;
KW Ha-RAS protein; farnesyl-protein transferase;
KW carboxy methyl transferase.
XX
OS Synthetic.
XX
FN US5366871-A.
XX
PD 22-NOV-1994.
XX
PF 13-NOV-1991; 91US-0791935.
XX
FR 13-NOV-1991; 91US-0791935.
XX
PA (UTAH ) UNIV UTAH.
XX
PI Rechsteiner MC, Yoo YJ;
XX
DR WPI; 1995-005826/01.
XX
Assay for enzymes that modify peptide chains - using a substrate
comprising a ubiquitin-peptide extension contg. a sequence
modified by the enzyme
XX
Example 1; Column 9; 14pp; English.
XX
This sequence represents a ubiquitin-peptide extension which is used
in the method of the invention for assaying enzymes that modify peptide
chains. This peptide sequence represents an extension which is known
to be modified in the presence of an enzyme being assayed for, and the
reaction mixture formed is then analysed. This method may be used for
assaying protein kinases or enzymes which modify the C-terminal end of
Ha-RAS protein, such as farnesyl-protein transferase, or carboxy methyl
transferase. Peptides such as this are less expensive to synthesise
than standard peptides used in these methods and they may be purified
from bacterial extracts by simple acid extraction.
XX
Query Match      66.7%; Score 4; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 8 SVLS 11

RESULT 62
AAR67247
ID AAR67247 standard; Protein; 11 AA.
XX
AC AAR67247;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human secreted protein sequence encoded by gene 17 SEQ ID NO:341.
XX
KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; gene therapy; pathological condition;
KW autoimmune disease; rheumatoid arthritis; hyperproliferative disorder;
KW neoplasm; cardiovascular disorder; cardiac arrest; cerebral ischaemia;
KW cerebrovascular disorder; angiogenesis; nervous system disorder;
KW Alzheimer's disease; infection; ocular disorder; corneal infection;
KW wound healing; skin aging; food additive; preservative.

```

XX OS Homo sapiens.
 XX PN WO200070042-A1.
 XX PD 23-NOV-2000.
 XX PF 11-MAY-2000; 2000WO-US12788.
 XX PR 13-MAY-1999; 99US-0134068.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Ruben SM, Moore PA, Young PE, Komatsoulis GA, Birse CE;
 XX PI Duan RD, Florence KA, Soppet DR;
 XX DR WPI; 2000-679828/66.
 XX PT Isolated nucleic acid molecule encoding a human secreted protein is
 XX PT used in preventing, treating or ameliorating a medical condition -
 XX PS Disclosure; Page 1012; 1065pp; English.
 XX CC The polynucleotide sequences given in AAC99818 to AAC99977 encode the
 CC human secreted proteins given in AAB56077 to AAB56362. Human secreted
 CC proteins have activities based on the tissues and cells the genes are
 CC expressed in. Examples of activities include: immunosuppressive;
 CC antirheumatic; antiproliferative; antiproliferative; cytostatic; cardiac;
 CC vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial;
 CC virucide; fungicide; and ophthalmological. The human secreted
 CC polynucleotides and proteins can be used to prevent, treat or ameliorate
 CC a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
 CC dogs, chickens or sheep. They are also used in diagnosing a pathological
 CC condition or susceptibility to a pathological condition. Disorders which
 CC are diagnosed or treated include autoimmune diseases e.g. rheumatoid
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
 CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
 CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
 CC fungi and ocular disorders e.g. corneal infection. The proteins can also
 CC be used to aid wound healing and epithelial cell proliferation, to
 CC prevent skin aging due to sunburn, to maintain organs before
 CC transplantation, for supporting cell culture of primary tissues, to
 CC regenerate tissues and in chemotaxis. The proteins can also be used as a
 CC food additive or preservative to increase or decrease storage
 CC capabilities. AAC99809 to AAC99817 and AAB56076 represent sequences used
 CC in the exemplification of the present invention.
 XX SQ Sequence 11 AA;
 Query Match 66.7%; Score 4; DB 21; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SVLS 6
 ||||
 Db 8 SVLS 11
 RESULT 63
 ABP14552
 ID ABP14552 standard; Peptide; 11 AA.
 XX AC ABP14552;
 XX DT 15-JUL-2002 (first entry)
 XX DE HIV A03 super motif gag peptide #114.
 XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX OS Human immunodeficiency virus type 1.
 XX PN WO200124810-A1.

XX OS Human immunodeficiency virus type 1.
 XX PN WO200124810-A1.
 XX PD 12-APR-2001.
 XX PF 05-OCT-2000; 2000WO-US27766.
 XX PR 05-OCT-1999; 99US-0412863.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 XX PI Baker DM, Cellis E, Kubo RT, Grey HM;
 XX DR WPI; 2001-354887/37.
 XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 XX PT peptide groups, useful for vaccinating against HIV-1 -
 XX PS Claim 32; Page 166; 448pp; English.
 XX CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABU25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX SQ Sequence 11 AA;
 Query Match 66.7%; Score 4; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SVLS 6
 ||||
 Db 5 SVLS 8
 RESULT 64
 ABP17201
 ID ABP17201 standard; Peptide; 11 AA.
 XX AC ABP17201;
 XX DT 15-JUL-2002 (first entry)
 XX DE HIV B27 super motif gag peptide #77.
 XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX OS Human immunodeficiency virus type 1.
 XX PN WO200124810-A1.

```

XX PD 12-APR-2001.
XX PF 05-OCT-2000; 2000WO-US27766.
XX PR 05-OCT-1999; 99US-0412863.
XX XX
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX DR WPI; 2001-354887/37.
XX XX
XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV-1 -
XX PS Claim 32; Page 221; 448pp; English.
XX CC
XX CC The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (ABL25347 to
XX CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines,
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group-based vaccine approach is the ability
XX CC to combine selected groups (CTL and HTL), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be modulated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. ABP1501 to ABP25412
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 11 AA;
XX
Query Match 66.7%; Score 4; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 4 SVLS 7
|
|
|
|

RESULT 65
ABP17202
ID ABP17202 standard; Peptide; 11 AA.
XX AC
XX AC ABP17202;
XX DT 15-JUL-2002 (first entry)
XX DE HIV B27 super motif gag peptide #78.
XX XX
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX KW antigen; vaccine; HIV infection; immunisation; virucide.
XX OS Human immunodeficiency virus type 1.
XX PN WO200124810-A1.
XX PD 12-APR-2001.
XX PF
XX PR

```

```

PF 05-OCT-2000; 2000WO-US27766.
XX PF 05-OCT-1999; 99US-0412863.
XX XX
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX DR WPI; 2001-354887/37.
XX XX
XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV-1 -
XX PS Claim 32; Page 221; 448pp; English.
XX CC
XX CC The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (ABL25347 to
XX CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines,
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group-based vaccine approach is the ability
XX CC to combine selected groups (CTL and HTL), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be modulated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. ABP1501 to ABP25412
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 11 AA;
XX
Query Match 66.7%; Score 4; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 4 SVLS 7
|
|
|
|

RESULT 66
ABP18788
ID ABP18788 standard; Peptide; 11 AA.
XX AC
XX AC ABP18788;
XX DT 15-JUL-2002 (first entry)
XX DE HIV B62 super motif gag peptide #81.
XX XX
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX KW antigen; vaccine; HIV infection; immunisation; virucide.
XX OS Human immunodeficiency virus type 1.
XX PN WO200124810-A1.
XX PD 12-APR-2001.
XX PF 05-OCT-2000; 2000WO-US27766.
XX PR 05-OCT-1999; 99US-0412863.

```


XX PA (EPIM-) EPIMUNE INC.
 XX PA
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cellis E, Kubo RT, Grey HM;
 XX XX
 DR WPI; 2001-354887/37.
 XX XX
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 PT
 XX Claim 32; Page 254; 448pp; English.
 XX XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (AB125347 to
 CC AB23397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX XX
 SQ Sequence 11 AA;
 Query Match 66.7%; Score 4; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SVLS 6
 Db 1 SVLS 4
 RESULT 67
 AAW80388
 ID AAW80388 standard; Peptide; 12 AA.
 XX AC
 XX AAW80388;
 XX XX
 DT 14-JAN-1999 (first entry)
 XX XX
 DE Peptide eluted after biopanning against maltose binding protein.
 XX XX
 KW Intervening protein sequence; IVPS; protein splicing;
 KW protein production; maltose binding protein.
 XX XX
 OS Synthetic.
 OS US5834247-A.
 PN US5834247-A.
 XX PD
 PD 10-NOV-1998.
 XX XX
 XX 05-MAR-1997; 97US-0811492.
 XX XX
 PR 05-MAR-1997; 97US-0811492.
 PR 09-DEC-1992; 92US-0004139.
 PR 03-NOV-1993; 93US-0146885.
 PR 28-JUN-1995; 95US-0496247.
 PR 29-DEC-1995; 95US-0580555.

XX PA (NEWE) NEW ENGLAND BIOLABS INC.
 XX PA
 PI Adam E, Chong SSC, Comb DG, Hodges RA, Jack WE;
 PI Noren CJ, Perler FB, Southworth M, Xu M;
 XX XX
 DR WPI; 1999-008713/01.
 XX XX
 XX New modified target proteins - which have controllable intervening
 PT protein sequence which can facilitate production, purification,
 PT labelling or isolation of target proteins
 XX XX
 PS Example 22; Fig 36; 123pp; English.
 XX XX
 CC AAW80372-93 represent peptides eluted after biopanning against
 CC maltose binding protein, in the course of the invention. The
 CC specification describes IVPS (intervening protein sequence)
 CC regions which encode peptides which are removed via protein
 CC splicing to form the native protein. The specification describes
 CC a modified protein comprising a target protein or portion, fused
 CC either internally or terminally, to a IVPS, or to an amino- or
 CC carboxyl-terminal element of a IVPS. The IVPS are capable of
 CC excision from or cleavage of the modified protein upon predetermined
 CC conditions, in cis or trans, e.g. temperature increase, deglycosylation,
 CC unblocking of amino acid residues, treatment with chemical reagents.
 CC The methods can be used for modifying, producing, purifying, labelling
 CC or isolating target proteins such as enzymes, toxins, cytokines,
 CC glycoproteins and growth factors.
 XX XX
 SQ Sequence 12 AA;
 Query Match 66.7%; Score 4; DB 20; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SVLS 6
 Db 7 SVLS 10
 RESULT 68
 AAB06328
 ID AAB06328 standard; peptide; 12 AA.
 XX XX
 AC AAB06328;
 XX XX
 DT 03-OCT-2000 (first entry)
 XX XX
 DE Sterol-regulatory element-binding protein 2 10mer.
 XX XX
 KW Sterol-regulatory element-binding protein 2; SREBP-2;
 KW subtilisin-kexin isoenzyme 1; SKI-1;
 KW pro-brain-derived neurotrophic factor; proBDNF; antilipaeamic;
 KW cyostatic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;
 KW liver steatosis; Ras-dependent cancer; restenosis;
 KW amyloid protein formation.
 XX XX
 OS Mammalia.
 OS Synthetic.
 XX XX
 PN WO2000026348-A2.
 XX XX
 PD 11-MAY-2000.
 XX XX
 XX 04-NOV-1999; 99WO-CA01058.
 PF PF
 XX 04-NOV-1998; 98CA-2249648.
 PR PR
 XX (RECL-) INST RECH CLINIQUES MONTREAL.
 PA PA
 XX Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;
 PI WPI; 2000-365601/31.
 XX DR

XX Novel soluble proteic fragment of subtilisin-kexin isoenzyme for
PT producing a polypeptide useful for treating hypercholesterolemia, liver
PT steatosis and amyloidosis, comprises a specific amino acid se
XX
XX Example 6; Page 53; 119pp; English.
XX
XX The present sequence is a 10mer of sterol-regulatory element-binding
CC protein 2 (SRBP-2), which is cleaved by subtilisin-kexin isoenzyme 1
CC (SKI-1), a type-1 membrane-bound proteinase. Fluorescence resonance
CC energy transfer (FRET)-based proteolysis assays were performed on a large
CC number of synthetic peptides based on potential cleavage sites in the
CC SKI-1 prodomain, proBDNF and the loop region of SRBP-2. Like SRBP-2,
CC proBDNF is processed by SKI-1. The present peptide was efficiently
CC cleaved by recombinant SKI-1. Peptides which bind to and are cleaved by
CC SKI-1 may be used for monitoring SKI-1 activity, for screening inhibitors
CC of SKI-1 activity, or for screening enhancers of SKI-1 activity. Proteic
CC fragments of SKI-1 which bind to the SKI-1 catalytic site may be used as
CC inhibitors of SKI-1 activity. They may be used to treat diseases
CC involving overexpression of SKI-1 or SKI-1 substrate. Such diseases
CC include hypercholesterolaemia, high levels of fatty acids, lipids or
CC farnesyl pyrophosphate, liver steatosis, Ras-dependent cancer, restenosis
CC and amyloid protein formation.
XX
SQ Sequence 12 AA;

Query Match 66.7%; Score 4; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
|||
Db 6 SVLS 9

RESULT 69
ABG78536
ID ABG78536 standard; Peptide; 12 AA.
XX
AC ABG78536;
XX
DT 29-NOV-2002 (first entry)
XX
DE Multiple sclerosis associated feature (MSF) tryptic digest peptide #24.
XX
KW Multiple sclerosis; MS; multiple sclerosis associated feature; MSAP;
KW human; multiple sclerosis-associated protein isoform; MSPI;
KW antiinflammatory; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200259604-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-GB00330.
XX
PR 26-JAN-2001; 2001US-264404P.
PR 20-NOV-2001; 2001US-331647P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAc, Perekh RB, Rohlf C;
XX
DR WPI; 2002-599812/64.
XX
PT Screening or diagnosing multiple sclerosis (MS), useful for e.g.
PT determining the stage or severity of MS, comprises detecting the
PT presence of MS-associated features or protein isoforms by 2-dimensional
PT electrophoresis -
XX
PS Disclosure; Page 20; 128pp; English.
XX

CC This invention relates to a novel method for screening or diagnosing
CC multiple sclerosis (MS) in a subject to determine the stage or severity
CC of MS, to identify a subject at risk of developing MS or to monitor the
CC effect of a therapy administered. The method comprises analysing a
CC sample body fluid from the subject by two-dimensional electrophoresis
CC and detecting the presence of multiple sclerosis-associated features
CC (MSFs), or multiple sclerosis-associated protein isoforms (MSPIs).
CC The MSF's of the invention correspond to spots identified on a 2D gel
CC. These proteins may have antiinflammatory or neuroprotective activity.
CC The methods of the invention and the compositions are useful for
CC clinical screening, diagnosis and treatment of MS, for monitoring the
CC effectiveness of MS treatment, for selecting participants in clinical
CC trials, for identifying patients most likely to respond to a particular
CC therapeutic treatment and for screening and developing drugs for
CC treatment of MS. Agents that modulate the expression or activity of an
CC MSPI are useful for treating MS, for preventing or delaying the onset or
CC development of MS, to prevent or delay the progression of MS, or to
CC ameliorate the symptoms MS. Nucleic acids comprising a sequence encoding
CC an MSPI, MSPI-related polypeptide, or their fragments are useful for
CC promoting MSPI function by gene therapy. The present sequence represents
CC a human multiple sclerosis associated feature tryptic digest
CC peptide of the invention.
XX
SQ Sequence 12 AA;

Query Match 66.7%; Score 4; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQSV 4
|||
Db 5 PQSV 8

RESULT 70
AAP50642
ID AAP50642 standard; Protein; 13 AA.
XX
AC AAP50642;
XX
DT 25-MAR-2003 (updated)
DT 09-JAN-2003 (updated)
DT 21-NOV-1991 (first entry)
XX
DE Sequence (b) of a synthetic polypeptide corresponding in amino acid
DE sequence to at least a portion of a naturally occurring proteinoid
DE translated from a messenger RNA present substantially only in brain
DE cells.
XX
KW Neurotransmitter; neuromodulator; neuroactive; brain cell proteinoid.
XX
OS Synthetic.
XX
PN AU8430813-A.
XX
PD 24-JAN-1985.
XX
PF 18-JUL-1984; 84AU-0030813.
XX
PR 21-JUL-1983; 83US-0516136.
PR 03-JUN-1987; 87US-0058620.
XX
PA (SCRI) SCRIPPS CLINIC & RES FOUND.
XX
PI Sutcliffe JG;
XX
DR WPI; 1985-062448/11.
XX
PT New synthetic poly;peptide(s) - useful as neuro-active agents and
PT for diagnosis of brain cell proteinoid(s)
XX
PS Claim 4; Page 80; 97pp; English.
XX

CC The peptides of the invention (AAP50641-P50648) can pass from the
 CC blood stream through the blood-brain barrier and into brain cell
 CC tissues. They may be neuroactive, e.g. some cpds. have
 CC neurotransmitter-like and neuromodulating activity. The patent
 CC application outlines procedures that are useful in identifying
 CC proteinoids that are translated from brain-specific mRNA and for
 CC preparing synthetic polypeptides whose AA residue sequences
 CC correspond substantially to the AA residue sequences of at least a
 CC portion of those proteinoids. The adult male rat was chosen as a
 CC model. Four brain-specific clones of Class III were described as
 CC exemplary. These clones are designated p1A75, p1B236, p1B208 and
 CC p0-40 (see AAN50473-N50475, AAN50520).
 CC (Updated on 09-JAN-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 13 AA;

Query Match 66.7%; Score 4; DB 6; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
 |||||
 Db 8 SVLS 11

RESULT 71

AAW92320
 ID AAW92320 standard; peptide; 13 AA.

XX AC AAW92320;

XX XX 09-APR-1999 (first entry)

DE E2A/pbx1 immunogenic fusion peptide #5.

XX E2A; pbx1; fusion protein; antigen; monoclonal antibody; diagnosis;
 KW epitope; acute lymphoblastic leukemia.

OS Synthetic.

XX US5858682-A.

XX PD 12-JAN-1999.

XX PF 02-AUG-1996; 96US-0691997.

XX PR 02-AUG-1996; 96US-0691997.

XX (PHAR-) PHARMINGEN.

XX PI Gruenwald S, Monell C, Sang B;

XX DR WPI; 1999-119870/10.

XX Monoclonal antibody specific for E2A/pbx1 fusion protein - useful
 PT for diagnosis of acute lymphoblastic leukemia

XX PS Disclosure; Column 25-26; 21pp; English.

XX This sequence represents a peptide used in a method for constructing
 CC antigenic E2A/pbx1 fusion proteins used for raising monoclonal
 CC antibodies which specifically bind with an E2A/pbx1 fusion epitope. This
 CC peptide can be used for the diagnosis of acute lymphoblastic leukemia.

XX SQ Sequence 13 AA;

Query Match 66.7%; Score 4; DB 20; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
 |||||

Db 5 SVLS 8

RESULT 72

AAAG68083

ID AAG68083 standard; peptide; 13 AA.

XX AC AAG68083;

XX DT 17-DEC-2001 (first entry)

XX DE Antitumour peptide hck 503-515.

XX Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
 KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
 KW cyclophilin B gene; HLA-A2402.

OS Homo sapiens.

XX JP2001245675-A.

XX PD 11-SEP-2001.

XX PF 25-DEC-2000; 2000JP-0393047.

XX PR 28-DEC-1999; 99JP-0374322.

XX PA (ITOY/) ITO Y.

XX DR WPI; 2001-610076/70.

XX PT New peptides for recognizing cancer cells with tumor specific cytotoxic
 PT T lymphocytes and for treating cancer -

XX PS Claim 8; Page 2; 14pp; Japanese.

XX The present invention describes peptides recognising cancer cells with
 CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
 CC cancer cells with tumour specific CTLs are selected from: (1) peptides
 CC of sequences (AAG68066 to AAG68069); (2) peptides containing the above
 CC mentioned sequences; (3) peptides having 70 % or more of homogeneity
 CC with the above mentioned sequences; and (4) peptides with one or more
 CC deleted, substituted, added or inserted amino acid(s) of the above
 CC mentioned sequences, particularly those having recognising property due
 CC to HLA-A2402 binding CTL, especially having at least 5 amino acids,
 CC used for medicine, particularly anticancer agents, derived from
 CC antitumour antigenic peptides of lck, src family, SART-1, SART-3 or
 CC cyclophilin B genes. The antitumour peptides have cytostatic activities.
 CC The peptides are used for the treatment of cancer. The peptides cause
 CC activation of CTL in cancer patients. The present sequence represents
 CC a peptide from the present invention.

XX SQ Sequence 13 AA;

Query Match 66.7%; Score 4; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5
 |||||
 Db 6 QSVL 9

RESULT 73

AAAG68084

ID AAG68084 standard; peptide; 13 AA.

XX AC AAG68084;

XX DT 17-DEC-2001 (first entry)

XX DE Antitumour peptide blk 482-494.

KW Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
 KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
 KW cyclophilin B gene; HLA-A2402.

XX Homo sapiens.

PN JP2001245675-A.

XX 11-SEP-2001.

PD 25-DEC-2000; 2000JP-0393047.

XX 28-DEC-1999; 99JP-0374322.

XX (ITOY/) ITO Y.

PA WPI; 2001-610076/70.

XX New peptides for recognizing cancer cells with tumor specific cytotoxic
 PT T lymphocytes and for treating cancer -

PS Claim 8; Page 2; 14pp; Japanese.

XX The present invention describes peptides recognising cancer cells with
 CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
 CC cancer cells with tumour specific CTLs are selected from: (1) peptides
 CC of sequences (AAG68066 to AAG68069); (2) peptides containing the above
 CC mentioned sequences; (3) peptides having 70 % or more of homogeneity
 CC with the above mentioned sequences; and (4) peptides with one or more
 CC deleted, substituted, added or inserted amino acid(s) of the above
 CC mentioned sequences, particularly those having recognising property due
 CC to HLA-A2402 binding CTL, especially those having at least 5 amino acids,
 CC used for medicine, particularly anticancer agents, derived from
 CC antitumour antigenic peptides of lck, src family, SART-1, SART-3 or
 CC cyclophilin B genes. The antitumour peptides have cytostatic activities.
 CC The peptides are used for the treatment of cancer. The peptides cause
 CC activation of CTL in cancer patients. The present sequence represents
 CC a peptide from the present invention.

XX Sequence 13 AA;

Query Match 66.7%; Score 4; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5

Db 6 QSVL 9

RESULT 74

AAB31919

ID AAB31919 standard; peptide; 13 AA.

XX AAB31919;

XX 15-MAY-2001 (first entry)

XX Amino acid sequence of a peptide fragment of a human protein.

XX Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
 KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
 KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
 KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
 KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.

XX Homo sapiens.

XX WO200105422-A2.

PN 25-JAN-2001.

PD 17-JUL-2000; 2000WO-FR02057.

XX Tumor antigen peptides which induce tumor-specific cytotoxic T-cells
 PT and polynucleotides encoding them for treatment of cancer -

XX 15-JUL-1999; 99FR-0009372.
 PR (INNR) BIOMERIEUX STELHYS.

XX Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;

XX WPI; 2001-159475/16.

XX Detecting, preventing and treating degenerative, neurological and
 PT autoimmune diseases, particularly multiple sclerosis, using specified
 PT polypeptides or related nucleic acid or ligand -

XX Claim 7; Page 205; 209pp; French.

XX The present sequence represents a peptide fragment of a human protein,
 CC which is used in the method of the invention. The specification describes
 CC a method which uses at least one polypeptide or polynucleotide sequence
 CC belonging to the perlecan, precursor of the retinol-binding plasma
 CC protein, precursor of the ganglioside GM2 activator, calgranulin B or
 CC saposin B protein families. The method is used for detecting,
 CC preventing or treating a degenerative, neurological and/or auto-immune
 CC disease. The polynucleotides and polypeptides are used for diagnosis,
 CC prognosis, prevention and treatment of multiple sclerosis (in its
 CC various forms and phases). They may also be useful in cases of
 CC e.g. Alzheimer's and Parkinson's diseases, amyotrophic lateral sclerosis,
 CC rheumatoid polyarthritis and lupus erythematosus, including use as
 CC vaccines and in gene therapy (expression of sense or antisense
 CC sequences). They can also be used to assess efficacy of potential
 CC therapeutic agents, particularly compounds that reduce or inhibit
 CC toxicity towards glial cells.

XX Sequence 13 AA;

Query Match 66.7%; Score 4; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6

Db 3 SVLS 6

RESULT 75

AAB73149

ID AAB73149 standard; Peptide; 13 AA.

XX AAB73149;

XX 09-MAY-2001 (first entry)

XX Tumour antigen peptide #33.

XX Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.

XX Homo sapiens.

XX WO200111044-A1.

XX 15-FEB-2001.

XX 03-AUG-2000; 2000WO-JP05220.

XX 05-AUG-1999; 99JP-0222101.

XX (ITOH/) ITOH K.

XX Itoh K;

XX WPI; 2001-191541/19.

XX Tumor antigen peptides which induce tumor-specific cytotoxic T-cells
 PT and polynucleotides encoding them for treatment of cancer -

XX Example 6; Page 36; 75pp; Japanese.
PS
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer.
XX
SQ Sequence 13 AA;
Query Match 66.7%; Score 4; DB 22; Length 13;
Best Local Similarity 100.0%; Pred.No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 QSVL 5
Db 6 QSVL 9
Search completed: November 25, 2003, 19:27:14
Job time : 16.314 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 9.62791 Seconds
(without alignments)
114.943 Million cell updates/sec

Title: US-09-641-801-26

Perfect score: 6

Sequence: 1 PQSVLS 6

Scoring table: OLIGO
Gapex 60.0 , Gapext 60.0

Searched: 673684 seqs, 18443283 residues

Word size: 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	100.0	6	15	US-10-281-652-26
2	4	66.7	7	12	US-10-271-708-22
3	4	66.7	8	12	US-10-209-187A-5
4	4	66.7	8	14	US-10-061-395-58
5	4	66.7	8	15	US-10-052-942-64
6	4	66.7	9	14	US-10-062-257-7
7	4	66.7	9	14	US-10-062-257-8
8	4	66.7	9	14	US-10-062-257-9
9	4	66.7	10	11	US-09-572-404B-1808
10	4	66.7	10	11	US-09-572-404B-1810
11	4	66.7	10	11	US-09-865-548A-152
12	4	66.7	11	11	US-09-986-480-341
13	4	66.7	12	10	US-09-242-450A-9
14	4	66.7	12	15	US-10-254-446A-214
15	4	66.7	14	10	US-09-242-450A-8

16	4	66.7	14	15	US-10-097-065-571	Sequence 571, App
17	4	66.7	15	10	US-09-791-378-194	Sequence 194, App
18	4	66.7	15	12	US-09-933-767-582	Sequence 582, App
19	4	66.7	15	15	US-10-023-282-582	Sequence 582, App
20	4	66.7	17	11	US-09-563-222-14	Sequence 14, Appl
21	4	66.7	17	12	US-10-272-248-23	Sequence 23, Appl
22	4	66.7	17	12	US-10-029-386-34123	Sequence 34123, A
23	4	66.7	19	11	US-09-876-904A-142	Sequence 142, App
24	4	66.7	19	15	US-10-219-834-128	Sequence 128, App
25	4	66.7	20	9	US-09-864-761-48427	Sequence 48427, A
26	4	66.7	20	12	US-10-195-730-116	Sequence 116, App
27	4	66.7	20	12	US-10-272-248-24	Sequence 24, Appl
28	4	66.7	20	12	US-09-962-756-1150	Sequence 1150, Ap
29	3	50.0	4	8	US-08-839-248-1	Sequence 1, Appli
30	3	50.0	4	8	US-08-424-550B-538	Sequence 538, App
31	3	50.0	4	9	US-09-770-967-1	Sequence 1, Appli
32	3	50.0	4	9	US-09-858-369-1	Sequence 1, Appli
33	3	50.0	4	9	US-09-757-251-2	Sequence 2, Appli
34	3	50.0	4	9	US-09-784-897A-1	Sequence 1, Appli
35	3	50.0	4	9	US-09-770-983-1	Sequence 1, Appli
36	3	50.0	4	9	US-09-834-765-742	Sequence 742, App
37	3	50.0	4	9	US-09-853-918-12	Sequence 12, Appl
38	3	50.0	4	9	US-09-828-325A-2	Sequence 2, Appli
39	3	50.0	4	9	US-09-757-217A-2	Sequence 2, Appli
40	3	50.0	4	10	US-09-828-259A-2	Sequence 2, Appli
41	3	50.0	4	10	US-09-751-100B-20	Sequence 20, Appl
42	3	50.0	4	10	US-09-784-818-1	Sequence 1, Appli
43	3	50.0	4	12	US-09-756-248-1	Sequence 1, Appli
44	3	50.0	4	12	US-09-932-165-1436	Sequence 1436, Ap
45	3	50.0	4	12	US-10-087-942-6	Sequence 6, Appli
46	3	50.0	4	12	US-10-083-894-17	Sequence 17, Appl
47	3	50.0	4	12	US-10-352-704-27	Sequence 27, Appl
48	3	50.0	4	12	US-10-317-644-6	Sequence 6, Appli
49	3	50.0	4	15	US-10-087-905-6	Sequence 6, Appli
50	3	50.0	4	15	US-10-211-088-360	Sequence 360, App
51	3	50.0	5	9	US-09-803-854-4	Sequence 4, Appli
52	3	50.0	5	10	US-09-924-824-16	Sequence 16, Appl
53	3	50.0	5	10	US-09-924-824-17	Sequence 17, Appl
54	3	50.0	5	10	US-09-751-100B-43	Sequence 43, Appl
55	3	50.0	5	12	US-10-268-552-16	Sequence 16, Appl
56	3	50.0	5	12	US-10-268-552-17	Sequence 17, Appl
57	3	50.0	5	12	US-10-076-047A-197	Sequence 197, App
58	3	50.0	5	12	US-10-076-047A-251	Sequence 251, App
59	3	50.0	5	12	US-10-076-047A-296	Sequence 296, App
60	3	50.0	5	12	US-10-319-402-25	Sequence 25, Appl
61	3	50.0	5	12	US-10-352-704-29	Sequence 29, Appl
62	3	50.0	5	15	US-10-206-699-55	Sequence 55, Appl
63	3	50.0	6	8	US-08-681-219-11	Sequence 11, Appl
64	3	50.0	6	9	US-09-742-582-22	Sequence 22, Appl
65	3	50.0	6	10	US-09-924-824-27	Sequence 27, Appl
66	3	50.0	6	10	US-09-924-824-28	Sequence 28, Appl
67	3	50.0	6	10	US-09-924-824-37	Sequence 37, Appl
68	3	50.0	6	10	US-09-924-824-38	Sequence 38, Appl
69	3	50.0	6	10	US-09-924-824-44	Sequence 44, Appl
70	3	50.0	6	10	US-09-873-233A-15	Sequence 15, Appl
71	3	50.0	6	11	US-09-742-580-22	Sequence 22, Appl
72	3	50.0	6	11	US-09-742-581-22	Sequence 22, Appl
73	3	50.0	6	12	US-10-268-552-30	Sequence 30, Appl
74	3	50.0	6	12	US-10-268-552-31	Sequence 31, Appl
75	3	50.0	6	12	US-10-268-552-40	Sequence 40, Appl
76	3	50.0	6	12	US-10-268-552-41	Sequence 41, Appl
77	3	50.0	6	12	US-10-268-552-47	Sequence 47, Appl
78	3	50.0	6	12	US-09-935-384-746	Sequence 746, App
79	3	50.0	6	12	US-10-092-138-9	Sequence 9, Appli
80	3	50.0	6	12	US-10-319-402-27	Sequence 27, Appl
81	3	50.0	6	12	US-10-352-704-31	Sequence 31, Appl
82	3	50.0	6	12	US-09-799-576A-9	Sequence 9, Appli
83	3	50.0	6	14	US-10-156-820-54	Sequence 54, Appl
84	3	50.0	7	9	US-09-896-251-30	Sequence 30, Appl
85	3	50.0	7	9	US-09-896-251-32	Sequence 32, Appl
86	3	50.0	7	9	US-09-896-251-33	Sequence 33, Appl
87	3	50.0	7	9	US-09-896-251-33	Sequence 33, Appl
88	3	50.0	7	9	US-09-896-251-40	Sequence 40, Appl

89 3 50.0 7 9 US-09-896-251-45 Sequence 45, Appl
90 3 50.0 7 9 US-09-896-245-30 Sequence 30, Appl
91 3 50.0 7 9 US-09-896-245-32 Sequence 32, Appl
92 3 50.0 7 9 US-09-896-245-33 Sequence 33, Appl
93 3 50.0 7 9 US-09-896-245-40 Sequence 40, Appl
94 3 50.0 7 9 US-09-896-245-45 Sequence 45, Appl
95 3 50.0 7 9 US-09-896-245-40 Sequence 9, Appl
96 3 50.0 7 9 US-09-989-789-751 Sequence 751, App
97 3 50.0 7 9 US-09-989-789-953 Sequence 953, App
98 3 50.0 7 9 US-09-989-789-955 Sequence 955, App
99 3 50.0 7 9 US-09-989-789-3232 Sequence 3232, Ap
100 3 50.0 7 9 US-09-989-789-3955 Sequence 3955, Ap

ALIGNMENTS

RESULT 1
US-10-281-652-26
; Sequence 26, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTEININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-26

Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POSVLS 6
 |||||
Db 1 POSVLS 6

RESULT 2
US-10-271-708-22
; Sequence 22, Application US/10271708
; Publication No. US20030162200A1
; GENERAL INFORMATION:
; APPLICANT: CHOO, Yen
; APPLICANT: LIU, Xiaohai
; APPLICANT: BALASUBRAMANIAN, Shankar
; APPLICANT: PATEL, Sachin D.
; APPLICANT: ISALAN, Mark
; TITLE OF INVENTION: METHODS FOR MODULATING TELOMERASE ACTIVITY
; FILE REFERENCE: SABT-036/01US (8325-2014.01)
; CURRENT APPLICATION NUMBER: US/10/271,708
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 7
; TYPE: PRT.

; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: F2 residue
US-10-271-708-22

Query Match 66.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
 |||||
Db 3 SVLS 6

RESULT 3
US-10-209-187A-5
; Sequence 5, Application US/10209187A
; Publication No. US20030148383A1
; GENERAL INFORMATION:
; APPLICANT: Maurer-Stroh, Sebastian
; APPLICANT: Eisenhaber, Birgit
; APPLICANT: Eisenhaber, Frank
; TITLE OF INVENTION: Methods for Identifying Proteins with N-Terminal N-Myristoyl
; FILE REFERENCE: 0652.2560000
; CURRENT APPLICATION NUMBER: US/10/209,187A
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: EP 01 118 627.7
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Synthetic octapeptide
US-10-209-187A-5

Query Match 66.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
 |||||
Db 5 SVLS 8

RESULT 4
US-10-061-395-58
; Sequence 58, Application US/10061395
; Publication No. US20020192675A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Smith, Ernest S.
; TITLE OF INVENTION: Methods of Identifying Regulator Molecules
; FILE REFERENCE: 1821.0080003
; CURRENT APPLICATION NUMBER: US/10/061,395
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/271,423
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/265,880
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/265,589
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Myristoylation signal sequence from HIV (HTLV-III) gag
US-10-061-395-58

```
Query Match      66.7%; Score 4; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
   ||||
Db 5 SVLS 8

RESULT 5
US-10-052-942-64
; Sequence 64, Application US/10052942
; Publication No. US2003010402A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Smith, Ernest
; APPLICANT: Wei, Chungwen
; TITLE OF INVENTION: Methods of Producing or Identifying Intrabodies in Eukaryotic Cell
; FILE REFERENCE: 1821.0030004
; CURRENT APPLICATION NUMBER: US/10/052,942
; CURRENT FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: 60/298,095
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/271,422
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/263,200
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/263,225
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 64
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: signal sequence
US-10-052-942-64

Query Match      66.7%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
   ||||
Db 5 SVLS 8

RESULT 6
US-10-062-257-7
; Sequence 7, Application US/10062257
; Publication No. US20020128201A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; TITLE OF INVENTION: Tumor antigen
; FILE REFERENCE: GP00-1017
; CURRENT APPLICATION NUMBER: US/10/062,257
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-257-7

Query Match      66.7%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5
   ||||
Db 6 QSVL 9

RESULT 7
US-10-062-257-8
; Sequence 8, Application US/10062257
; Publication No. US20020128201A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; TITLE OF INVENTION: Tumor antigen
; FILE REFERENCE: GP00-1017
; CURRENT APPLICATION NUMBER: US/10/062,257
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-257-8

Query Match      66.7%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5
   ||||
Db 6 QSVL 9

RESULT 8
US-10-062-257-9
; Sequence 9, Application US/10062257
; Publication No. US20020128201A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; TITLE OF INVENTION: Tumor antigen
; FILE REFERENCE: GP00-1017
; CURRENT APPLICATION NUMBER: US/10/062,257
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-257-9

Query Match      66.7%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5
   ||||
Db 6 QSVL 9

RESULT 9
US-09-572-404B-1808
; Sequence 1808, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1808
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
```


FEATURE:
; OTHER INFORMATION: sequence located in EVX1 at 384-393 and may interact with Sequences
; OTHER INFORMATION: in this patent.
US-09-572-404B-1808

Query Match
Best Local Similarity 66.7%; Score 4; DB 11; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 4 SVLS 7

RESULT 10
US-09-572-404B-1810
; Sequence 1810, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; PRIOR FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1810
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in EVX1 at 383-392 and may interact with Sequences
; OTHER INFORMATION: in this patent.
US-09-572-404B-1810

Query Match
Best Local Similarity 66.7%; Score 4; DB 11; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 5 SVLS 8

RESULT 11
US-09-865-548A-152
; Sequence 152, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 152
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-152

Query Match
Best Local Similarity 66.7%; Score 4; DB 11; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 5 SVLS 8

RESULT 12
US-09-986-480-341
; Sequence 341, Application US/09986480
; Publication No. US20030027999A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 143 Human Secreted Proteins
; FILE REFERENCE: P8500P1
; CURRENT APPLICATION NUMBER: US/09/986,480
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/12788
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/134,068
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 456
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 341
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-986-480-341

Query Match
Best Local Similarity 66.7%; Score 4; DB 11; Length 11;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 8 SVLS 11

RESULT 13
US-09-242-450A-9
; Sequence 9, Application US/09242450A
; Patent No. US20020155552A1
; GENERAL INFORMATION:
; APPLICANT: Bergmann, Johanna
; TITLE OF INVENTION: "PRIONS", HIGHLY SPECIFIC MARKERS FOR NONINVASIVE PRE-SYMPTOMATIC DETECTION OF TSE DISEASES AND TARGETS FOR THERAPEUTIC REAGENTS
; FILE REFERENCE: 830006-2001
; CURRENT APPLICATION NUMBER: US/09/242,450A
; CURRENT FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: PRT
; ORGANISM: mouse
; US-09-242-450A-9

Query Match
Best Local Similarity 66.7%; Score 4; DB 10; Length 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 POSV 4
Db 5 POSV 8

RESULT 14
US-10-254-446A-214
; Sequence 214, Application US/10254446A
; Publication No. US20030113714A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M
; APPLICANT: Smalley, Richard E.

; APPLICANT: Ryan, Esther
; APPLICANT: Lee, Seung-Wuk
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
; FILE REFERENCE: 119927-1066
; CURRENT APPLICATION NUMBER: US/10/254,446A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/325,664
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 214
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopar
US-10-254-446A-214

Query Match 66.7%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQSV 4
|
|
|
|
Db 8 PQSV 11

RESULT 15
US-09-242-450A-8
; Sequence 8, Application US/09242450A
; Patent No. US20020155552A1
; GENERAL INFORMATION:
; APPLICANT: Bergmann, Johanna
; TITLE OF INVENTION: "PRIONINS", HIGHLY SPECIFIC MARKERS FOR NONINVASIVE PRE-SYMPTOM
; TITLE OF INVENTION: DETECTION OF TSE DISEASES AND TARGETS FOR THERAPEUTIC REAGENTS
; FILE REFERENCE: 830006-2001
; CURRENT APPLICATION NUMBER: US/09/242,450A
; CURRENT FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-242-450A-8

Query Match 66.7%; Score 4; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQSV 4
|
|
|
|
Db 7 PQSV 10

RESULT 16
US-10-097-065-571
; Sequence 571, Application US/10097065
; Publication No. US20030055236A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: P2021P1
; CURRENT APPLICATION NUMBER: US/10/097,065
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057

; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,008
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,365
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 571
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-065-571

Query Match 66.7%; Score 4; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
|
|
|
|
Db 5 SVLS 8

RESULT 17
US-09-791-378-194
; Sequence 194, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 194
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-194

Query Match 66.7%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
|
|
|
|
Db 7 SVLS 10

RESULT 18
US-09-933-767-582
; Sequence 582, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:

; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,881
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,880
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,896
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,020
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,876
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,895
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,884
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,894
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,971
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,882
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,899
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,893
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,900
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,901
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,892
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,915
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,019
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,972
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,916
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,373
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,875
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,374
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,917
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,949
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06

; PRIOR APPLICATION NUMBER: 60/048,883
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,897
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,898
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,962
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,963
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,877
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,878
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 582
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-933-767-582

Query Match 66.7%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 11 SVLS 14

RESULT 19
US-10-023-282-582
; Sequence 582, Application US/10023282
; Publication No. US2003002893A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/10/023,282
; CURRENT FILING DATE: 2001-12-20
; EARLIER APPLICATION NUMBER: 09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04

```
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
```

```
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 582
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-282-582

Query Match      66.7%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVLS 6
      ||||
Db      11 SVLS 14

RESULT 20
US-09-563-222-14
; Sequence 14, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-14

Query Match      66.7%; Score 4; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QSVL 5
      ||||
Db      4 QSVL 7

RESULT 21
US-10-272-248-23
; Sequence 23, Application US/10272248
; Publication No. US20030176337A1
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
```

; APPLICATION NUMBER: US/10/272,248
; FILING DATE: 15-Oct-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/593,321
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/307,200
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-272-248-23

Query Match 66.7%; Score 4; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 14 SVLS 17

RESULT 22
US-10-029-386-34123
; Sequence 34123, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEONICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34123
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007281.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
US-10-029-386-34123

Query Match 66.7%; Score 4; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 10 SVLS 13

RESULT 23
US-09-876-904A-142
; Sequence 142, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOsome COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 142
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Bos sp.
; FEATURE:
; OTHER INFORMATION: Karyophilic peptide
US-09-876-904A-142

Query Match 66.7%; Score 4; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSVL 5
Db 15 QSVL 18

RESULT 24
US-10-219-834-128
; Sequence 128, Application US/10219834
; Publication No. US20030096751A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE
; FILE REFERENCE: D0191 NP
; CURRENT APPLICATION NUMBER: US/10/219,834
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/313,658
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/340,703
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: US 60/318,675
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/355,596
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/333,417
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/338,367
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-834-128

Query Match 66.7%; Score 4; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 5 SVLS 8

RESULT 25
US-09-864-761-48427
; Sequence 48427, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng

```
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48427
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO L78810.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN ET474, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96
; OTHER INFORMATION: EST_HUMAN HIT: BE621144.1, EVALUATE 2.00e-03
US-09-864-761-48427

Query Match 66.7%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 12 SVLS 15

RESULT 26
US-10-195-730-116
; Sequence 116, Application US/10195730
; Publication No. US2003014492A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al
; TITLE OF INVENTION: 101 Human Secreted Proteins
; FILE REFERENCE: P2017P1
; CURRENT APPLICATION NUMBER: US/10/195,730

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48427
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO L78810.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN ET474, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96
; OTHER INFORMATION: EST_HUMAN HIT: BE621144.1, EVALUATE 2.00e-03
US-09-864-761-48427

Query Match 66.7%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 12 SVLS 15

RESULT 26
US-10-195-730-116
; Sequence 116, Application US/10195730
; Publication No. US2003014492A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al
; TITLE OF INVENTION: 101 Human Secreted Proteins
; FILE REFERENCE: P2017P1
; CURRENT APPLICATION NUMBER: US/10/195,730
```

```
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: US/09/281,976
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/060,837
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (20)
; OTHER INFORMATION: Xaa equals stop translation
US-10-195-730-116

Query Match 66.7%; Score 4; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 5 SVLS 8

RESULT 27
US-10-272-248-24
; Sequence 24, Application US/10272248
; Publication No. US20030176337A1
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; Karunaratne, Nedra
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/272,248
; FILING DATE: 15-Oct-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/593,321
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/307,200
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-272-248-24
```

Query Match 66.7%; Score 4; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5
Db 16 QSVL 19

RESULT 28
US-09-962-756-1150
; Sequence 1150, Application US/09962756
; Publication No. US20030195147A1
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAEFFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-40510S1
; CURRENT APPLICATION NUMBER: US/09/962,756
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1150
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (11)
; OTHER INFORMATION: Unknown amino acid; translation read-through at
; OTHER INFORMATION: TGA stop codon
US-09-962-756-1150

Query Match 66.7%; Score 4; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5
Db 2 QSVL 5

RESULT 29
US-08-839-248-1
; Sequence 1, Application US/08839248A
; Publication No. US20020034725A1
; GENERAL INFORMATION:
; APPLICANT: McKenna, Gillies
; APPLICANT: Muschel, Ruth J
; APPLICANT: Bernhard, Eric J
; APPLICANT: Sebt, Said M
; APPLICANT: Hamilton, Andrew D
; TITLE OF INVENTION: Sensitization of Cells to Radiation Therapy
; FILE REFERENCE: 09596-201
; CURRENT APPLICATION NUMBER: US/08/839,248A
; CURRENT FILING DATE: 1997-04-15
; EARLIER APPLICATION NUMBER: 60/015,477
; EARLIER FILING DATE: 1996-04-15
; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: H-ras farnesyltransferase recognition motif
US-08-839-248-1

Query Match 50.0%; Score 3; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
Db 2 VLS 4

RESULT 30
US-08-424-550B-538
; Sequence 538, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATTIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESS: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMESKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 538:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-538

Query Match 50.0%; Score 3; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQS 3
|||

```

Db          2 PQS 4

RESULT 31
US-09-770-967-1
; Sequence 1, Application US/09770967
; Patent No. US20020010184A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Bergman, Jeffrey M.
; TITLE OF INVENTION: Inhibitors of Prenyl-Protein Transferase
; FILE REFERENCE: 20495
; CURRENT APPLICATION NUMBER: US/09/770,967
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/183,651
; PRIOR FILING DATE: 2000-2-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homosapien
US-09-770-967-1

Query Match          50.0%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 VLS 6
           |||
Db          2 VLS 4

RESULT 32
US-09-858-369-1
; Sequence 1, Application US/09858369
; Patent No. US2002022633A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Williams, Theresa M.
; APPLICANT: Stump, Craig A.
; TITLE OF INVENTION: Inhibitors of Prenyl-Protein Transferase
; FILE REFERENCE: 20673
; CURRENT APPLICATION NUMBER: US/09/858,369
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/215,655
; PRIOR FILING DATE: 2000/06/30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homosapien
US-09-858-369-1

Query Match          50.0%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 VLS 6
           |||
Db          2 VLS 4

RESULT 33
US-09-757-251-2
; Sequence 2, Application US/09757251
; Patent No. US20020049217A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: S. Jane deSolms
; APPLICANT: Suzanne C. MacTough
; APPLICANT:

```

```

; APPLICANT: Anthony W. Shaw
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20604Y
; CURRENT APPLICATION NUMBER: US/09/757,251
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175,784
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: N-terminus of Ras protein
US-09-757-251-2

Query Match          50.0%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 VLS 6
           |||
Db          2 VLS 4

RESULT 34
US-09-784-897A-1
; Sequence 1, Application US/09784897A
; Patent No. US20020052363A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Bergman, Jeffrey M.
; TITLE OF INVENTION: PRENYL-PROTEIN TRANSFERASE INHIBITORS
; FILE REFERENCE: 20497
; CURRENT APPLICATION NUMBER: US/09/784,897A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/183,449
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic sequence
US-09-784-897A-1

Query Match          50.0%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 VLS 6
           |||
Db          2 VLS 4

RESULT 35
US-09-770-983-1
; Sequence 1, Application US/09770983
; Patent No. US20020052380A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Bergman, Jeffrey M.
; TITLE OF INVENTION: Inhibitors of Prenyl-Protein Transferase
; FILE REFERENCE: 20309
; CURRENT APPLICATION NUMBER: US/09/770,983
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/183,650
; PRIOR FILING DATE: 2000-2-18

```


; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homosapiens
US-09-770-983-1

Query Match 50.0%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
|||
Db 2 VLS 4

RESULT 36
US-09-834-765-742
; Sequence 742, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 742
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-742

Query Match 50.0%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
|||
Db 1 SVL 3

RESULT 37
US-09-853-918-12
; Sequence 12, Application US/09853918
; Patent No. US20020068346A1
; GENERAL INFORMATION:
; APPLICANT: Krystek, Stanley R.
; APPLICANT: Sheriff, Steven
; APPLICANT: Witmer, Mark R.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Yan, Ning
; APPLICANT: Mouravieff, Julie E.
; APPLICANT: Einspahr, Howard M.
; APPLICANT: Kish, Kevin
; TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
; FILE REFERENCE: DE24NP
; CURRENT APPLICATION NUMBER: US/09/853,918
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,448
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 65

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-918-12

Query Match 50.0%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POS 3
|||
Db 2 POS 4

RESULT 38
US-09-828-325A-2
; Sequence 2, Application US/09828325A
; Patent No. US20020068747A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Craig A. Stump
; APPLICANT: Theresa M. Williams
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20636Y
; CURRENT APPLICATION NUMBER: US/09/828,325A
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/196,244
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: N-terminus of Ras protein
US-09-828-325A-2

Query Match 50.0%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
|||
Db 2 VLS 4

RESULT 39
US-09-757-217A-2
; Sequence 2, Application US/09757217A
; Patent No. US20020099007A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: S. Jane deSolms
; APPLICANT: Gerald E. Stokker
; APPLICANT: Anthony W. Shaw
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20603Y
; CURRENT APPLICATION NUMBER: US/09/757,217A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/175,801
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: N-terminus of Ras protein
US-09-757-217A-2

Query Match 50.0%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
|||
Db 2 VLS 4

RESULT 40
US-09-828-259A-2
; Sequence 2, Application US/09828259A
; Patent No. US20020123497A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Diem N. Nguyen
; APPLICANT: Craig A. Stump
; APPLICANT: Theresa M. Williams
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20637Y
; CURRENT APPLICATION NUMBER: US/09/828,259A
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,951
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: N-terminus of Ras protein
US-09-828-259A-2

Query Match 50.0%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
|||
Db 2 VLS 4

RESULT 41
US-09-751-100B-20
; Sequence 20, Application US/09751100B
; Patent No. US20020142436A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Human Adenylate Cyclase and Use Therefor
; FILE REFERENCE: P27948A
; CURRENT APPLICATION NUMBER: US/09/751,100B
; CURRENT FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Mouse
US-09-751-100B-20

Query Match 50.0%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
|||
Db 2 VLS 4

RESULT 42
US-09-784-818-1

; Sequence 1, Application US/09784818
; Publication No. US20020193283A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Bergman, Jeffrey M.
; TITLE OF INVENTION: PRENYL-PROTEIN TRANSFERASE INHIBITORS
; FILE REFERENCE: 20496
; CURRENT APPLICATION NUMBER: US/09/784,818
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,451
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic sequence
US-09-784-818-1

Query Match 50.0%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
|||
Db 2 VLS 4

RESULT 43
US-09-756-248-1
; Sequence 1, Application US/09756248
; Publication No. US20030134860A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinsmore, Christopher J.
; TITLE OF INVENTION: Inhibitors Of Prenyl-Protein Transferase
; FILE REFERENCE: 20341
; CURRENT APPLICATION NUMBER: US/09/756,248
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/175,706
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homosapien
US-09-756-248-1

Query Match 50.0%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
|||
Db 2 VLS 4

RESULT 44
US-09-932-165-1436
; Sequence 1436, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE

```

; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatP2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1436
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1436

Query Match          50.0%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVL 5
Db      1 SVL 3

RESULT 45
US-10-087-942-6
; Sequence 6, Application US/10087942
; Publication No. US20030165808A1
; GENERAL INFORMATION:
; APPLICANT: Haaland, Perry D.
; APPLICANT: Sherman, Douglas B.
; APPLICANT: Stewart II, Walter W.
; APPLICANT: Lloyd, Sheila A.
; APPLICANT: Campbell, Robert L.
; TITLE OF INVENTION: METHODS, APPARATUS AND COMPUTER PROGRAM PRODUCTS FOR
; TITLE OF INVENTION: FORMULATING CULTURE MEDIA
; FILE REFERENCE: P3250
; CURRENT APPLICATION NUMBER: US/10/087,942
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US/09/359,260
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hypothetical
US-10-087-942-6

Query Match          50.0%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 VLS 6
Db      1 VLS 3

RESULT 46
US-10-083-894-17
; Sequence 17, Application US/10083894
; Publication No. US20030170766A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Michael S.
; APPLICANT: Goldstein, Joseph L.

```

```

; Reiss, Yuval
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; IDENTIFICATION, CHARACTERIZATION, AND INHIBITION OF
; FARNESYL PROTEIN TRANSFERASE
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Artold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/083,894
; FILING DATE: 27-Feb-2002
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/937,893
; FILING DATE: 18-APR-1991
; APPLICATION NUMBER: US 07/615,713
; FILING DATE: 20-NOV-1990
; APPLICATION NUMBER: US 07/510,706
; FILING DATE: 18-APR-1990
; APPLICATION NUMBER: NOT APPLICABLE
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:249/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-083-894-17

Query Match          50.0%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 VLS 6
Db      2 VLS 4

RESULT 47
US-10-352-704-27
; Sequence 27, Application US/10352704
; Publication No. US20030176690A1
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; a Solid Support and Apparatus Permitting its
; Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; STATE: D.C.
; COUNTRY: U.S.A.

```

ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/352,704
FILING DATE: 28-Jan-2003
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/358,556A
FILING DATE: 14-DEC-1994
APPLICATION NUMBER: FR 9315164
FILING DATE: 16-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-352-704-27

Query Match 50.0%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4
Db 2 QSV 4

RESULT 48
US-10-317-644-6
Sequence 6, Application US/10317644
Publication No. US20030181355A1
GENERAL INFORMATION:
APPLICANT: Glenn, Jeffrey S.
TITLE OF INVENTION: METHOD FOR INHIBITION OF VIRAL INFECTION
FILE REFERENCE: 24004-20524.21
CURRENT APPLICATION NUMBER: US/10/317,644
CURRENT FILING DATE: 2002-12-11
PRIOR APPLICATION NUMBER: US 09/687,267
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 09/028,655
PRIOR FILING DATE: 1998-02-24
PRIOR APPLICATION NUMBER: US 08/347,448
PRIOR FILING DATE: 1995-06-23
PRIOR APPLICATION NUMBER: US 07/890,754
PRIOR FILING DATE: 1992-05-29
PRIOR APPLICATION NUMBER: PCT/US98/05247
PRIOR FILING DATE: 1993-06-01
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Mimic of a prenyl group
US-10-317-644-6

Query Match 50.0%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 VLS 6
Db 2 VLS 4

RESULT 49
US-10-087-905-6
Sequence 6, Application US/10087905
Publication No. US20030022152A1
GENERAL INFORMATION:
APPLICANT: Haaland, Perry D.
APPLICANT: Sherman, Douglas B.
APPLICANT: Stewart II, Walter W.
APPLICANT: Lloyd, Sheila A.
APPLICANT: Campbell, Robert L.
TITLE OF INVENTION: METHODS, APPARATUS AND COMPUTER PROGRAM PRODUCTS FOR FORMULATING CULTURE MEDIA
FILE REFERENCE: P3250
CURRENT APPLICATION NUMBER: US/10/087,905
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US/09/359,260
PRIOR FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: hypothetical
US-10-087-905-6

Query Match 50.0%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
Db 1 VLS 3

RESULT 50
US-10-211-088-360
Sequence 360, Application US/10211088
Publication No. US20030104479A1
GENERAL INFORMATION:
APPLICANT: Bright, Gary R.
APPLICANT: Premkumar, D. David
APPLICANT: Chen, Yih-Tai
TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular
FILE REFERENCE: 01-1022-US
CURRENT APPLICATION NUMBER: US/10/211,088
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/309,395
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/341,589
PRIOR FILING DATE: 2001-12-13
NUMBER OF SEQ ID NOS: 366
SOFTWARE: PatentIn version 3.1
SEQ ID NO 360
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Post-translational modification site
US-10-211-088-360

Query Match 50.0%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
|||
Db 2 VLS 4

RESULT 51

US-09-803-854-4
; Sequence 4, Application US/09803854
; Patent No. US20010046686A1
; GENERAL INFORMATION:
; APPLICANT: Albert J. Wong
; APPLICANT: David K. Moscatello
; APPLICANT: Allan Lipton
; APPLICANT: Kim E. Ieitzel
; TITLE OF INVENTION: Sensitive Detection of Wild-Type and
; TITLE OF INVENTION: Mutant EGFR by Specific ELISA Assays in Any Biological
; TITLE OF INVENTION: Sample
; FILE REFERENCE: W0N01-NP003
; CURRENT APPLICATION NUMBER: US/09/803,854
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/188,424
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-803-854-4

Query Match 50.0%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
|||
Db 1 VLS 3

RESULT 52

US-09-924-824-16
; Sequence 16, Application US/09924824
; Patent No. US20020103136A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Feng, Dong-Mei
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
; TITLE OF INVENTION: PROSTATE CANCER
; FILE REFERENCE: 20183Y
; CURRENT APPLICATION NUMBER: US/09/924,824
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/076,860
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic amino acid sequence
US-09-924-824-16

Query Match 50.0%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4
|||
Db 3 QSV 5

RESULT 53

US-09-924-824-17
; Sequence 17, Application US/09924824
; Patent No. US20020103136A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Feng, Dong-Mei
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
; TITLE OF INVENTION: PROSTATE CANCER
; FILE REFERENCE: 20183Y
; CURRENT APPLICATION NUMBER: US/09/924,824
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/076,860
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic amino acid sequence
; NAME/KEY: VARIANT
; LOCATION: (2)...(2)
; OTHER INFORMATION: clclohexylglycine
US-09-924-824-17

Query Match 50.0%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4
|||
Db 3 QSV 5

RESULT 54

US-09-751-100B-43
; Sequence 43, Application US/09751100B
; Patent No. US20020142436A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Human Adenylate Cyclase and Use Therefor
; FILE REFERENCE: P27948A
; CURRENT APPLICATION NUMBER: US/09/751,100B
; CURRENT FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mouse
US-09-751-100B-43

Query Match 50.0%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
|||
Db 3 VLS 5

RESULT 55

US-10-268-552-16
; Sequence 16, Application US/10268552
; Publication No. US2003013927A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: DeFeo-Jones, Deborah
; APPLICANT: Jones, Raymond E.
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
; TITLE OF INVENTION: PROSTATE CANCER
US-10-268-552-16

FILE REFERENCE: 20771
; CURRENT APPLICATION NUMBER: US/10/268,552
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,351
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid Sequence
US-10-268-552-16

Query Match 50.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSV 4
|||
Db 3 QSV 5

RESULT 56
US-10-268-552-17
; Sequence 17, Application US/10268552
; Publication No. US2003013927A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: DeFeo-Jones, Deborah
; APPLICANT: Jones, Raymond E.
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
; TITLE OF INVENTION: PROSTATE CANCER
; FILE REFERENCE: 20771
; CURRENT APPLICATION NUMBER: US/10/268,552
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,351
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid Sequence
; NAME/KEY: VARIANT
; LOCATION: (2)...(2)
; OTHER INFORMATION: Xaa = cyclohexylglycine
US-10-268-552-17

Query Match 50.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSV 4
|||
Db 3 QSV 5

RESULT 57
US-10-076-047A-197
; Sequence 197, Application US/10076047A
; Publication No. US20030152935A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer
; FILE REFERENCE: 2543-1-026
; CURRENT APPLICATION NUMBER: US/10/076,047A
; CURRENT FILING DATE: 2002-02-13

; PRIOR APPLICATION NUMBER: GB 9919258.5
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: GB 0007754.5
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/GB00/03143
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 351
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 197
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-047A-197

Query Match 50.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVL 5
|||
Db 1 SVL 3

RESULT 58
US-10-076-047A-251
; Sequence 251, Application US/10076047A
; Publication No. US20030152935A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer
; FILE REFERENCE: 2543-1-026
; CURRENT APPLICATION NUMBER: US/10/076,047A
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: GB 9919258.5
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: GB 0007754.5
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/GB00/03143
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 351
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 251
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-047A-251

Query Match 50.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVL 5
|||
Db 1 SVL 3

RESULT 59
US-10-076-047A-296
; Sequence 296, Application US/10076047A
; Publication No. US20030152935A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer
; FILE REFERENCE: 2543-1-026
; CURRENT APPLICATION NUMBER: US/10/076,047A
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: GB 9919258.5
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: GB 0007754.5
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/GB00/03143

```
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 351
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-047A-296

Query Match          50.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVL 5
Db      1 SVL 3

RESULT 60
US-10-319-402-25
; Sequence 25, Application US/10319402
; Publication No. US20030176699A1
; GENERAL INFORMATION:
; APPLICANT: Joyce, Michael
; APPLICANT: Williams, Mark
; APPLICANT: Hindsgaul, Ole
; APPLICANT: Tyrrell, D. Lorne
; TITLE OF INVENTION: Inhibitors of Hepatitis C Virus Protease
; FILE REFERENCE: UALB-002
; CURRENT APPLICATION NUMBER: US/10/319,402
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 60/340,574
; PRIOR FILING DATE: 2001-12-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Domain in NS4A that binds to NS3 as discussed in the specification
; OTHER INFORMATION: (e.,g page 37)
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(5)
; OTHER INFORMATION: This sequence is shown in the specification using one-letter code
US-10-319-402-25

Query Match          50.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 VLS 6
Db      1 VLS 3

RESULT 61
US-10-352-704-29
; Sequence 29, Application US/10352704
; Publication No. US20030176690A1
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; a Solid Support and Apparatus Permitting its
; Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; STATE: D.C

Query Match          50.0%; Score 3; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/352,704
FILING DATE: 28-Jan-2003
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/358,556A
FILING DATE: 14-DEC-1994
APPLICATION NUMBER: FR 9315164
FILING DATE: 16-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-352-704-29

Query Match          50.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QSV 4
Db      2 QSV 4

RESULT 62
US-10-206-699-55
; Sequence 55, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-55

Query Match          50.0%; Score 3; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 PQS 3
|||
Db 1 PQS 3

RESULT 63

US-08-681-219-11
; Sequence 11, Application US/08681219
; Publication No. US20020058607A1
; GENERAL INFORMATION:
; APPLICANT: Takaaki Sato and Junn Yanagisawa
; TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
; TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF
; TITLE OF INVENTION: (PDZ/DHR) DOMAIN AND USES THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681.219
; FILING DATE: 22-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/48962/JPW/JKM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-681-219-11

Query Match 50.0%; Score 3; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSV 4
|||
Db 3 QSV 5

RESULT 64

US-09-742-582-22
; Sequence 22, Application US/09742582
; Patent No. US20010012615A1
; GENERAL INFORMATION:
; APPLICANT: Heidler, Steven A
; APPLICANT: Radding, Jeffrey A
; TITLE OF INVENTION: IPC SYNTHASE GENES FROM FUNGI
; FILE REFERENCE: X-11242 Sequence List
; Patent No. US20010012615A1
; CURRENT APPLICATION NUMBER: US/09/742,582
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/041,075
; PRIOR FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-09-742-582-22

Query Match 50.0%; Score 3; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVL 5
|||
Db 2 SVL 4

RESULT 65

US-09-924-824-27
; Sequence 27, Application US/09924824
; Patent No. US20020103136A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Feng, Dong-Mei
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
; TITLE OF INVENTION: PROSTATE CANCER
; FILE REFERENCE: 20183Y
; CURRENT APPLICATION NUMBER: US/09/924,824
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/076,860
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic amino acid sequence
US-09-924-824-27

Query Match 50.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSV 4
|||
Db 4 QSV 6

RESULT 66

US-09-924-824-28
; Sequence 28, Application US/09924824
; Patent No. US20020103136A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Feng, Dong-Mei
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
; TITLE OF INVENTION: PROSTATE CANCER
; FILE REFERENCE: 20183Y
; CURRENT APPLICATION NUMBER: US/09/924,824
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/076,860
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic amino acid sequence
; NAME/KEY: VARIANT
; LOCATION: (3)...(3)
; OTHER INFORMATION: cyclohexylglycine
US-09-924-824-28

Query Match 50.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4
|||
Db 4 QSV 6

RESULT 67
US-09-924-824-37
; Sequence 37, Application US/09924824
; Patent No. US20020103136A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Feng, Dong-Mei
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
; TITLE OF INVENTION: PROSTATE CANCER
; FILE REFERENCE: 20183Y
; CURRENT APPLICATION NUMBER: US/09/924,824
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/076,860
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic amino acid sequence
US-09-924-824-37

Query Match 50.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4
|||
Db 4 QSV 6

RESULT 68
US-09-924-824-38
; Sequence 38, Application US/09924824
; Patent No. US20020103136A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Feng, Dong-Mei
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
; TITLE OF INVENTION: PROSTATE CANCER
; FILE REFERENCE: 20183Y
; CURRENT APPLICATION NUMBER: US/09/924,824
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/076,860
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic amino acid sequence
; NAME/KEY: VARIANT
; LOCATION: (3)...(3)
; OTHER INFORMATION: cyclohexylglycine
US-09-924-824-38

Query Match 50.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4
|||
Db 4 QSV 6

RESULT 69
US-09-924-824-44
; Sequence 44, Application US/09924824
; Patent No. US20020103136A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Feng, Dong-Mei
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
; TITLE OF INVENTION: PROSTATE CANCER
; FILE REFERENCE: 20183Y
; CURRENT APPLICATION NUMBER: US/09/924,824
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/076,860
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic amino acid sequence
; NAME/KEY: VARIANT
; LOCATION: (3)...(3)
; OTHER INFORMATION: cyclohexylglycine
US-09-924-824-44

Query Match 50.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4
|||
Db 4 QSV 6

RESULT 70
US-09-873-233A-15
; Sequence 15, Application US/09873233A
; Patent No. US20020146434A1
; GENERAL INFORMATION:
; APPLICANT: UEDA, Shigeharu
; APPLICANT: KATANABE, Michiko
; APPLICANT: KAWANISHI, Hitomi
; TITLE OF INVENTION: GENE CODING FOR THE MEASLES VIRUS MUTANT ANTIGEN
; FILE REFERENCE: 0216-0451P
; CURRENT APPLICATION NUMBER: US/09/873,233A
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Measles virus
; FEATURE:
; OTHER INFORMATION: Attenuated measles virus NA strain
US-09-873-233A-15

Query Match 50.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4
|||
Db 2 QSV 4

```
RESULT 71
US-09-742-580-22
; Sequence 22, Application US/09742580
; Publication No. US20030022342A1
; GENERAL INFORMATION:
; APPLICANT: Heidler, Steven A
; TITLE OF INVENTION: IPC SYNTHASE GENES FROM FUNGI
; FILE REFERENCE: X-11242 Sequence 1st
; CURRENT APPLICATION NUMBER: US/09/742,580
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/041,075
; PRIOR FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-09-742-580-22

Query Match      50.0%; Score 3; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SVL 5
Db      2 SVL 4

RESULT 72
US-09-742-581-22
; Sequence 22, Application US/09742581
; Publication No. US20030022343A1
; GENERAL INFORMATION:
; APPLICANT: Heidler, Steven A
; TITLE OF INVENTION: IPC SYNTHASE GENES FROM FUNGI
; FILE REFERENCE: X-11242 Sequence 1st
; CURRENT APPLICATION NUMBER: US/09/742,581
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/041,075
; PRIOR FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-09-742-581-22

Query Match      50.0%; Score 3; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SVL 5
Db      2 SVL 4

RESULT 73
US-10-268-552-30
; Sequence 30, Application US/10268552
; Publication No. US20030133927A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Defeo-Jones, Deborah
; APPLICANT: Jones, Raymond E.
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
; FILE REFERENCE: 20771
; CURRENT APPLICATION NUMBER: US/10/268,552
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,351

US-10-268-552-40
; Sequence 40, Application US/10268552
; Publication No. US20030133927A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Defeo-Jones, Deborah
; APPLICANT: Jones, Raymond E.
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
; FILE REFERENCE: 20771
; CURRENT APPLICATION NUMBER: US/10/268,552
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,351

US-10-268-552-31
; Sequence 31, Application US/10268552
; Publication No. US20030133927A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Defeo-Jones, Deborah
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
; FILE REFERENCE: 20771
; CURRENT APPLICATION NUMBER: US/10/268,552
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,351
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid Sequence
; NAME/KEY: VARIANT
; LOCATION: (3)...(3)
; OTHER INFORMATION: Xaa = cyclohexylglycine
US-10-268-552-31

Query Match      50.0%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 QSV 4
Db      4 QSV 6

RESULT 75
US-10-268-552-40
; Sequence 40, Application US/10268552
; Publication No. US20030133927A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Defeo-Jones, Deborah
; APPLICANT: Jones, Raymond E.
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
; FILE REFERENCE: 20771
; CURRENT APPLICATION NUMBER: US/10/268,552
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,351

US-10-268-552-30
; Sequence 30, Application US/10268552
; Publication No. US20030133927A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Defeo-Jones, Deborah
; APPLICANT: Jones, Raymond E.
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
; FILE REFERENCE: 20771
; CURRENT APPLICATION NUMBER: US/10/268,552
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,351

US-10-268-552-31
; Sequence 31, Application US/10268552
; Publication No. US20030133927A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Defeo-Jones, Deborah
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
; FILE REFERENCE: 20771
; CURRENT APPLICATION NUMBER: US/10/268,552
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,351
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid Sequence
; NAME/KEY: VARIANT
; LOCATION: (3)...(3)
; OTHER INFORMATION: Xaa = cyclohexylglycine
US-10-268-552-31

Query Match      50.0%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 QSV 4
Db      4 QSV 6

RESULT 75
US-10-268-552-40
; Sequence 40, Application US/10268552
; Publication No. US20030133927A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Defeo-Jones, Deborah
; APPLICANT: Jones, Raymond E.
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
; FILE REFERENCE: 20771
; CURRENT APPLICATION NUMBER: US/10/268,552
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,351
```

```
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid Sequence
US-10-268-552-40
```

```
Query Match      50.0%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QSV 4
        |||
Db       4 QSV 6
```

```
Search completed: November 25, 2003, 20:37:03
Job time : 10.6279 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 4.84884 Seconds
(without alignments)
52.356 Million cell updates/sec

Title: US-09-641-801-26
Perfect score: 6
Sequence: 1 PQSVLS 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

- Database : Issued Patents AA.*
- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	6	100.0	6	4	US-09-641-803-26	Sequence 26, Appl	
2	6	100.0	20	3	US-08-505-250-12	Sequence 12, Appl	
3	6	100.0	20	4	US-08-505-250-12	Sequence 12, Appl	
4	4	66.7	4	2	US-08-691-997-12	Sequence 12, Appl	
5	4	66.7	5	2	US-08-691-997-11	Sequence 11, Appl	
6	4	66.7	5	4	US-09-360-237-10	Sequence 10, Appl	
7	4	66.7	5	4	US-09-522-666-31	Sequence 31, Appl	
8	4	66.7	6	2	US-08-691-997-3	Sequence 3, Appl	
9	4	66.7	7	4	US-09-537-817B-7	Sequence 7, Appl	
10	4	66.7	8	2	US-08-373-190-39	Sequence 39, Appl	
11	4	66.7	8	2	US-08-350-260A-382	Sequence 382, App	
12	4	66.7	8	2	US-08-438-190A-39	Sequence 39, Appl	
13	4	66.7	8	3	US-08-350-215-39	Sequence 39, Appl	
14	4	66.7	8	3	US-08-287-145A-39	Sequence 39, Appl	
15	4	66.7	8	4	US-09-556-111-39	Sequence 39, Appl	
16	4	66.7	8	4	US-09-104-337A-382	Sequence 382, App	
17	4	66.7	9	2	US-08-691-997-9	Sequence 9, Appl	
18	4	66.7	10	4	US-09-298-924-39	Sequence 39, Appl	
19	4	66.7	11	1	US-07-791-935B-13	Sequence 13, Appl	
20	4	66.7	12	2	US-08-811-492-150	Sequence 150, App	
21	4	66.7	13	2	US-08-691-997-8	Sequence 8, Appl	
22	4	66.7	13	4	US-09-522-666-30	Sequence 30, Appl	
23	4	66.7	13	4	US-09-257-825B-22	Sequence 22, Appl	
24	4	66.7	13	6	5242798-11	Patent No. 5242798	
25	4	66.7	14	1	US-07-791-935B-9	Sequence 9, Appl	
26	4	66.7	14	2	US-08-691-997-4	Sequence 4, Appl	
27	4	66.7	15	1	US-08-268-251-5	Sequence 5, Appl	

28	4	66.7	15	1	US-08-342-411A-21	Sequence 21, Appl
29	4	66.7	15	1	US-08-397-633A-80	Sequence 80, Appl
30	4	66.7	15	1	US-08-397-633A-81	Sequence 81, Appl
31	4	66.7	15	1	US-08-397-633A-83	Sequence 83, Appl
32	4	66.7	15	3	US-08-684-187-4	Sequence 4, Appl
33	4	66.7	15	4	US-09-537-817B-2	Sequence 2, Appl
34	4	66.7	15	4	US-09-205-258-582	Sequence 582, App
35	4	66.7	15	5	PCT-US93-01112-5	Sequence 5, Appl
36	4	66.7	16	2	US-08-480-190-37	Sequence 37, Appl
37	4	66.7	16	2	US-08-488-379-37	Sequence 37, Appl
38	4	66.7	16	4	US-09-360-237-55	Sequence 55, Appl
39	4	66.7	16	4	US-08-475-399A-37	Sequence 37, Appl
40	4	66.7	16	5	PCT-US93-07545-37	Sequence 37, Appl
41	4	66.7	17	1	US-08-360-125-19	Sequence 19, Appl
42	4	66.7	17	2	US-08-450-578-19	Sequence 19, Appl
43	4	66.7	17	2	US-09-017-628-19	Sequence 19, Appl
44	4	66.7	17	2	US-09-014-880-19	Sequence 19, Appl
45	4	66.7	17	3	US-08-658-857B-23	Sequence 23, Appl
46	4	66.7	17	3	US-08-763-226C-23	Sequence 23, Appl
47	4	66.7	17	3	US-09-307-200-23	Sequence 23, Appl
48	4	66.7	17	4	US-08-450-363-19	Sequence 19, Appl
49	4	66.7	17	4	US-09-593-321-23	Sequence 23, Appl
50	4	66.7	19	1	US-08-519-777-15	Sequence 15, Appl
51	4	66.7	19	1	US-08-742-035-15	Sequence 15, Appl
52	4	66.7	19	2	US-08-777-019-15	Sequence 15, Appl
53	4	66.7	19	2	US-08-777-143-15	Sequence 15, Appl
54	4	66.7	19	3	US-08-775-414-15	Sequence 15, Appl
55	4	66.7	19	3	US-08-931-858E-15	Sequence 15, Appl
56	4	66.7	19	3	US-08-981-739-15	Sequence 15, Appl
57	4	66.7	19	4	US-09-128-026-15	Sequence 15, Appl
58	4	66.7	19	4	US-09-257-825B-23	Sequence 23, Appl
59	4	66.7	20	3	US-08-658-857B-24	Sequence 24, Appl
60	4	66.7	20	3	US-08-763-226C-24	Sequence 24, Appl
61	4	66.7	20	3	US-09-307-200-24	Sequence 24, Appl
62	4	66.7	20	4	US-09-593-321-24	Sequence 24, Appl
63	3	50.0	4	1	US-07-772-087-8	Sequence 8, Appl
64	3	50.0	4	1	US-08-199-778-4	Sequence 4, Appl
65	3	50.0	4	1	US-08-240-712-5	Sequence 5, Appl
66	3	50.0	4	1	US-08-387-156-22	Sequence 22, Appl
67	3	50.0	4	1	US-08-443-890-5	Sequence 5, Appl
68	3	50.0	4	2	US-08-667-001-13	Sequence 13, Appl
69	3	50.0	4	2	US-08-694-865-28	Sequence 28, Appl
70	3	50.0	4	2	US-08-358-556A-27	Sequence 27, Appl
71	3	50.0	4	2	US-08-637-759B-200	Sequence 200, App
72	3	50.0	4	2	US-08-429-964-19	Sequence 19, Appl
73	3	50.0	4	2	US-08-878-748-22	Sequence 22, Appl
74	3	50.0	4	2	US-08-707-082A-18	Sequence 18, Appl
75	3	50.0	4	3	US-08-582-076-2	Sequence 2, Appl
76	3	50.0	4	3	US-08-871-355A-200	Sequence 200, App
77	3	50.0	4	3	US-09-124-491-28	Sequence 28, Appl
78	3	50.0	4	3	US-09-195-578-11	Sequence 11, Appl
79	3	50.0	4	3	US-08-894-173-20	Sequence 20, Appl
80	3	50.0	4	3	US-09-140-557-11	Sequence 11, Appl
81	3	50.0	4	3	US-09-170-951-11	Sequence 11, Appl
82	3	50.0	4	3	US-09-164-482-11	Sequence 11, Appl
83	3	50.0	4	3	US-09-330-970-16	Sequence 16, Appl
84	3	50.0	4	3	US-09-330-970-34	Sequence 34, Appl
85	3	50.0	4	3	US-09-058-562-5	Sequence 5, Appl
86	3	50.0	4	3	US-09-398-193-20	Sequence 20, Appl
87	3	50.0	4	3	US-09-167-180-11	Sequence 11, Appl
88	3	50.0	4	4	US-09-360-237-11	Sequence 11, Appl
89	3	50.0	4	4	US-09-360-233-38	Sequence 38, Appl
90	3	50.0	4	4	US-09-426-533-1	Sequence 1, Appl
91	3	50.0	4	4	US-09-516-945-1	Sequence 1, Appl
92	3	50.0	4	4	US-09-201-945-200	Sequence 200, App
93	3	50.0	4	4	US-09-757-218-2	Sequence 2, Appl
94	3	50.0	4	4	US-09-516-757-1	Sequence 1, Appl
95	3	50.0	4	4	US-09-516-750-1	Sequence 1, Appl
96	3	50.0	4	4	US-09-342-577-2	Sequence 2, Appl
97	3	50.0	4	4	US-09-516-756-1	Sequence 1, Appl
98	3	50.0	4	4	US-09-828-061A-2	Sequence 2, Appl
99	3	50.0	4	4	US-09-463-917-1	Sequence 1, Appl
100	3	50.0	4	4	US-09-347-673-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-641-803-26
; Sequence 26, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-26

Query Match 100.0%; Score 6; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Qy 1 PQSVLS 6
Db 1 PQSVLS 6
|||

RESULT 2
US-08-505-250-12
; Sequence 12, Application US/08505250
; Patent No. 6183983
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kokichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Sakagami, Masahiro
; APPLICANT: Taniguchi, Makoto
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
; FILE REFERENCE: 110-511
; CURRENT APPLICATION NUMBER: US/08/505,250
; CURRENT FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: PCT/JP95/00298
; EARLIER FILING DATE: 1995-02-27
; EARLIER APPLICATION NUMBER: JP 198187/94
; EARLIER FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-08-505-250-12

Query Match 100.0%; Score 6; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.67; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Qy 1 PQSVLS 6
Db 2 PQSVLS 7
|||

RESULT 3
US-08-505-250-12
; Sequence 12, Application US/08505250
; Patent No. 6322996
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kokichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Sakagami, Masahiro
; APPLICANT: Taniguchi, Makoto
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
; FILE REFERENCE: 110-511
; CURRENT APPLICATION NUMBER: US/08/505,250
; CURRENT FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: PCT/JP95/00298
; PRIOR FILING DATE: 1995-02-27
; PRIOR APPLICATION NUMBER: JP 198187/94
; PRIOR FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-08-505-250-12

Query Match 100.0%; Score 6; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.67; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Qy 1 PQSVLS 6
Db 2 PQSVLS 7
|||

RESULT 4
US-08-691-997-12
; Sequence 12, Application US/08691997
; Patent No. 5858682
; GENERAL INFORMATION:
; APPLICANT: Gruenwald, Stefan
; APPLICANT: Sang, Bi-Ching
; APPLICANT: Monell, Craig
; TITLE OF INVENTION: E2A/dbx1 FUSION PROTEIN
; TITLE OF INVENTION: SPECIFIC MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,997

```
;
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 219/251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-691-997-12

Query Match 66.7%; Score 4; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 1 SVLS 4

RESULT 5
US-08-691-997-11
; Sequence 11, Application US/08691997
; Patent No. 5858682
; GENERAL INFORMATION:
; APPLICANT: Gruenwald, Stefan
; APPLICANT: Sang, Bi-Ching
; APPLICANT: Monell, Craig
; TITLE OF INVENTION: E2A/px1 FUSION PROTEIN
; TITLE OF INVENTION: SPECIFIC MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,997
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 219/251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 11:
```

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-691-997-11

Query Match 66.7%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 2 SVLS 5

RESULT 6
US-09-360-237-10
; Sequence 10, Application US/09360237
; Patent No. 632962
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: CHENG, DONG
; APPLICANT: ESPENSHADE, PETER J.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: RAWSON, ROBERT B.
; APPLICANT: SAKAI, JURO
; TITLE OF INVENTION: STEROL-REGULATED SITE-1 PROTEASE AND ASSAYS OF
; TITLE OF INVENTION: MODULATORS THEREOF
; FILE REFERENCE: UTXD:567
; CURRENT APPLICATION NUMBER: US/09/360,237
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/096,571
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
; US-09-360-237-10

Query Match 66.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 2 SVLS 5

RESULT 7
US-09-522-666-31
; Sequence 31, Application US/09522666
; Patent No. 6333167
; GENERAL INFORMATION:
; APPLICANT: Shuey, David
; APPLICANT: Quinet, Elaine
; TITLE OF INVENTION: Methods and Reagents for Identifying Inhibitors of
; TITLE OF INVENTION: Proteolysis of Membrane-Associated Proteins
; FILE REFERENCE: 6-00
; CURRENT APPLICATION NUMBER: US/09/522,666
; CURRENT FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:amino acid
; OTHER INFORMATION: sequence within human, hamster SREBP-2 recognized
; OTHER INFORMATION: by Site-1 protease
US-09-522-666-31

Query Match          66.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
   ||||
Db  2 SVLS 5

RESULT 8
US-08-691-997-3
; Sequence 3, Application US/08691997
; Patent No. 5858682
; GENERAL INFORMATION:
; APPLICANT: Gruenwald, Stefan
; APPLICANT: Sang, Bi-Ching
; APPLICANT: Monelli, Craig
; TITLE OF INVENTION: E2A/pbx1 FUSION PROTEIN
; TITLE OF INVENTION: SPECIFIC MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,997
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 219/251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-691-997-3

Query Match          66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
   ||||
Db  3 SVLS 6

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:amino acid
; OTHER INFORMATION: sequence within human, hamster SREBP-2 recognized
; OTHER INFORMATION: by Site-1 protease
US-09-522-666-31

Query Match          66.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
   ||||
Db  2 SVLS 5

RESULT 9
US-09-537-817B-7
; Sequence 7, Application US/09537817B
; Patent No. 6417327
; GENERAL INFORMATION:
; APPLICANT: Shuichi Oka
; APPLICANT: Yoshimitsu Yamazaki
; APPLICANT: Toru Imamura
; APPLICANT: Yasuko Fujita
; APPLICANT: Saori Yamamoto
; APPLICANT: Yukiko Okita
; APPLICANT: Kazuo Ozawa
; APPLICANT: Reiko Akakura
; APPLICANT: Chikako Ito
; TITLE OF INVENTION: PEPTIDE CAPABLE OF REGULATING
; TITLE OF INVENTION: PHYSIOLOGICAL FUNCTION OF FGF-5 AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITION CONTAINING THE PEPTIDE
; FILE REFERENCE: 08206-012001
; CURRENT APPLICATION NUMBER: US/09/537,817B
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: JP 88364/1999
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: JP 6643/2000
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEQ ID NO:7 represents a partial sequence
; OTHER INFORMATION: (corresponding to amino acids 111-117) of the
; OTHER INFORMATION: amino acid sequence of mouse FGF-5.
US-09-537-817B-7

Query Match          66.7%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
   ||||
Db  4 SVLS 7

RESULT 10
US-08-373-190-39
; Sequence 39, Application US/08373190
; Patent No. 5851829
; GENERAL INFORMATION:
; APPLICANT: MARASCO, WAYNE
; APPLICANT: HASELTINE, WILLIAM
; TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF PROTEINS
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,190
; FILING DATE: 17-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06735
```

```

; FILING DATE: 16-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41956-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: STRE UR 2002
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-373-190-39

Query Match 66.7%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 5 SVLS 8

RESULT 11
US-08-350-260A-382
; Sequence 382, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: banding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: EISENSTEIN, RONALD I.
; REGISTRATION NUMBER: 30628
; REFERENCE/DOCKET NUMBER: 41956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; 
```

```

; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 382:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-350-260A-382

Query Match 66.7%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 1 SVLS 4

RESULT 12
US-08-438-190A-39
; Sequence 39, Application US/08438190A
; Patent No. 5965371
; GENERAL INFORMATION:
; APPLICANT: MARASCO, WAYNE
; APPLICANT: HASELTINE, WILLIAM
; TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,190A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: EISENSTEIN, RONALD I.
; REGISTRATION NUMBER: 30628
; REFERENCE/DOCKET NUMBER: 41956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; 
```



```
; TOPOLOGY: linear
US-08-438-190A-39
Query Match          66.7%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 5 SVLS 8

RESULT 13
US-08-350-215-39
; Sequence 39, Application US/08350215
; Patent No. 6004940
; GENERAL INFORMATION:
; APPLICANT: MARASCO, WAYNE A.
; TITLE OF INVENTION: INTRACELLULAR TARGETING OF ENDOGENOUS
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/287,145A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US/08/438,190
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: EISENSTEIN, RONALD I.
; REGISTRATION NUMBER: 30628
; REFERENCE/DOCKET NUMBER: 41956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-287-145A-39
Query Match          66.7%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 5 SVLS 8

RESULT 14
US-09-287-145A-39
; Sequence 39, Application US/09287145A
; Patent No. 6072036
; GENERAL INFORMATION:
; APPLICANT: MARASCO, WAYNE
; TITLE OF INVENTION: INTRACELLULAR BINDING OF
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 78

US-08-350-215-39
Query Match          66.7%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 5 SVLS 8

RESULT 15
US-09-556-111-39
; Sequence 39, Application US/09556111
; Patent No. 6329173
; GENERAL INFORMATION:
; APPLICANT: MARASCO, WAYNE
; TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
; PROTEINS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/556,111
; FILING DATE: 21-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,190
```

```

; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: EISENSTEIN, RONALD I.
; REGISTRATION NUMBER: 30628
; REFERENCE/DOCKET NUMBER: 41956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-556-111-39

Query Match      66.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SVLS 6
Db      5 SVLS 8
      |||||

RESULT 16
US-09-104-337A-382
; Sequence 382, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 382:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 382:
US-09-104-337A-382

Query Match      66.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SVLS 6
Db      1 SVLS 4
      |||||

RESULT 17
US-08-691-997-9
; Sequence 9, Application US/08691997
; Patent No. 5858682
; GENERAL INFORMATION:
; APPLICANT: Gruenwald, Stefan
; APPLICANT: Sang, Bi-Ching
; APPLICANT: Monell, Craig
; TITLE OF INVENTION: E2A/pbx1 FUSION PROTEIN
; TITLE OF INVENTION: SPECIFIC MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,997
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 219/251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-691-997-9

```

Query Match 66.7%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 4 SVLS 7

RESULT 18
US-09-298-924-39
; Sequence 39, Application US/09298924
; Patent No. 6391595
; GENERAL INFORMATION:
; APPLICANT: KATO, Masaru
; MIURA, Yutaka
; KETTOKU, Masako
; IWAMATSU, Akihiro
; KOBAYASHI, Kazuo
; KOMEDA, Toshihiro
; TITLE OF INVENTION: NOVEL TRANSFERASE AND AMYLASE, PROCESS
; FOR PRODUCING THE ENZYMES, USE THEREOF, AND GENE CODING
; FOR THE SAME
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; City: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,924
; FILING DATE: 26-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/750,569
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 7-120673
; FILING DATE: 21-APR-1995
; APPLICATION NUMBER: JP 6-311185
; FILING DATE: 21-NOV-1994
; APPLICATION NUMBER: JP 6-286917
; FILING DATE: 21-NOV-1994
; APPLICATION NUMBER: JP 6-290394
; FILING DATE: 31-OCT-1994
; APPLICATION NUMBER: JP 6-194223
; FILING DATE: 18-AUG-1994
; APPLICATION NUMBER: JP 6-133354
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 49441/110
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-298-924-39

Query Match 66.7%; Score 4; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 64;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 2 SVLS 5

RESULT 19
US-07-791-935B-13
; Sequence 13, Application US/07791935B
; Patent No. 5366871
; GENERAL INFORMATION:
; APPLICANT: RECHSTEINER, MARTIN C.
; APPLICANT: YOO, YUNG JOON
; TITLE OF INVENTION: UBIQUITIN-PEPTIDE EXTENSIONS AS
; ENZYME SUBSTRATES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thorpe, No. 5366871th & Western
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
; COMPUTER: compaq LTE/286
; OPERATING SYSTEM: DOS 4.01
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,935B
; FILING DATE: 19911113
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: na
; ATTORNEY/AGENT INFORMATION:
; NAME: Western, M. Wayne
; REGISTRATION NUMBER: 22,788
; REFERENCE/DOCKET NUMBER: T310
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801) 566-6633
; TELEFAX: (801) 566-0750
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acid residues
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-791-935B-13

Query Match 66.7%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 8 SVLS 11

RESULT 20
US-08-811-492-150
; Sequence 150, Application US/08811492
; Patent No. 5834247
; GENERAL INFORMATION:
; APPLICANT: COMB, DONALD G.
; APPLICANT: PERLER, FRANCINE B.
; APPLICANT: JACK, WILLIAM E.
; APPLICANT: XU, MING-QUN
; APPLICANT: HODGES, ROBERT A.
; APPLICANT: NOREN, CHRISTOPHER J.
; APPLICANT: CHONG, SHAO-RONG S.C.
; APPLICANT: ADAM, ERIC

```

; APPLICANT: SOUTHWORTH, MAURICE
; TITLE OF INVENTION: MODIFIED PROTEINS, METHODS OF THEIR
; TITLE OF INVENTION: PRODUCTION AND METHODS FOR PURIFICATION OF TARGET
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 155
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC\ DOS\MS\ DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,492
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/580,555
; FILING DATE: 29-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,247
; FILING DATE: 28-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,885
; FILING DATE: 03-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/004,139
; FILING DATE: 09-DEC-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Gregory D
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-036C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-927-5054
; TELEFAX: 509-927-1705
; TELEX:
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-811-492-150

Query Match 66.7%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 7 SVLS 10
|||
|||

RESULT 21
US-08-691-997-8
; Sequence 8, Application US/08691997
; Patent No. 5858682
; GENERAL INFORMATION:
; APPLICANT: Gruenwald, Stefan
; APPLICANT: Sang, Bi-Ching
; APPLICANT: Monell, Craig
; TITLE OF INVENTION: E2A/px1 FUSION PROTEIN
; TITLE OF INVENTION: SPECIFIC MONOCLONAL

```

```

; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,997
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 219/251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-691-997-8

Query Match 66.7%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 5 SVLS 8
|||
|||

RESULT 22
US-09-522-666-30
; Sequence 30, Application US/09522666
; Patent No. 6333167
; GENERAL INFORMATION:
; APPLICANT: Shuey, David
; APPLICANT: Quinet, Elaine
; TITLE OF INVENTION: Methods and Reagents for Identifying Inhibitors of
; TITLE OF INVENTION: Proteolysis of Membrane-Associated Proteins
; FILE REFERENCE: 6-00
; CURRENT APPLICATION NUMBER: US/09/522,666
; CURRENT FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:amino acid
; OTHER INFORMATION: sequence encompassing Site-1 protease cleavage
; OTHER INFORMATION: site within SREPB-2
US-09-522-666-30

```

```
Query Match          66.7%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVLS 6
      |||||
Db      8 SVLS 11

RESULT 23
US-09-257-825B-22
; Sequence 22, Application US/09257825B
; Patent No. 6403352
; GENERAL INFORMATION:
; APPLICANT: Poovaiah, Bachettira W.
; APPLICANT: Patil, Shameekumar
; APPLICANT: Takezawa, Daisuke
; TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants
; FILE REFERENCE: 4630-51993
; CURRENT APPLICATION NUMBER: US/09/257,825B
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: US 08/655,352
; PRIOR FILING DATE: 1996-05-23
; PRIOR APPLICATION NUMBER: US 60/014,743
; PRIOR FILING DATE: 1996-03-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 22
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Lilium longiflorum
US-09-257-825B-22

Query Match          66.7%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVLS 6
      |||||
Db      9 SVLS 12

RESULT 24
5242798-11
; Patent No. 5242798
; APPLICANT: SUTCLIFFE, J. GERGOR
; TITLE OF INVENTION: SYNTHETIC POLYPEPTIDES CORRESPONDING
; TO PORTIONS OF PROTEINOIDS TRANSLATED FROM BRAIN-SPECIFIC MRNAS,
; RECEPTORS, METHODS AND DIAGNOSTICS USING THE SAME
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/476,961
; FILING DATE: 07-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 58,620
; FILING DATE: 03-JUN-1987
; APPLICATION NUMBER: 516,136
; FILING DATE: 21-JUL-1983
; SEQ ID NO:11:
; LENGTH: 13
5242798-11

Query Match          66.7%; Score 4; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVLS 6
      |||||
Db      8 SVLS 11

RESULT 25
US-07-791-935B-9
```

```
; Sequence 9, Application US/07791935B
; Patent No. 5366871
; GENERAL INFORMATION:
; APPLICANT: RECHSTEINER, MARTIN C.
; APPLICANT: YOO, YUNG JOON
; TITLE OF INVENTION: UBIQUITIN-PEPTIDE EXTENSIONS AS
; ENZYME SUBSTRATES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thorpe, No. 5366871th & Western
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
; COMPUTER: compaq LTE/286
; OPERATING SYSTEM: DOS 4.01
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA: US/07/791,935B
; FILING DATE: 19911113
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: na
; ATTORNEY/AGENT INFORMATION:
; NAME: Western, M. Wayne
; REGISTRATION NUMBER: 22,788
; REFERENCE/DOCKET NUMBER: T310
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801) 566-6633
; TELEFAX: (801) 566-0750
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acid residues
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-791-935B-9

Query Match          66.7%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVLS 6
      |||||
Db      11 SVLS 14

RESULT 26
US-08-691-997-4
; Sequence 4, Application US/08691997
; Patent No. 5858682
; GENERAL INFORMATION:
; APPLICANT: Gruenwald, Stefan
; APPLICANT: Sang, Bi-Ching
; APPLICANT: Monell, Craig
; TITLE OF INVENTION: E2A/pbx1 FUSION PROTEIN
; SPECIFIC MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
```

```
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691.997
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34.613
; REFERENCE/DOCKET NUMBER: 219/251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-691-997-4

Query Match 66.7%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 3 SVLS 6

RESULT 27
US-08-268-251-5
; Sequence 5, Application US/08268251
; Patent No. 5585475
; GENERAL INFORMATION:
; APPLICANT: Jamieson, Gordon A
; APPLICANT: Dedman, John R
; APPLICANT: Kaetzel, Marcia A
; TITLE OF INVENTION: Calmodulin-Binding Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,251
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/831,219
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Grant D
; REGISTRATION NUMBER: 31,259
; REFERENCE/DOCKET NUMBER: 272.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 5:
```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-268-251-5

Query Match 66.7%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 10 SVLS 13

RESULT 28
US-08-342-411A-21
; Sequence 21, Application US/08342411A
; Patent No. 5639616
; GENERAL INFORMATION:
; APPLICANT: LIAO, Shutsung
; APPLICANT: SONG, Ching
; TITLE OF INVENTION: UBIQUITOUS NUCLEAR RECEPTOR:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,411A
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KITCHELL, BARBARA S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARCD154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-342-411A-21

Query Match 66.7%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 8 SVLS 11

RESULT 29
US-08-397-633A-80
; Sequence 80, Application US/08397633A
; Patent No. 5773577
```

```

; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-633A-80
;
; Query Match 66.7%; Score 4; DB 1; Length 15;
; Best Local Similarity 100.0%; Pred. No. 94;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 3 SVLS 6
Db 1 SVLS 4

; RESULT 30
; US-08-397-633A-81
; Sequence 81, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-633A-81
;
; Query Match 66.7%; Score 4; DB 1; Length 15;
; Best Local Similarity 100.0%; Pred. No. 94;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 3 SVLS 6
Db 1 SVLS 4

; RESULT 31
; US-08-397-633A-83
; Sequence 83, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-633A-83
;
; Query Match 66.7%; Score 4; DB 1; Length 15;
; Best Local Similarity 100.0%; Pred. No. 94;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 3 SVLS 6

```

Db 1 SVLS 4

RESULT 32

US-08-684-187-4

; Sequence 4, Application US/08684187A

; Patent No. 6020171

; GENERAL INFORMATION:

; APPLICANT: SAITO, ATSUSHI

; APPLICANT: SHINAGAWA, HIDEO

; APPLICANT: NAKATA, ATSUGO

; TITLE OF INVENTION: METHOD OF PREPARING PLASMID HAVING BOTH EXPRESSING

; TITLE OF INVENTION: ABILITY OF RETROVIRAL GENE AND PROCESSING ABILITY AFTER

; TITLE OF INVENTION: TRANSLATION AND RESULTANT PLASMID AND EXPRESSION

; TITLE OF INVENTION: PRODUCTS THEREOF

; FILE REFERENCE: 96-0747/1c(wmc)/653

; CURRENT APPLICATION NUMBER: US/08/684,187A

; CURRENT FILING DATE: 1996-07-19

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: N-TERMINAL

; OTHER INFORMATION: AMINO ACID SEQUENCE

US-08-684-187-4

Query Match 66.7%; Score 4; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 94;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6

Db 5 SVLS 8

RESULT 33

US-09-537-817B-2

; Sequence 2, Application US/09537817B

; Patent No. 6417327

; GENERAL INFORMATION:

; APPLICANT: Shuichi Oka

; APPLICANT: Yoshimitsu Yamazaki

; APPLICANT: Toru Imamura

; APPLICANT: Yasuko Fujita

; APPLICANT: Saori Yamamoto

; APPLICANT: Yukiko Okita

; APPLICANT: Kazuo Ozawa

; APPLICANT: Reiko Akakura

; APPLICANT: Chikako Ito

; TITLE OF INVENTION: PEPTIDE CAPABLE OF REGULATING

; TITLE OF INVENTION: PHYSIOLOGICAL FUNCTION OF FGF-5 AND PHARMACEUTICAL

; TITLE OF INVENTION: COMPOSITION CONTAINING THE PEPTIDE

; FILE REFERENCE: 08206-012001

; CURRENT APPLICATION NUMBER: US/09/537,817B

; CURRENT FILING DATE: 2001-08-23

; PRIOR APPLICATION NUMBER: JP 88364/1999

; PRIOR FILING DATE: 1999-03-30

; PRIOR APPLICATION NUMBER: JP 6643/2000

; PRIOR FILING DATE: 2000-01-14

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: SEQ ID NO:2 represents a partial sequence

; OTHER INFORMATION: (corresponding to amino acids 103-117) of the

; OTHER INFORMATION: amino acid sequence of mouse FGF-5.

US-09-537-817B-2

Query Match 66.7%; Score 4; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 94;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6

Db 12 SVLS 15

RESULT 34

US-09-205-258-582

; Sequence 582, Application US/09205258

; Patent No. 6525174

; GENERAL INFORMATION:

; APPLICANT: Young et al.

; TITLE OF INVENTION: 207 Human Secreted Proteins

; FILE REFERENCE: P2007P1

; CURRENT APPLICATION NUMBER: US/09/205,258

; CURRENT FILING DATE: 1998-12-04

; EARLIER APPLICATION NUMBER: PCT/US98/11422

; EARLIER FILING DATE: 1998-06-04

; EARLIER APPLICATION NUMBER: 60/048,885

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,375

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,881

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,880

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,896

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,020

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,876

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,895

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,884

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,894

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,971

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,964

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,882

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,899

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,893

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,900

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,901

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,892

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,915

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,019

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,970

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,972

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,916

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,373

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,875

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,374

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,862
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 582
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-582

Query Match 66.7%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
DB 11 SVLS 14

RESULT 35
PCT-US93-01112-5
Sequence 5, Application PC/TUS9301112
GENERAL INFORMATION:
APPLICANT: Jamieson, Gordon A
APPLICANT: Dedman, John R
APPLICANT: Kaetzel, Marcia A
TITLE OF INVENTION: Calmodulin-Binding Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSER: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01112
FILING DATE: 19930208
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,219
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:

NAME: Green, Grant D
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 272.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2706
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-01112-5

Query Match 66.7%; Score 4; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
DB 10 SVLS 13

RESULT 36
US-08-480-190-37
Sequence 37, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-37

```
Query Match          66.7%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVLS 6
Db      5 SVLS 8

RESULT 37
US-08-488-379-37
; Sequence 37, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-488-379-37

Query Match          66.7%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVLS 6
Db      5 SVLS 8

RESULT 38
US-09-360-237-55
; Sequence 55, Application US/09360237
; Patent No. 6322962
```

```
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: CHENG, DONG
; APPLICANT: ESPENSHADE, PETER J.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: RAWSON, ROBERT B.
; APPLICANT: SAKAI, JURO
; TITLE OF INVENTION: STEROL-REGULATED SITE-1 PROTEASE AND ASSAYS OF
; FILE REFERENCE: UTXD:567
; CURRENT APPLICATION NUMBER: US/09/360,237
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/096,571
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-360-237-55

Query Match          66.7%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVLS 6
Db      7 SVLS 10

RESULT 39
US-08-475-399A-37
; Sequence 37, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,399A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00246/168003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-507
```

```
/ TELEFAX: 617/542-890
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-475-399A-37

Query Match 66.7%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 5 SVLS 8

RESULT 40
PCT-US93-07545-37
; Sequence 37, Application PC/TUS9307545
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07545
; FILING DATE: 19930811
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PCT-US93-07545-37

Query Match 66.7%; Score 4; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 5 SVLS 8

RESULT 41
US-08-360-125-19
; Sequence 19, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human antibody GAH
; CELL LINE:
; ORGANELLER:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
```

```

; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-19
Query Match 66.7%; Score 4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5
Db 4 QSVL 7

RESULT 42
US-08-450-578-19
; Sequence 19, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,578
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids

```

```

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human antibody GAH
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-19
Query Match 66.7%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5
Db 4 QSVL 7

RESULT 43
US-09-017-628-19
; Sequence 19, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: TAGAWA, Toshiaki
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITO, No. 5990287ihiko
; APPLICANT: NAGAIKE, Kazuhiro
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; FILE REFERENCE: 177/527361KH
; CURRENT APPLICATION NUMBER: US/09/017,628
; CURRENT FILING DATE: 1998-02-02
; EARLIER APPLICATION NUMBER: 08/360,125
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 17

```

;; TYPE: PRT
;; ORGANISM: Unknown
;; FEATURE:
;; OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-19

Query Match 66.7%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 QSVL 5
Db 4 QSVL 7

RESULT 44
US-09-014-880-19
; Sequence 19, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,880
; FILING DATE: January 28, 1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,578
; FILING DATE: May 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; CELL TYPE: Hybridoma producing human antibody GAH
US-09-014-880-19

Query Match 66.7%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 QSVL 5

Db 4 QSVL 7

RESULT 45
US-08-658-857B-23
; Sequence 23, Application US/08658857B
; Patent No. 6040435
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Karunaratne, Nedra
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,857B
; FILING DATE: May 31, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/460,464
; FILING DATE: June 2, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-658-857B-23

Query Match 66.7%; Score 4; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 14 SVLS 17

RESULT 46
US-08-763-226C-23
; Sequence 23, Application US/08763226C
; Patent No. 6057291
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Karunaratne, Nedra
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

```

; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/763,226C
; FILING DATE: 10-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/658,857
; FILING DATE: 31-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/014001
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-763-226C-23

Query Match 66.7%; Score 4; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 14 SVLS 17

RESULT 47
US-09-307-200-23
; Sequence 23, Application US/09307200
; Patent No. 6297215
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Karunaratne, Nedra
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/307,200
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/763,226
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/014001
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

```

```

US-09-307-200-23

Query Match 66.7%; Score 4; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 14 SVLS 17

RESULT 48
US-08-450-363-19
; Sequence 19, Application US/08450363
; Patent No. 6436434
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 6436434hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,363
; FILING DATE: May 25, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human antibody GAH

```

```
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
;
US-08-450-363-19
Query Match 66.7%; Score 4; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5
Db 4 QSVL 7

RESULT 49
US-09-593-321-23
; Sequence 23, Application US/09593321
; Patent No. 6465429
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Karunaratne, Nedra
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/593,321
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/307,200
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/014001
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-593-321-23

Query Match 66.7%; Score 4; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 14 SVLS 17

RESULT 50
US-08-519-777-15
; Sequence 15, Application US/08519777
; Patent No. 5739307
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/519,777
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 953095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-519-777-15

Query Match 66.7%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 16 SVLS 19

RESULT 51
US-08-742-035-15
; Sequence 15, Application US/08742035
; Patent No. 5747655
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
```

```
; APPLICANT: KOTZBAUER, PAUL T.
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,035
; FILING DATE: 01-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/519,777
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 953095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-742-035-15

Query Match 66.7%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 16 SVLS 19
|||||

RESULT 52
US-08-777-019-15
; Sequence 15, Application US/08777019
; Patent No. 5817622
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,019
; FILING DATE: 30-DEC-1996
```

```
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/519,777
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 953095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-777-019-15

Query Match 66.7%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 16 SVLS 19
|||||

RESULT 53
US-08-777-143-15
; Sequence 15, Application US/08777143
; Patent No. 5843914
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,143
; FILING DATE: 30-DEC-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/519,777
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 953095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-777-143-15
```



```
Query Match 66.7%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 3 SVLS 6
Db 16 SVLS 19

RESULT 54
US-08-775-414-15
; Sequence 15, Application US/08775414
; Patent No. 6090778
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/775.414
; FILING DATE: 31-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965805
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-775-414-15

Query Match 66.7%; Score 4; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 3 SVLS 6
Db 16 SVLS 19

RESULT 55
US-08-931-858E-15
; Sequence 15, Application US/08931858E
; Patent No. 6222022
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; APPLICANT: KLEIN, ROBERT
; APPLICANT: DESAUVAGE, FRED
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
; NUMBER OF SEQUENCES: 239
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931.858E
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 971486
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-931-858E-15

Query Match 66.7%; Score 4; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 3 SVLS 6
Db 16 SVLS 19

RESULT 56
US-08-981-739-15
; Sequence 15, Application US/08981739
; Patent No. 6232449
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981.739
; FILING DATE: 31-Aug-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/03461
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
```



```
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-658-857B-24

Query Match 66.7%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSVL 5
Db 16 QSVL 19

RESULT 60
US-08-763-226C-24
; Sequence 24, Application US/08763226C
; Patent No. 6057291
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Karunaratne, Nedra
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/763,226C
; FILING DATE: 10-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/658,857
; FILING DATE: 31-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-763-226C-24

Query Match 66.7%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSVL 5
Db 16 QSVL 19

RESULT 61
US-09-307-200-24
; Sequence 24, Application US/09307200
; Patent No. 6297215
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Karunaratne, Nedra
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/307,200
; FILING DATE: 09/307,200
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/307,200
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-307-200-24

Query Match 66.7%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSVL 5
Db 16 QSVL 19

RESULT 62
US-09-593-321-24
; Sequence 24, Application US/09593321
; Patent No. 6465429
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Karunaratne, Nedra
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/593,321
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/307,200
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-593-321-24

Query Match 66.7%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSVL 5
Db 16 QSVL 19
```

```

; REFERENCE/DOCKET NUMBER: 07420/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-593-321-24

Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5
Db 16 QSVL 19

RESULT 63
US-07-772-087-8
; Sequence 8, Application US/07772087
; Patent No. 5275945
; GENERAL INFORMATION:
; APPLICANT: HSIAC, Hung-Yu
; APPLICANT: FODGE, Douglas W.
; APPLICANT: LALONDE, James J.
; TITLE OF INVENTION: ALKALINE PROTEASES STABLE IN HEAVY-DUTY
; TITLE OF INVENTION: DETERGENT LIQUIDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07772,087
; FILING DATE: 19911008
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16754/115 CHCO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacillus
; STRAIN: KPI239 from B. alcalophilus
US-07-772-087-8

Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4

```

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/240,712
;; FILING DATE: 09-MAY-1994
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/09752
;; FILING DATE: 13-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: COOPER, IVER P
;; REGISTRATION NUMBER: 28,005
;; REFERENCE/DOCKET NUMBER: ANDERSON=6
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; TELEX: 248633
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-240-712-5

Query Match 50.0%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
Db 1 VLS 3

RESULT 66
US-08-397-156-22
; Sequence 22, Application US/08387156
; Patent No. 5723129
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HUW P.A.
; TITLE OF INVENTION: GHRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 635 BRYANT STREET
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,156
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,932
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,171
; FILING DATE: 16-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0016.21

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 617-8999
;; TELEFAX: (415) 327-3231
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-387-156-22

Query Match 50.0%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
Db 2 VLS 4

RESULT 67
US-08-443-890-5
; Sequence 5, Application US/08443890
; Patent No. 5739011
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DAVID C.
; APPLICANT: MATHews, ANTONY JAMES
; APPLICANT: STETLER, GARY L.
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
; TITLE OF INVENTION: HEMOGLOBINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,890
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/240,712
; FILING DATE: 09-MAY-1994
; APPLICATION NUMBER: PCT/US92/09752
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: ANDERSON=6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-443-890-5

Query Match 50.0%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
|||
Db 1 VLS 3

RESULT 68

US-08-667-001-13
; Sequence 13, Application US/08667001
; Patent No. 5827827
; GENERAL INFORMATION:
; APPLICANT: Janda, Kim D.
; APPLICANT: Wirsching, Peter
; TITLE OF INVENTION: HIV-1 PROTEASE INHIBITOR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10666 No. 5827827th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,001
; FILING DATE: 20-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/335,039
; FILING DATE: 16-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lewis, Donald G.
; REGISTRATION NUMBER: 28,636
; REFERENCE/DOCKET NUMBER: TSRI 282.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note= "sequence = R" in formula
; OTHER INFORMATION:
US-08-667-001-13

Query Match 50.0%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4
|||
Db 2 QSV 4

RESULT 69

US-08-694-865-28
; Sequence 28, Application US/08694865
; Patent No. 5837268
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: MANN, JOHN G.
; TITLE OF INVENTION: GRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS LLP
; STREET: 285 HAMILTON AVENUE, SUITE 200
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/694,865
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 9001-0016.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)327-3400
; TELEFAX: (415)327-3231
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-694-865-28

Query Match 50.0%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
|||
Db 2 VLS 4

RESULT 70

US-08-358-556A-27
; Sequence 27, Application US/08358556A
; Patent No. 5869643
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; TITLE OF INVENTION: a Solid Support and Apparatus Permitting its
; TITLE OF INVENTION: Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409

REFERENCE/DOCKET NUMBER: 10577/P58418
TELEPHONE: (202)638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-556A-27

Query Match 50.0%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4

Db 2 QSV 4

RESULT 71

US-08-637-759B-200
Sequence 200, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 200:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-637-759B-200

Query Match 50.0%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4

Db 1 QSV 3

RESULT 72

US-08-429-964-19
Sequence 19, Application US/08429964
Patent No. 5962243
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: REISS, YUVAL
APPLICANT: JAMES, GUY L.
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
TRANSFERASE INHIBITORS
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,964
FILING DATE: 27-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,625
FILING DATE: 16-FEB-1993
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/822,011
FILING DATE: ABANDONED
CLASSIFICATION: 435
APPLICATION NUMBER: PCT/US/91/02650
FILING DATE: 18-APR-1991
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/615,715
FILING DATE: 20-NOV-1990
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/510,706
FILING DATE: 18-APR-1990 (ABANDONED)
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:432/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-429-964-19

Query Match 50.0%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6

Db 2 VLS 4

RESULT 73
 US-08-878-748-22
 ; Sequence 22, Application US/08878748
 ; Patent No. 5969126
 ; GENERAL INFORMATION:
 ; APPLICANT: POTTER, ANDREW A.
 ; APPLICANT: REDMOND, MARK J.
 ; APPLICANT: HUGHES, HUW P.A.
 ; TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: REED & ROBINS
 ; STREET: 635 BRYANT STREET
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: UNITED STATES OF AMERICA
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/878,748
 ; FILING DATE: 19-JUN-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/387,156
 ; FILING DATE: 10-FEB-1995
 ; APPLICATION NUMBER: US 07/960,932
 ; FILING DATE: 14-OCT-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/779,171
 ; FILING DATE: 16-OCT-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: ROBINS, ROBERTA L.
 ; REGISTRATION NUMBER: 33,208
 ; REFERENCE/DOCKET NUMBER: 9001-0016.21
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 617-8999
 ; TELEFAX: (415) 327-3231
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-878-748-22

Query Match 50.0%; Score 3; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
 |||
 Db 2 VLS 4

RESULT 74
 US-08-707-082A-18
 ; Sequence 18, Application US/08707082A
 ; Patent No. 5990277
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Levitzki, Chaim Gilon and Hadas Reuveni
 ; TITLE OF INVENTION: SEMIPEPTOID FARNESYL PROTEIN TRANSFERASE
 ; TITLE OF INVENTION: INHIBITORS AND ANALOGS THEREOF
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Mark M. Friedman c/o Robert Sheinbein
 ; STREET: 2940 Birchtree lane
 ; CITY: Silver Spring
 ; STATE: Maryland

; COUNTRY: United States of America
 ; ZIP: 20906
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
 ; COMPUTER: Twinhead* Slimnote-890TX
 ; OPERATING SYSTEM: MS DOS version 6.2,
 ; OPERATING SYSTEM: Windows version 3.11
 ; SOFTWARE: Word for Windows version 2.0 converted to
 ; SOFTWARE: an ASCII file
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/707,082A
 ; FILING DATE: 3 SEP 1996
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Friedmam, Mark M.
 ; REGISTRATION NUMBER: 33,883
 ; REFERENCE/DOCKET NUMBER: 325/7
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 972-3-5625553
 ; TELEFAX: 972-3-5625554
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-707-082A-18
 ; Query Match 50.0%; Score 3; DB 2; Length 4;
 ; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 ; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
 |||
 Db 2 VLS 4

RESULT 75
 US-08-582-076-2
 ; Sequence 2, Application US/08582076
 ; Patent No. 6011175
 ; GENERAL INFORMATION:
 ; APPLICANT: SEPTI, SAID
 ; APPLICANT: HAMILTON, ANDREW
 ; TITLE OF INVENTION: INHIBITION OF FARNESYLTRANSFERASE
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DABRY & CUSHMAN
 ; STREET: 1100 NEW YORK AVENUE, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/582,076
 ; FILING DATE: 02-JAN-1996
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOKULIS, PAUL N.
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: 220007/6137
 ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-582-076-2

Query Match 50.0%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 VLS 6
|||
Db 2 VLS 4

Search completed: November 25, 2003, 20:30:02
Job time : 5.84884 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 15.093 seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-27

Perfect score: 22

Sequence: 1 LSQPKVLPVKAVPQDMPIQ 22

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	18.2	10	2 A61218	alpha-gliadin 4Ha
2	4	18.2	10	2 B61218	alpha-gliadin 6Ha
3	4	18.2	11	2 PC4267	ribosomal protein
4	4	18.2	13	2 S09395	hypothetical prote
5	4	18.2	15	2 A49155	vasotocin-associat
6	4	18.2	17	2 JQ2030	hypothetical 1.9K
7	4	18.2	18	2 PNO149	beta-gliadine l3 -
8	4	18.2	19	2 S69153	Neb-colloostatin -
9	4	18.2	19	2 A37968	neural surface pro
10	4	18.2	20	2 S63602	glutathione S-tran
11	3	13.6	6	2 A35890	RNA-directed DNA p
12	3	13.6	7	2 PQ0663	membrane protein -
13	3	13.6	7	2 PC1316	large granule l3 c
14	3	13.6	8	2 B24749	neuropeptide B - b
15	3	13.6	8	2 A14683	aspartate transami
16	3	13.6	9	2 S78426	52.5K protein - sp
17	3	13.6	9	2 PC7073	ubiquinol-cytochro
18	3	13.6	10	1 XASNPC	angiotensin-conver
19	3	13.6	10	2 A46491	C3 homology HX - in
20	3	13.6	10	2 A44646	neurotoxin-associa
21	3	13.6	10	2 I44644	neurotoxin-associa
22	3	13.6	10	2 JP0072	ribosomal protein
23	3	13.6	10	2 PC4374	telomeric and tetr
24	3	13.6	11	2 De0691	phycobilisome 9K 1
25	3	13.6	11	2 S68637	acetylcholinestera
26	3	13.6	12	1 A43975	locustamyotropin -
27	3	13.6	12	2 S25485	transcription fact
28	3	13.6	12	2 S43013	hypothetical prote
29	3	13.6	12	2 PA0037	plastocyanin 2 - A

30	13.6	12	2 PA0030	protein QA300025 -
31	13.6	12	2 PA0098	ribosomal protein
32	13.6	12	2 A61503	sterol carrier pro
33	13.6	12	2 S74196	3-hydroxy-3-methyl
34	13.6	13	2 S12388	argA protein - sal
35	13.6	13	2 G22565	R-phycocerythrin ga
36	13.6	13	2 S09018	hemolytic protein
37	13.6	13	2 PL0157	Ig kappa chain V-I
38	13.6	13	2 B58864	dipeptidyl-peptida
39	13.6	13	2 C61576	ribosomal protein
40	13.6	14	2 JN0389	histamine-releasin
41	13.6	14	2 C33098	223K exoantigen -
42	13.6	14	2 S45655	cathepsin L (SC 3.
43	13.6	14	2 S38307	DEB-A protein - fr
44	13.6	14	2 S14336	mastoparan B - hor
45	13.6	14	2 A23996	beta-granin - rat
46	13.6	15	2 I49420	placental lactogen
47	13.6	15	2 PNO117	hemoglobin alpha c
48	13.6	15	2 PH0216	agarase (EC 3.2.1.
49	13.6	15	2 T09463	ribosomal protein
50	13.6	15	2 PA0056	protein QF200002 -
51	13.6	15	2 B61457	alpha-glucosidase
52	13.6	15	2 PT0090	alpha-glucosidase
53	13.6	15	2 D46743	corneal keratan su
54	13.6	15	2 G24417	interphotoreceptor
55	13.6	15	2 S62675	collagen type I -
56	13.6	15	2 PH1590	Ig H chain V-D-J r
57	13.6	15	2 A31902	bone acidic glycop
58	13.6	16	2 A27803	myosin light chain
59	13.6	16	2 PA0048	protein QA100047 -
60	13.6	16	2 PS0256	22K protein 4208 -
61	13.6	16	2 S38292	30K allergen - rye
62	13.6	16	2 A23992	melatin-omochrome
63	13.6	16	2 S65709	major allergen Myr
64	13.6	16	2 S68730	bleomycin-binding
65	13.6	17	2 I65274	glutathione S-tran
66	13.6	17	2 A29834	trp leader peptide
67	13.6	17	2 A36727	cytochrome C551 -
68	13.6	17	2 A49237	45/47K antigen - M
69	13.6	17	2 S59481	hydroxyproline-ric
70	13.6	17	2 S28839	RNA-binding protei
71	13.6	17	2 A22595	bombolitin I - Ame
72	13.6	17	2 B22595	bombolitin II - Am
73	13.6	17	2 C22595	bombolitin III - A
74	13.6	17	2 D22595	bombolitin IV - Am
75	13.6	17	2 PT0234	Ig heavy chain CRD
76	13.6	18	1 DRUFPD	pigment-dispersing
77	13.6	18	2 A24749	neuropeptide A - b
78	13.6	18	2 I40062	shikimate 5-dehydr
79	13.6	18	2 S13974	chlorophyll a/b-bi
80	13.6	18	2 A45590	beta-pigment-dispe
81	13.6	18	2 B48408	21K high mobility
82	13.6	18	2 A56798	dermatan sulfate p
83	13.6	18	2 S09026	carboxylesterase (
84	13.6	18	2 S19914	choline O-acetyltr
85	13.6	18	2 S38009	oviducin - golden
86	13.6	19	2 C56049	superoxide dismuta
87	13.6	19	2 A41299	T-cell receptor al
88	13.6	19	2 D24417	interphotoreceptor
89	13.6	19	2 I40063	shikimate 5-dehydr
90	13.6	19	2 C61079	24K protein List
91	13.6	19	2 PQ6678	photosystem I 8.0K
92	13.6	19	2 A48408	21K high mobility
93	13.6	19	2 A49192	transhyretin - bu
94	13.6	19	2 A60326	cholecystokinin-58
95	13.6	19	2 S02808	nucleolin - bovine
96	13.6	19	2 S78411	ribosomal protein
97	13.6	19	2 S68394	H+-transporting tw
98	13.6	20	2 A39328	notechis II-5b non
99	13.6	20	2 S09022	carboxylesterase (
100	13.6	20	2 S09025	carboxylesterase (

ALIGNMENTS

```
RESULT 1
A61218
alpha-gliadin 4Ha - grass (Haynaldia villosa) (fragment)
C:Species: Haynaldia villosa, Dasyphyrum villosum
C>Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Mar-1999
C:Accession: A61218
R:Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.
Biochem. Genet. 29, 207-211, 1991
A:Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia villosa
A:Reference number: A61218; MUID:91315394; PMID:1859356
A:Accession: A61218
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <SHE>
C:Keywords: seed; storage protein

Query Match      18.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 PVPQ 11
DB      5 PVPQ 8

RESULT 2
B61218
alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)
C:Species: Haynaldia villosa, Dasyphyrum villosum
C>Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Mar-1999
C:Accession: B61218
R:Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.
Biochem. Genet. 29, 207-211, 1991
A:Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia villosa
A:Reference number: A61218; MUID:91315394; PMID:1859356
A:Accession: B61218
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <SHE>
C:Keywords: seed; storage protein

Query Match      18.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 PVPQ 11
DB      5 PVPQ 8

RESULT 3
PC4267
ribosomal protein L12.1 - rice (fragment)
C:Species: Oryza sativa (rice)
C>Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C:Accession: PC4267
R:Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.
submitted to JIFAD, April 1997
A:Reference number: PC4267
A:Accession: PC4267
A:Molecule type: protein
A:Residues: 1-11 <KAW>
A:Experimental source: strain Japonica Nihonbare

Query Match      18.2%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PKVL 7
DB      4 PVPQ 7

RESULT 4
S09395
hypothetical protein - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
C:Accession: S09395
R:Gisselmann, G.; Sewing, S.; Madsen, B.W.; Mallart, A.; Angaut-Petit, D.; Mueller-Hoeberich, J.
EMBO J. 8, 2359-2364, 1989
A:Title: The interference of truncated with normal potassium channel subunits leads to a reduction in the current
A:Reference number: S09395; MUID:90005442; PMID:2551680
A:Accession: S09395
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <GIS>

Query Match      18.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 LPVP 10
DB      5 LPVP 8

RESULT 5
A49155
vasotocin-associated neurophysin - African toad (fragment)
N:Alternate names: MSRL-neurophysin
C:Species: Bufo regularis (African toad)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2001
C:Accession: A49155
R:Chauvet, J.; Ouedraogo, Y.; Michel, G.; Acher, R.
Comp. Biochem. Physiol. Comp. Physiol. 104, 497-502, 1993
A:Title: Vasotocin and hydrin 2 (vasotocinyl-Gly) in the African toad Bufo regularis
A:Reference number: A49155; MUID:93230882; PMID:8097151
A:Accession: A49155
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <CHA>
A>Note: sequence extracted from NCBI backbone (NCBIP:129814)
C:Superfamily: oxytocin-neurophysin
C:Keywords: neuropeptide

Query Match      18.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 AVPQ 16
DB      6 AVPQ 9

RESULT 6
JQ2030
hypothetical 1.9K protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis vi
N:Alternate names: OR2 mini gene protein
C:Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNVP
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C:Accession: JQ2030
R:Russell, R.L.Q.; Rohrmann, G.F.
J. Gen. Virol. 74, 1191-1195, 1993
A:Title: Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus
A:Reference number: PQ0633; MUID:93286576; PMID:8389803
A:Accession: JQ2030
A:Molecule type: DNA
A:Residues: 1-17 <RUS>
A:Cross-references: DBJ:D13375; NID:G222217; PIDN:BAA02640.1; PID:di003144; PID:G22:

Query Match      18.2%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
```


A:Reference number: JQ2191; MUID:93389433; PMID:8397280
 A:Accession: PQ0663
 A:Molecule type: mRNA
 A:Residues: 1-7 <BRI>
 A:Cross-references: GB:Z14976; NID:9311650; PID:CAA78699.1; PID:9584083
 C:Comment: This virus is coronavirus related to human coronavirus 229E.
 C:Keywords: membrane protein

Query Match 13.6%; Score 3; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
 |||
 Db 2 KVL 4

RESULT 13

PC1316
 large granule L3 chain - horseshoe crab (Tachyplesus tridentatus) (fragment)
 C:Species: tachyplesus tridentatus
 C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 C:Accession: PC1316
 R:Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa
 J. Biochem. 114, 307-316, 1993
 A>Title: Separation of large and small granules from horseshoe crab (Tachyplesus tridentat
 A:Reference number: PC1309; MUID:94110249; PMID:8282718
 A:Accession: PC1316
 A:Molecule type: protein
 A:Residues: 1-7 <SHI>
 C:Comment: This protein participates in immobilization of invading microbes.

Query Match 13.6%; Score 3; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4
 |||
 Db 2 SQP 4

RESULT 14

B24749
 neuropeptide B - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2000
 C:Accession: B24749
 R:Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.
 Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985
 A>Title: Isolation, sequencing, synthesis, and pharmacological characterization of two B
 A:Reference number: A94074; MUID:86067985; PMID:3865193
 A:Accession: B24749
 A:Molecule type: protein
 A:Residues: 1-8 <YAN>
 C:Superfamily: unassigned animal peptides
 C:Keywords: neuropeptide

Query Match 13.6%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
 |||
 Db 5 PQR 7

RESULT 15

A14683
 aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (fragm
 N:Alternate names: aspartate aminotransferase, mitochondrial
 C:Species: Gallus gallus (chicken)
 C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
 C:Accession: A14683

R:Wilson, K.J.; Hunziker, P.; Hughes, G.J.
 FEBS Lett. 108, 98-102, 1979
 A>Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.
 A:Reference number: A14683; MUID:80092116; PMID:520566
 A:Accession: A14683
 A:Molecule type: protein
 A:Residues: 1-8 <WIL>
 C:Keywords: aminotransferase; mitochondrion

Query Match 13.6%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPK 5
 |||
 Db 6 QPK 8

RESULT 16

S78426
 S2.5K protein - spiny lobster (fragment)
 C:Species: Panulirus argus (spiny lobster)
 C>Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 19-May-2000
 C:Accession: S78426
 R:James, M.O.; Boyle, S.M.; Trapido-Rosenthal, H.G.; Smith, W.C.; Greenberg, R.M.; St
 Arch. Biochem. Biophys. 329, 31-38, 1996
 A>Title: cDNA and protein sequence of a major form of P450, CYP2L, in the hepatopancri
 A:Reference number: S68856; MUID:96201120; PMID:8619632
 A:Accession: S78426
 A:Molecule type: protein
 A:Residues: 1-9 <JAM>
 A:Experimental source: hepatopancreas microsomes

Query Match 13.6%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
 |||
 Db 5 KVL 7

RESULT 17

PC7073
 ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 03-Jun-2002
 C:Accession: PC7073
 R:Tsuigita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y
 Electrophoresis 21, 1853-1871, 2000
 A>Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles
 A:Reference number: PC7072
 A:Accession: PC7073
 A:Molecule type: protein
 A:Residues: 1-9 <TSU>
 C:Keywords: brain; core protein; oxidoreductase

Query Match 13.6%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKV 6
 |||
 Db 6 PKV 8

RESULT 18

XASNPC
 angiotensin-converting enzyme inhibitor - aspic viper
 C:Species: Vipera aspis (aspic viper)
 C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 08-Dec-1995
 C:Accession: A60377
 R:Komori, Y.; Sugihara, H.

```

Int. J. Biochem. 22, 767-771, 1990
A;Title: Characterization of a new inhibitor for angiotensin converting enzyme from the
A;Reference number: A60377; MUID:90382616; PMID:2169439
A;Accession: A60377
A;Molecule type: protein
A;Residues: 1-10 <KOM>
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid
F;I/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match      13.6%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PKV 6
      |||
Db      6 PKV 8

RESULT 19
A46491
C3 homolog HX - inshore hagfish (fragment)
C;Species: Eptatretus burgeri (inshore hagfish)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
C;Accession: A46491
E;Fujii, T.; Nakamura, T.; Sekizawa, A.; Tomonaga, S.
J. Immunol. 149, 117-123, 1992
A;Title: Isolation and characterization of a protein from hagfish serum that is homologous
A;Reference number: A46491; MUID:92091759; PMID:1727859
A;Accession: A46491
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <FOU>
A;Experimental source: serum
A;Note: sequence extracted from NCBI backbone (NCBIP:71420)
C;Superfamily: alpha-2-macroglobulin

Query Match      13.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 KVL 7
      |||
Db      2 KVL 4

RESULT 20
A46466
neurotoxin-associated protein type A Hn+ 57K chain - Clostridium botulinum (fragment)
C;Species: Clostridium botulinum
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C;Accession: A46466
R;Somers, B.; DasGupta, B.R.
J. Protein Chem. 10, 415-425, 1991
A;Title: Clostridium botulinum types A, B, Cl, and E produce proteins with or without he
A;Reference number: A46444; MUID:92143938; PMID:1781887
A;Contents: type A
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SOM>
A;Note: sequence extracted from NCBI backbone (NCBIP:83774)
A;Note: 6-Trp was also found
C;Keywords: hemagglutinin

Query Match      13.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 VLP 8
      |||
Db      7 VLP 9

Int. J. Biochem. 22, 767-771, 1990
A;Title: Characterization of a new inhibitor for angiotensin converting enzyme from the
A;Reference number: A60377; MUID:90382616; PMID:2169439
A;Accession: A60377
A;Molecule type: protein
A;Residues: 1-10 <KOM>
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid
F;I/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match      13.6%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PKV 6
      |||
Db      6 PKV 8

RESULT 19
A46491
C3 homolog HX - inshore hagfish (fragment)
C;Species: Eptatretus burgeri (inshore hagfish)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
C;Accession: A46491
E;Fujii, T.; Nakamura, T.; Sekizawa, A.; Tomonaga, S.
J. Immunol. 149, 117-123, 1992
A;Title: Isolation and characterization of a protein from hagfish serum that is homologous
A;Reference number: A46491; MUID:92091759; PMID:1727859
A;Accession: A46491
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <FOU>
A;Experimental source: serum
A;Note: sequence extracted from NCBI backbone (NCBIP:71420)
C;Superfamily: alpha-2-macroglobulin

Query Match      13.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 KVL 7
      |||
Db      2 KVL 4

RESULT 20
A46466
neurotoxin-associated protein type A Hn+ 57K chain - Clostridium botulinum (fragment)
C;Species: Clostridium botulinum
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C;Accession: A46466
R;Somers, B.; DasGupta, B.R.
J. Protein Chem. 10, 415-425, 1991
A;Title: Clostridium botulinum types A, B, Cl, and E produce proteins with or without he
A;Reference number: A46444; MUID:92143938; PMID:1781887
A;Contents: type A
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SOM>
A;Note: sequence extracted from NCBI backbone (NCBIP:83774)
A;Note: 6-Trp was also found
C;Keywords: hemagglutinin

Query Match      13.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 VLP 8
      |||
Db      7 VLP 9

```

```

RESULT 21
I44644
neurotoxin-associated protein type B Hn+ 57K chain - Clostridium botulinum (fragment)
C;Species: Clostridium botulinum
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C;Accession: I44644
R;Somers, B.; DasGupta, B.R.
J. Protein Chem. 10, 415-425, 1991
A;Title: Clostridium botulinum types A, B, Cl, and E produce proteins with or without
A;Reference number: A46444; MUID:92143938; PMID:1781887
A;Contents: type B
A;Accession: I44644
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SOM>
A;Note: sequence extracted from NCBI backbone (NCBIP:83783)
C;Keywords: hemagglutinin

Query Match      13.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 VLP 8
      |||
Db      7 VLP 9

RESULT 22
JP0072
ribosomal protein L32 - Lactobacillus plantarum (fragment)
C;Species: Lactobacillus plantarum
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
C;Accession: JP0072
R;Ochi, K.
submitted to JIPID, February 1994
A;Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal
A;Reference number: JP0042
A;Accession: JP0072
A;Molecule type: protein
A;Residues: 1-10 <OCH>
C;Keywords: protein biosynthesis; ribosome

Query Match      13.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 AVP 15
      |||
Db      1 AVP 3

RESULT 23
PC4374
telomeric and tetraplex DNA binding protein qTBP42 IV - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C;Accession: PC4374
R;Sarif, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A;Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the
A;Reference number: PC4371; MUID:97445086; PMID:9299414
A;Accession: PC4374
A;Molecule type: protein
A;Residues: 1-10 <SAR>
C;Comment: This protein binds either strand of the telomeric DNA as well as unimolecu

Query Match      13.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 KVL 7
      |||

```

```

F:12/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match      13.6%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 AVP 15
Db      2 AVP 4

RESULT 27
S25485
transcription factor NF1 - rat
N:Alternate names: HNF1 protein; LFBI protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 15-Oct-1999
C:Accession: S25485; S50121
R:Tomei, L.; Piaggio, G.; Toniatti, C.; Lazzaro, D.; de Francesco, R.; Pozzi, L.; Ger-
submitted to the EMBL Data Library, August 1992
A:Description: LFBI/HNF1 acts as a repressor of its own transcription.
A:Reference number: S25485
A:Accession: S25485
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <TOM>
A:Cross-references: EMBL:X67649; NID:g56575; PIDN:CAA47891.1; PID:g56576
R:Piaggio, G.; Tomei, L.; Toniatti, C.; de Francesco, R.; Gerstner, J.; Cortese, R.
Nucleic Acids Res. 22, 4284-4290, 1994
A:Title: LFBI/HNF1 acts as a repressor of its own transcription.
A:Reference number: S50121; MUID:95023202; PMID:7937157
A:Accession: S50121
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <PTA>
A:Cross-references: EMBL:X67649; NID:g56575; PIDN:CAA47891.1; PID:g56576
C:Superfamily: transcription factor HNF-1; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match      13.6%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LSQ 3
Db      5 LSQ 7

RESULT 28
S43013
hypothetical protein URF-2X - Yersinia enterocolitica transposon TN3926
C:Species: Yersinia enterocolitica
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1999
C:Accession: S43013
R:Osbourne, S.E.V.; Turner, A.K.; Grinstead, J.
submitted to the EMBL Data Library, March 1994
A:Description: The structure of the bacterial transposable element, Tn3926.
A:Reference number: S43011
A:Accession: S43013
A:Molecule type: DNA
A:Residues: 1-12 <OSB>
A:Cross-references: EMBL:X78059; NID:g460067; PIDN:CAA54979.1; PID:g460070
C:Genetics:
A:Mobile element: transposon TN3926

Query Match      13.6%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SQP 4
Db      4 SQP 6

```

RESULT 29

PA0037
 plastocyanin 2 - Arabidopsis thaliana (fragment)
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
 C;Accession: PA0037
 R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 Submitted to JIPID, July 1994
 A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis
 A;Reference number: PA0001
 A;Accession: PA0037
 A;Molecule type: protein
 A;Residues: 1-12 <KAM>
 A;Experimental source: stem

Query Match 13.6%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLP 8
 Db 5 VLP 7

RESULT 30

PA0030
 protein QA300025 - Arabidopsis thaliana (fragment)
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C;Accession: PA0030
 R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 Submitted to JIPID, July 1994
 A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis
 A;Reference number: PA0001
 A;Accession: PA0030
 A;Molecule type: protein
 A;Residues: 1-12 <KAM>
 A;Experimental source: seed
 C;Keywords: seed

Query Match 13.6%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 PIQ 22
 Db 4 PIQ 6

RESULT 31

PA0098
 ribosomal protein S3 - fungus (Fusarium sporotrichioides) (fragment)
 C;Species: Fusarium sporotrichioides
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C;Accession: PA0098
 R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 Submitted to JIPID, October 1994
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
 A;Reference number: PA0051
 A;Accession: PA0098
 A;Molecule type: protein
 A;Residues: 1-12 <CHO>

Query Match 13.6%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVP 10
 Db 5 PVP 7

RESULT 32

A61503
 sterol carrier protein-2-like protein - chicken (fragment)
 C;Species: Gallus gallus (chicken)
 C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 11-May-2000
 C;Accession: A61503
 R;Reinhart, M.P.; Avarit, S.J.; Foglia, T.
 Comp. Biochem. Physiol. B 100, 243-248, 1991
 A;Title: Purification, characterization and comparison with mammalian SCP-2 of a chicken sterol carrier protein-2-like protein
 A;Reference number: A61503; MUID:92191564; PMID:11799965
 A;Accession: A61503
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-12 <REI>

Query Match 13.6%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PKV 6
 Db 6 PKV 8

RESULT 33

S74196
 3-hydroxy-3-methylglutaryl CoA synthase homolog - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 01-May-1998
 C;Accession: S74196
 R;Taketani, S.; Yoshinaga, T.; Furukawa, T.; Kohno, H.; Tokunaga, R.; Nishimura, K.; Eura, J. Biochem. 230, 760-765, 1995
 A;Title: Induction of terminal enzymes for heme biosynthesis during differentiation of bovine erythroid cells
 A;Reference number: S65629; MUID:95331315; PMID:7607249
 A;Accession: S74196
 A;Molecule type: protein
 A;Residues: 1-12 <TAK>
 A;Experimental source: liver

Query Match 13.6%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 AVP 15
 Db 5 AVP 7

RESULT 34

S12388
 argA protein - Salmonella typhimurium (fragment)
 C;Species: Salmonella typhimurium
 C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
 C;Accession: S12388
 R;Shyanala, V.; Schneider, E.; Ames, G.F.L.
 EMBO J. 9, 939-946, 1990
 A;Title: Tandem chromosomal duplications: role of REP sequences in the recombination of the argA gene
 A;Reference number: S12388; MUID:90183995; PMID:2178927
 A;Accession: S12388
 A;Molecule type: DNA
 A;Residues: 1-13 <SHY>
 C;Genetics:
 A;Gene: argA

Query Match 13.6%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVL 7
 Db 6 KVL 8

RESULT 35

G22565
 R-phycoerythrin gamma-B chain - red alga (Gastrocloonium coulteri) (fragment)
 C:Species: Gastrocloonium coulteri
 C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
 C:Accession: G22565
 R:Klotz, A. V.; Glazer, A. N.
 J. Biol. Chem. 260, 4856-4863, 1985
 A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
 A:Reference number: A22565; MUID:85182601; PMID:3886644
 A:Accession: G22565
 A:Molecule type: protein
 A:Residues: 1-13 <KLO>

Query Match 13.6%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VPQ 11

|||

DB 6 VPQ 8

|||

RESULT 36

S09018
 hemolytic protein A1 - edible frog (fragment)
 C:Species: Rana esculenta (edible frog)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
 C:Accession: S09018
 R:Simmaco, M.; De Biase, D.; Severini, C.; Aita, M.; Erspamer, G. F.; Barra, D.; Bossa, F.
 Biochim. Biophys. Acta 1033, 318-323, 1990
 A:Title: Purification and characterization of bioactive peptides from skin extracts of R.
 A:Reference number: S09018; MUID:90198965; PMID:2317508
 A:Accession: S09018
 A:Molecule type: protein
 A:Residues: 1-13 <STM>

Query Match 13.6%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQ 3

|||

DB 9 LSQ 11

|||

RESULT 37

PL0157
 Ig kappa chain V-II region (anti-myelin-associated glycoprotein, PEC) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-Feb-1997
 C:Accession: PL0157; C61458
 R:Brouet, J. C.; Dellagi, K.; Gendron, M. C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
 J. Exp. Med. 170, 1551-1558, 1989
 A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-associated glycoprotein.
 A:Reference number: A61458; MUID:90039128; PMID:2478651
 A:Accession: PL0157

A:Molecule type: protein
 A:Residues: 1-13 <BRO>

A:Accession: C61458

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <BR2>

C:Comment: This protein is one of monoclonal IgM reactive with myelin-associated glycoprotein; heterotetramer; immunoglobulin

Query Match 13.6%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9

|||

DB 11 LPV 13

|||

RESULT 38

B56864
 dipeptidyl-peptidase IV (EC 3.4.14.5) - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
 C:Accession: B56864
 R:Plakidou-Dymock, S.; McGivan, J. D.
 Biochim. Biophys. Acta 1145, 105-112, 1993
 A:Title: The oligomeric structure of renal
 A:Reference number: A56864; MUID:93136203; PMID:8093665
 A:Accession: B56864
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13 <PLA>
 A:Experimental source: renal brush-border membrane vesicles
 C:Keywords: dipeptidylpeptidase hydrolase

Query Match 13.6%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7

|||

DB 6 KVL 8

|||

RESULT 39

C61576
 ribosomal protein L30 - Actinomadura malachitica (fragment)
 C:Species: Actinomadura malachitica
 C:Date: 20-Oct-1994 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
 C:Accession: C61576
 R:Ochi, K.; Miyadoh, S.; Tamura, T.
 Int. J. Syst. Bacteriol. 41, 234-239, 1991
 A:Title: Polyacrylamide gel electrophoresis analysis of ribosomal protein AT-L30 as
 A:Reference number: A61576; MUID:91307971; PMID:18554638
 A:Accession: C61576
 A:Molecule type: protein
 A:Residues: 1-13 <OCH>
 C:Keywords: protein biosynthesis; ribosome

Query Match 13.6%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAV 14

|||

DB 9 KAV 11

|||

RESULT 40

JN0389
 histamine-releasing peptide I - oriental hornet
 N:Alternate names: venom protein HR-1
 C:Species: Vespa orientalis (oriental hornet)
 C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 23-Aug-1997
 C:Accession: JN0389; S06445
 R:Miroschnikov, A. I.; Snezhkova, L. G.; Nazimov, I. V.; Reshetova, O. I.; Rozinov, B. V.;
 Bioorg. Khim. 7, 1467-1477, 1981
 A:Title: Structure and properties of histamine releasing peptides from the venom of
 A:Reference number: JN0389
 A:Accession: JN0389
 A:Molecule type: protein
 A:Residues: 1-14 <MIR>

R:Tuichibaev, M. U.; Akhmedova, N. U.; Kazakov, I.; Korneev, A. S.; Gagel'gans, A. I.
 Biochemistry (N.Y.) 53, 183-190, 1988
 A:Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis
 A:Reference number: S06445
 A:Accession: S06445
 A:Molecule type: protein
 A:Residues: 1-14 <TUI>

C:Superfamily: mastoparan
C;Keywords: amidated carboxyl end; venom
F;14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVL 7
Db 12 KVL 14

RESULT 41
C33098
223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C;Accession: C33098
R;Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A;Reference number: A33098
A;Accession: C33098
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <NIC>

Query Match 13.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLP 8
Db 1 VLP 3

RESULT 42
S45655
cathepsin L (EC 3.4.22.15) 2 - liver fluke (fragment)
N;Alternate names: cysteine proteinase
C;Species: Fasciola hepatica (liver fluke)
C;Date: 10-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996
C;Accession: S45655
R;Dowd, A.J.; Smith, A.M.; McGonigle, S.; Dalton, J.P.
Eur. J. Biochem. 223, 91-98, 1994
A;Title: Purification and characterisation of a second cathepsin L proteinase secreted by
A;Reference number: S45655; MUID:94307282; PMID:8033913
A;Accession: S45655
A;Molecule type: protein
A;Residues: 1-14 <DOW>
C;Keywords: cysteine proteinase; hydrolase

Query Match 13.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 AVP 15
Db 1 AVP 3

RESULT 43
S38307
DEB-A protein - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 17-Mar-1999
C;Accession: S38307
R;Wang, G.L.; Goldstein, E.S.
Biochim. Biophys. Acta 1216, 94-104, 1993
A;Title: An AP-1 binding site in the upstream region of DEB-A is part of a developmental
A;Reference number: S38307; MUID:94032494; PMID:8218421
A;Accession: S38307
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-14 <WAN>

Query Match 13.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 MPI 21
Db 1 MPI 3

RESULT 44
S14336
mastoparan B - hornet (Vespa basalis)
C;Species: Vespa basalis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Apr-1999
C;Accession: S14336
R;Ho, C.L.; Hwang, L.L.
Biochem. J. 274, 453-456, 1991
A;Title: Structure and biological activities of a new mastoparan isolated from the ve
A;Reference number: S14336; MUID:91174755; PMID:2006909
A;Accession: S14336
A;Molecule type: protein
A;Residues: 1-14 <HOC>
A;Experimental source: venom
C;Function:
A;Description: possesses a potent hemolytic activity which acts in synergy with the le
C;Keywords: amidated carboxyl end; mast cell; venom
F;14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVL 7
Db 12 KVL 14

RESULT 45
A23996
beta-granin - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Jun-1993
C;Accession: A23996
R;Hutton, J.C.; Hansen, F.; Peshavaria, M.
FEBS Lett. 188, 336-340, 1985
A;Title: Beta-granins: 21 kDa co-secreted peptides of the insulin granule closely rel
A;Reference number: A23996; MUID:85285598; PMID:3896848
A;Accession: A23996
A;Molecule type: protein
A;Residues: 1-14 <HUT>

Query Match 13.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPV 9
Db 1 LPV 3

RESULT 46
I49420
placental lactogen I - western wild mouse (fragment)
C;Species: Mus spretus (western wild mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: I49420
R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau,
Mamm. Genome 5, 349-355, 1994
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A;Reference number: I49334; MUID:94319082; PMID:8043949

A;Accession: I49420
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-15 <RES>
 C;Superfamily: prolactin

Query Match 13.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
 ||||
 Db 3 KVL 5

RESULT 47
 PN0117
 hemoglobin alpha chain - red fox (fragment)
 C;Species: Vulpes vulpes (red fox)
 C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 19-May-2000
 C;Accession: PN0117
 R;Sukhomlinov, B.F.; Konoshenko, S.V.
 Mol. Biol. (Mosk.) 5, 415-418, 1971
 A;Title: Study on N-terminal sequence of the haemoglobin of Vulpes vulpes fox.
 A;Reference number: PN0117
 A;Accession: PN0117
 A;Molecule type: protein
 A;Residues: 1-15 <SUK>
 C;Superfamily: globin; globin homology
 C;Keywords: blood; erythrocyte; heme; heterotetramer; oxygen carrier

Query Match 13.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAV 14
 ||||
 Db 7 KAV 9

RESULT 48
 PH0216
 agarase (EC 3.2.1.81) - Pseudomonas sp. (fragment)
 N;Alternate names: agarose 4-glycanohydrolase
 C;Species: Pseudomonas sp.
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 06-Dec-1996
 C;Accession: PH0216
 R;Yamamura, I.; Matsumoto, T.; Funatsu, M.; Shigeiri, H.; Shibata, T.
 Agric. Biol. Chem. 55, 2531-2536, 1991
 A;Title: Purification and some properties of agarase from Pseudomonas sp. PT-5.
 A;Reference number: PH0216
 A;Accession: PH0216
 A;Molecule type: protein
 A;Residues: 1-15 <YAM>
 A;Experimental source: strain PT-5
 A;Note: the isoelectric point of this enzyme is 3.6
 C;Comment: This enzyme is stable from pH6 to 9 and has its maximum activity at pH8.5.
 C;Comment: This enzyme rapidly reduces the viscosity of agarose solution and the activity
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 13.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVP 15
 ||||
 Db 7 AVP 9

RESULT 49
 T09463
 ribosomal protein S14 - brown alga (Pylaiella littoralis) mitochondrion (fragment)

C;Species: mitochondrion Pylaiella littoralis
 C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
 C;Accession: T09463
 R;Rousvoal, S.; Oudot, M.; Fontaine, J.; Kloareg, B.; Goer, S.L.
 J. Mol. Biol. 277, 1047-1057, 1998
 A;Title: Witnessing the evolution of transcription in mitochondria: The mitochondria:
 A;Reference number: Z16681; MUID:98239704; PMID:9571021
 A;Accession: T09463
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-15 <ROU>
 A;Cross-references: EMBL:AF034976; NID:G3243103; PID:G3243104
 A;Experimental source: strain Roscoff
 C;Genetics:

A;Gene: rps14
 A;Genome: mitochondrion
 C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 13.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
 ||||
 Db 6 VLP 8

RESULT 50
 PA0056
 protein QF200002 - fungus (Fusarium sporotrichioides) (fragment)
 C;Species: Fusarium sporotrichioides
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C;Accession: PA0056
 R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JPIID, October 1994
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporot
 A;Reference number: PA0051
 A;Accession: PA0056
 A;Molecule type: protein
 A;Residues: 1-15 <CHO>

Query Match 13.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAV 14
 ||||
 Db 3 KAV 5

RESULT 51
 B61457
 alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)
 C;Species: Tetrahymena pyriformis
 C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-Dec-1999
 C;Accession: B61457
 R;Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.
 J. Protozool. 36, 562-567, 1989
 A;Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purific
 A;Reference number: A61457; MUID:90095988; PMID:2689637
 A;Accession: B61457
 A;Molecule type: protein
 A;Residues: 1-15 <BAN>
 C;Genetics:

A;Genetic code: SGC5
 C;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; m

Query Match 13.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
 ||||

Db 1 VLP 3

RESULT 52

PT0090
 alpha-glucosidase (EC 3.2.1.20) - honeybee (fragment)
 C;Species: Apis mellifera (honeybee)
 C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 07-May-1999
 C;Accession: PT0090
 R;Kimura, A.; Takata, M.; Fukushi, Y.; Mori, H.; Matsui, H.; Chiba, S.
 Biosci. Biotechnol. Biochem. 61, 1091-1098, 1997
 A;Title: A catalytic amino acid and primary structure of active site in Aspergillus niger
 A;Reference number: PT0090; MUID:97399878; PMID:9255970
 A;Accession: PT0090
 A;Molecule type: protein
 A;Residues: 1-15 <KIM>
 C;Keywords: glycosidase; hydrolase

Query Match 13.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 AVP 15
 |||
 Db 9 AVP 11

RESULT 53

D46743
 corneal keratan sulfate proteoglycan core protein 25 - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C;Accession: D46743
 R;Funderburgh, J.L.; Funderburgh, M.L.; Brown, S.J.; Vergnes, J.P.; Hassell, J.R.; Mann, J. Biol. Chem. 268, 11874-11880, 1993
 A;Title: Sequence and structural implications of a bovine corneal keratan sulfate proteoglycan
 A;Reference number: A46743; MUID:93280153; PMID:8099356
 A;Accession: D46743
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-15 <FUN>

Query Match 13.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 MPI 21
 |||
 Db 2 MPI 4

RESULT 54

G24417
 interphotoreceptor retinoid-binding protein - hamster (fragment)
 N;Alternate names: interstitial retinol-binding protein
 C;Species: Cricetinae gen. sp. (hamster)
 C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 18-Jun-1993
 C;Accession: G24417
 R;Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B. FEBS Lett. 205, 309-312, 1986
 A;Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10 species
 A;Reference number: A91365; MUID:86301171; PMID:3743780
 A;Accession: G24417
 A;Molecule type: protein
 A;Residues: 1-15 <FON>

Query Match 13.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 PIQ 22
 |||
 Db 2 PIQ 4

RESULT 55

S62675
 collagen type I - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
 C;Accession: S62675
 R;Mizuno, M.; Kitafima, T.; Tomita, M.; Kuboki, Y. Biochim. Biophys. Acta 1310, 97-102, 1996
 A;Title: The osteoblastic MC3T3-E1 cells synthesized C-terminal propeptide of type I collagen
 A;Reference number: S62675; MUID:97386332; PMID:9244181
 A;Accession: S62675
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-15 <MIZ>

Query Match 13.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 QRD 18
 |||
 Db 8 QRD 10

RESULT 56

PH1590
 Ig H chain V-D-J region (wild-type clone 141) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C;Accession: PH1590
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P. J. Exp. Med. 178, 317-329, 1993
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A;Reference number: PH1580; MUID:93301609; PMID:8315387
 A;Accession: PH1590
 A;Molecule type: DNA
 A;Residues: 1-15 <LEV>
 A;Experimental source: bone marrow pre-B lymphocyte
 C;Keywords: immunoglobulin

Query Match 13.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 RDM 19
 |||
 Db 3 RDM 5

RESULT 57

A31902
 bone acidic glycoprotein-75 - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 31-Dec-1993
 C;Accession: A31902
 R;Gorski, J.P.; Shimizu, K. J. Biol. Chem. 263, 15938-15945, 1988
 A;Title: Isolation of new phosphorylated glycoprotein from mineralized phase of bone
 A;Reference number: A31902; MUID:89034045; PMID:2846530
 A;Accession: A31902
 A;Molecule type: protein
 A;Residues: 1-15 <GOR>
 A;Note: 14-Glu and 15-Glu were also found
 C;Keywords: glycoprotein

Query Match 13.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPV 9
 |||

```

Db          1 LPV 3

RESULT 58
A27803
myosin light chain, smooth muscle - turkey (fragment)
C:Species: Meleagris gallopavo (common turkey)
C>Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 29-Sep-1999
C:Accession: A27803
R:Benigur, A.R.; Robinson, E.A.; Appella, E.; Sellers, J.R.
J. Biol. Chem. 262, 7613-7617, 1987
A:Title: Sequence of the sites phosphorylated by protein kinase C in the smooth muscle
A:Reference number: A27803; MUID:87222380; PMID:584131
A:Accession: A27803
A:Molecule type: protein
A:Residues: 1-16 <BEN>
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: EF hand; muscle; smooth muscle

Query Match          13.6%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          15 POR 17
          |||
Db          14 POR 16

RESULT 59
PA0048
protein QA100047 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C:Accession: PA0048; PA0043
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional
A:Reference number: PA0001
A:Accession: PA0048
A:Molecule type: protein
A:Residues: 1-16 <KAM>
A:Experimental source: stem

Query Match          13.6%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          18 DMP 20
          |||
Db          5 DMP 7

RESULT 60
PS0256
22K protein 4208 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C:Accession: PS0256
R:Tsugita, A.; Miyatake, N.
submitted to JIPID, April 1993
A:Reference number: PS0208
A:Accession: PS0256
A:Molecule type: protein
A:Residues: 1-16 <TSU>
A:Experimental source: germ, strain Nihonbare
C:Comment: molecular weight 22K, pI 6.6.

Query Match          13.6%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          12 KAV 14
          |||

Db          2 KAV 4

RESULT 61
S38292
30K allergen - rye (fragment)
C:Species: Secale cereale (rye)
C>Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 07-May-1999
C:Accession: S38292
R:Peterson, A.; Schramm, G.; Becker, W.M.; Schlaak, M.
Biol. Chem. Hoppe-Seyler 374, 855-861, 1993
A:Title: Comparison of four grass pollen species concerning their allergens of grass
A:Reference number: S38288; MUID:94092339; PMID:7505588
A:Accession: S38292
A:Molecule type: protein
A:Residues: 1-16 <PET>

Query Match          13.6%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          3 QPK 5
          |||
Db          13 QPK 15

RESULT 62
A23992
melatin-ommochrome-stimulating hormone III - silkworm (fragment)
N:Alternate names: melanization and reddish coloration hormone III; MRCH III
C:Species: Bombyx mori (silkworm)
C>Date: 30-Jan-1988 #sequence_revision 30-Jan-1988 #text_change 18-Jun-1993
C:Accession: A23992
R:Matsumoto, S.; Isogai, A.; Suzuki, A.
FEBS Lett. 189, 115-118, 1985
A:Title: N-terminal amino acid sequence of an insect neurohormone, melanization and
A:Reference number: A23992; MUID:85285612; PMID:3896851
A:Accession: A23992
A:Molecule type: protein
A:Residues: 1-16 <MAT>
C:Keywords: hormone

Query Match          13.6%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          18 DMP 20
          |||
Db          5 DMP 7

RESULT 63
S65709
major allergen Myr p I - bulldog ant (Myrmecia pilosula) (fragment)
C:Species: Myrmecia pilosula
C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C:Accession: S65709
R:Street, M.D.; Donovan, G.R.; Baldo, B.A.
Biochim. Biophys. Acta 1305, 87-97, 1996
A:Title: Molecular cloning and characterization of the major allergen Myr p II from
A:Reference number: S65709; MUID:96180991; PMID:8605256
A:Accession: S65709
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <STR>

Query Match          13.6%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 PKV 6
          |||
Db          7 PKV 9

```

RESULT 64

S68730
bleomycin-binding protein - Streptomyces verticillus (fragment)
C:Species: Streptomyces verticillus
C:Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 17-Mar-1999
C:Accession: S68730
F:Sugiyama, M.; Kumagai, T.; Matsuo, H.; Bhuiyan, M.Z.A.; Ueda, K.; Mochizuki, H.; Nakamura
FEBS Lett. 362, 80-84, 1995
A:Title: Overproduction of the bleomycin-binding proteins from bleomycin-producing Streptomyces
al characterisation.
A:Reference number: S68730; PMID:95212588; PMID:7535252
A:Accession: S68730
A:Molecule type: protein
A:Residues: 1-16 <SUB>
A:Experimental source: ATCC 15003
C:Keywords: antibiotic resistance

Query Match	13.6%	Score 3;	DB 2;	Length 16;
Best Local Similarity	100.0%	Pred. No. 5e+03;		
Matches 3;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;			

Qy 13 AVP 15
7 AVP 9
Db

RESULT 65

I65274
glutathione S-transferase Ya subunit (put.) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Jun-1999
C:Accession: I65274
R:Rothkopf, G.S.; Telakowski-Hopkins, C.A.; Stotish, R.L.; Pickett, C.B.
Biochemistry 25, 993-1002, 1986
A:Title: Multiplicity of Glutathione S-transferase genes in the rat and association with
A:Reference number: I52395; MUID:8618772; PMID:2421763
A:Accession: I65274
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-17 <RES>
A:Cross-references: GB:M12894; NID:G204504; PIDN:AAA1289.1; PID:G204505
C:Superfamily: glutathione transferase

Query Match	13.6%	Score 3;	DB 2;	Length 17;
Best Local Similarity	100.0%;	Pred. No. 5.2e+03;		
Matches	3;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

QY	7 LPV 9
Db	1 LPV 3

RESULT 66

A29834
trp leader peptide - *Corynebacterium glutamicum*
C/Species: *Corynebacterium glutamicum*
C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Sep-1999
C/Accession: A29834; A29723; A29458; S13087; A48967
R/Matsui, K.; Miwa, K.; Sano, K.
J. Bacteriol. 169, 5330-5332, 1987
A/Title: Two single-base-pair substitutions causing desensitization to tryptophan feedback
A/Reference number: A29834; PMID:68032866; PMID:3667535
A/Contents: B. lactofermentum
A/Accession: A29834
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-17 <M>
A/Cross-references: GB:M17892; NID:G144101; PIDN:AAB59110.1; PID:G1129101
R/Matsui, K.; Sano, K.; Ohtsubo, E.
Nucleic Acids Res. 14, 10113-10114, 1986

A;Title: Complete nucleotide and deduced amino acid sequences of the *Brevibacterium* C
A;Reference number: A93606; MUID:87117512; PMID:3808947
A;Contents: B. lactofermentum
A;Accession: A24723
A;Molecule type: DNA
A;Residues: 1-17 <MA2>
A;Cross-references: GB:X04960; NID:g39591; PIDN:CAA28622.1; PID:g580785
R;Sano, K.; Matsui, K.
Gene 53, 191-200, 1987
A;Title: Structure and function of the trp operon control regions of *Brevibacterium* C
A;Reference number: A91575; MUID:87277409; PMID:3609747
A;Contents: B. lactofermentum
A;Accession: A29458
A;Molecule type: DNA
A;Residues: 1-17 <SAN>
R;Heery, D.M.; Dunican, L.K.
Nucleic Acids Res. 18, 7138, 1990
A;Title: Nucleotide sequence of the *Corynebacterium glutamicum* trpE gene.
A;Reference number: S13087; MUID:91088299; PMID:2263476
A;Accession: S13087
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-17 <HEE>
A;Cross-references: EMBL:X55994; NID:g40521; PIDN:CAA39466.1; PID:g580992
R;Heery, D.M.; Dunican, L.K.
Appl. Environ. Microbiol. 59, 791-799, 1993
A;Title: Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of *C*
A;Reference number: A48967; MUID:93243735; PMID:7683184

A;Accession: J04501
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-13 <HER>
A;Cross-references: GB:859239; NID:g299877; PID:g299878
A;Experimental source: ATCC 21850
A;Note: sequence extracted from NCBI backbone (NCBIN:130455, NCBI:P.130456)
C;Genetics:
A;Gene: trpL
A;Start codon: GTG
C;Superfamily: unassigned leader peptides

Query Match	13.6%	Score 3	DB 2	Length 17
Best Local Similarity	100.0%	Pred. No.	5.2e+03	
Matches 3	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0

Qy	1	LSQ	3
Db	6	LSO	8

RESULT 67

A36727
cytochrome c551 - Methylomonas sp. (fragment)
C:Species: Methylomonas sp.
C:Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 18-Jun-1993
C:Accession: A36727
R:DiSpirito, A.A.; Lipscomb, J.D.; Lidstrom, M.E.
J. Bacteriol. 172, 5360-5367, 1990
A:Title: Soluble cytochromes from the marine methanotroph Methylomonas sp.
A:Reference number: A36727; PMID:90368596; PMID:2168380
A:Accession: A36727
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <DIS>

Query Match 13.6%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels

Qy	11	QKA	13
Db	8	QKA	10

Db 8 OKA 10

RESULT 68

A49237
45/47K antigen - Mycobacterium bovis (fragment)
C:Species: Mycobacterium bovis
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 24-Feb-1995
C:Accession: A49237
R:Romain, F.; Laqueyrie, A.; Millitzer, P.; Pescher, P.; Chavarot, P.; Lagranderie, M.; Infect. Immun. 61, 742-750, 1993
A:Title: Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen complex, a
A:Reference number: A49237; MUID:93138802; PMID:8423100
A:Contents: BCG
A:Accession: A49237
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <ROM>
A>Note: sequence extracted from NCBI backbone (NCBIP:123246)

Query Match 13.6%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVP 10

DB 7 PVP 9

RESULT 69

S59481
hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)
C:Species: Phaseolus vulgaris (kidney bean)
C:Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 05-Dec-1998
C:Accession: S59481
R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
Plant Mol. Biol. 28, 1075-1087, 1995
A:Title: Specificity in the immobilisation of cell wall proteins in response to different
A:Reference number: S59481; MUID:96011753; PMID:7548825
A:Accession: S59481
A:Molecule type: protein
A:Residues: 1-17 <MOJ>

C:Keywords: glycoprotein; hydroxyproline
F:6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVP 10

DB 6 PVP 8

RESULT 70

S28839
RNA-binding protein, 28K - garden pea (fragment)
C:Species: Pisum sativum (garden pea)
C:Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Dec-1998
C:Accession: S28839
R:Subbaiah, C.C.; Tewari, K.K.
Eur. J. Biochem. 211, 171-179, 1993
A:Title: Purification and characterization of ribonucleoproteins from pea chloroplasts.
A:Reference number: S28837; MUID:93145944; PMID:8425527
A:Accession: S28839
A:Molecule type: protein
A:Residues: 1-17 <SUB>

A:Experimental source: cv. Arkel
C:Function:

A:Description: may be involved in post-transcriptional regulation of plastid genes
C:Keywords: chloroplast; transcription regulation

Query Match 13.6%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAV 14

DB 14 KAV 16

RESULT 71

A22595
bombolitin I - American common bumblebee
C:Species: Bombus pennsylvanicus (American common bumblebee)
C:Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 08-Dec-1995
C:Accession: A22595
R:Argiolas, A.; Pisano, J.J.
J. Biol. Chem. 260, 1437-1444, 1985
A:Title: Bombolitins, a new class of mast cell degranulating peptides from the venom
A:Reference number: A92504; MUID:85105003; PMID:2578459
A:Accession: A22595
A:Molecule type: protein
A:Residues: 1-17 <ARG>

C:Keywords: amidated carboxyl end; hemolysis; venom
F:17/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7

DB 12 KVL 14

RESULT 72

B22595
bombolitin II - American common bumblebee
C:Species: Bombus pennsylvanicus (American common bumblebee)
C:Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 08-Dec-1995
C:Accession: B22595
R:Argiolas, A.; Pisano, J.J.
J. Biol. Chem. 260, 1437-1444, 1985
A:Title: Bombolitins, a new class of mast cell degranulating peptides from the venom
A:Reference number: A92504; MUID:85105003; PMID:2578459
A:Accession: B22595
A:Molecule type: protein
A:Residues: 1-17 <ARG>

C:Keywords: amidated carboxyl end; hemolysis; venom
F:17/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7

DB 12 KVL 14

RESULT 73

B22595
bombolitin III - American common bumblebee
C:Species: Bombus pennsylvanicus (American common bumblebee)
C:Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 08-Dec-1995
C:Accession: B22595
R:Argiolas, A.; Pisano, J.J.
J. Biol. Chem. 260, 1437-1444, 1985
A:Title: Bombolitins, a new class of mast cell degranulating peptides from the venom
A:Reference number: A92504; MUID:85105003; PMID:2578459
A:Accession: B22595
A:Molecule type: protein
A:Residues: 1-17 <ARG>

C:Keywords: amidated carboxyl end; hemolysis; venom
F:17/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
|||
Db 12 KVL 14

RESULT 74

D22595
bombolitin IV - American common bumblebee
C;Species: Bombus pennsylvanicus (American common bumblebee)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 08-Dec-1995
C;Accession: D22595
R;Argiolas, A.; Pisano, J.J.
J. Biol. Chem. 260, 1437-1444, 1985
A;Title: Bombolitins, a new class of mast cell degranulating peptides from the venom of
A;Reference number: A92504; MUID:85105003; PMID:2578459
A;Accession: D22595
A;Molecule type: protein
A;Residues: 1-17 <ARG>
C;Keywords: amidated carboxyl end; hemolysis; venom
F;17/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
|||
Db 12 KVL 14

RESULT 75

PT0234
Ig heavy chain CRD3 region (clone 1-130) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0234
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0234
A;Molecule type: DNA
A;Residues: 1-17 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 13.6%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
|||
Db 5 KVL 7

Search completed: November 25, 2003, 19:36:11
Job time : 16.093 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 7.80233 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-27

Perfect score: 22

Sequence: 1 LSQPKVLVPQKAVPQDMPIQ 22

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	22.7	10	UPA5_HUMAN	P30091 homo sapien
2	4	18.2	14	TKN1_SCHGR	P82470 schistocerc
3	4	18.2	19	COOT_SARBU	Q09148 sarcophaga
4	4	18.2	20	YOA_H_KLEAE	P56506 klebsiella
5	3	13.6	8	NPB_BOVIN	P15507 bos taurus
6	3	13.6	9	FAR4_PENMO	P83319 penaeus mon
7	3	13.6	10	BPP_VIPAS	P31351 vipera aspi
8	3	13.6	10	UPA8_HUMAN	P30094 homo sapien
9	3	13.6	12	LMT1_LOCOMI	P22395 locusta mig
10	3	13.6	12	TM2A_METWA	P80652 methanosarc
11	3	13.6	13	RP65_HUMAN	P54963 homo sapien
12	3	13.6	13	FIBB_RABIT	P14478 oryctolagus
13	3	13.6	13	HPA1_RANES	P32415 rana escul
14	3	13.6	13	PEDI_HYDAT	P80578 hydra atten
15	3	13.6	13	TEME_RANTE	P56920 rana tempor
16	3	13.6	13	TEME_RANTE	P56921 rana tempor
17	3	13.6	14	CAT2_FASHE	P80342 fasciola he
18	3	13.6	14	MAST_VESBA	P21654 vespa basal
19	3	13.6	14	MAST_VESOR	P17238 vespa orien
20	3	13.6	14	TAT_HVI12	P12509 human immun
21	3	13.6	14	TAT_HVI128	P12511 human immun
22	3	13.6	14	UC15_MAIZE	P80621 zea mays (m
23	3	13.6	15	APP3_MALPA	P83137 malva parvi
24	3	13.6	15	IRBP_CRISP	P12665 cricetidae
25	3	13.6	15	MCA2_RHOOP	P56870 rhodococcus
26	3	13.6	15	RBS_PHYPA	P80657 physcomitre
27	3	13.6	15	UC29_MAIZE	P80635 zea mays (m
28	3	13.6	16	AF2S_MALPA	P83142 malva parvi
29	3	13.6	17	A45K_MYCBO	P80069 mycobacteri
30	3	13.6	17	SOLI_MEGFE	P10521 megabombus
31	3	13.6	17	BOL2_MEGFE	P07493 megabombus
32	3	13.6	17	BOL3_MEGFE	P07494 megabombus
33	3	13.6	17	BOL4_MEGFE	P07495 megabombus

ALIGNMENTS

RESULT 1

34	17	13.6	3	H2B3 ICTPU	P81904 ictalurus p
35	17	13.6	3	LPW_GORGL	P06556 corynebacte
36	17	13.6	3	UP34_UPEMJ	P82041 uperoleia m
37	17	13.6	3	UP35_UPEMJ	P82042 uperoleia m
38	18	13.6	3	AL13_CARMA	P81816 carcinus ma
39	18	13.6	3	ALL2_CYPDO	P82153 cydia pomon
40	18	13.6	3	D7A1_ACASC	P83402 acanthopagr
41	18	13.6	3	DRPH_UCAPU	P08871 uca pugilat
42	18	13.6	3	LCTN_LAMGL	P83315 lama glama
43	18	13.6	3	NPA_BOVIN	P15506 bos taurus
44	19	13.6	3	FIBB_PIG	P14477 sus scrofa
45	19	13.6	3	IRBP_CAVPO	P12666 cavia porce
46	20	13.6	3	ABP_PIG	Q9TRC7 sus scrofa
47	20	13.6	3	AF2L_MALPA	P83143 malva parvi
48	20	13.6	3	BIP_PHAVU	P80089 phaseolus v
49	20	13.6	3	CAT3_FASHE	Q09093 fasciola he
50	20	13.6	3	CD4_SHEEP	P05542 ovis aries
51	20	13.6	3	FIBB_ELEMA	P14538 elephas max
52	20	13.6	3	H2B1 ICTPU	P81903 ictalurus p
53	20	13.6	3	OAR_PHOPI	P14803 photinus py
54	2	9.1	4	DCM5_PSECH	P19918 pseudomonas
55	2	9.1	4	FFKA_ANTEL	P58705 anthopleura
56	5	9.1	5	BPP7_BOTIN	P30425 bothrops in
57	5	9.1	5	PRCT_PERAM	P01373 periplaneta
58	6	9.1	6	ACPH_RABIT	P25154 oryctolagus
59	6	9.1	6	EI01_LITRU	P82036 litorea rub
60	6	9.1	6	TRPI_PSEPU	P36414 pseudomonas
61	7	9.1	7	CARP_MYTED	P10420 mytilus edu
62	7	9.1	7	LANC_CARUI	P36960 carnobacter
63	7	9.1	7	TPFY_PACDA	P83455 pachymedusa
64	7	9.1	7	UF04_MOUSE	P38642 mus musculu
65	7	9.1	7	UN05_PINPS	P81675 pinus pinas
66	8	9.1	8	AL12_CARMA	P81815 carcinus ma
67	8	9.1	8	ALL6_CYPDO	P81821 carcinus ma
68	8	9.1	8	B44K_PORGI	P82157 cydia pomon
69	8	9.1	8	CAD1_ENTFA	P81886 porphyromon
70	8	9.1	8	CLP_THICU	P13268 enterococcu
71	8	9.1	8	COW2_CONPU	P80488 thiobacillu
72	8	9.1	8	CPD1_ENTFA	P58785 conus purpu
73	8	9.1	8	FUSS_FUSSO	P13269 enterococcu
74	8	9.1	8	PK3_PERAM	P81010 fusarium so
75	8	9.1	8	RS7_MYCIT	P82618 periplaneta
76	8	9.1	8	UC25_MAIZE	P33554 mycobacteri
77	8	9.1	8	UPA1_HUMAN	P80632 zea mays (m
78	8	9.1	8	VGLG_HSV2B	P10087 homo sapien
79	8	9.1	8	AL10_CARMA	P81780 herpes simp
80	9	9.1	9	ALC_CHLRE	P81813 carcinus ma
81	9	9.1	9	BS43_SERPL	P82678 chlamydomon
82	9	9.1	9	CONO_CONGE	P83375 serratia pl
83	9	9.1	9	COXE_THUOB	P05486 conus geogr
84	9	9.1	9	FAR1_CALVO	P80975 thunnus obe
85	9	9.1	9	FAR2_CALVO	P41856 calliphora
86	9	9.1	9	FAR3_CALVO	P41857 calliphora
87	9	9.1	9	FAR3_PENMO	P41858 calliphora
88	9	9.1	9	FAR5_PENMO	P83318 penaeus mon
89	9	9.1	9	FARA_CALVO	P83320 penaeus mon
90	9	9.1	9	FARB_ERYPA	P41865 calliphora
91	9	9.1	9	FLA2_TREHY	P19346 erythrocebu
92	9	9.1	9	FRF1_SARBU	P80159 treponema h
93	9	9.1	9	HUTU_KLEAE	P83350 sarcophaga
94	9	9.1	9	ISON_CYPCA	P12381 klebsiella
95	9	9.1	9	LITO_LITAU	P42993 cyprinus ca
96	9	9.1	9	LMT3_LOCOMI	P08945 litoria aur
97	9	9.1	9	MGMT_BOVIN	P41489 locusta mig
98	9	9.1	9	OXVA_SCYCA	P29177 bos taurus
99	9	9.1	9	OXVF_SCYCA	P42996 scyliorhinu
100	9	9.1	9		P42997 scyliorhinu

UPA5 HUMAN
ID PUA5 HUMAN STANDARD; PRT; 10 AA.
AC P30931;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092337; PubMed=1459037;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.85, ITS MW IS: 40 KDa.
CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
CC PROTEIN.
DR SWISS-2DPAGE; P30091; HUMAN.
FT NON TER 1 1
FT VARIANT 9 9 G->Y.
FT FTID=VAR_000002.
FT NON TER 10 10
FT SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;
Query Match 22.7%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 QPKVL 7
Db 3 QPKVL 7

RESULT 2
TKN1 SCHGR
ID TKN1 SCHGR STANDARD; PRT; 14 AA.
AC P82470;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tachykinin-1 (Scg-midgut-TK).
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
OX NCBI_TaxID=7010;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Midgut;
RX MEDLINE=20050081; PubMed=10581195;
RA Vellaert D., Baggerman G., Derua R., Waelkens E., Meeusen T.,
RA Van de Water G., De Loof A., Schoofs L.;
RT "Identification of a new tachykinin from the midgut of the desert
locust, Schistocerca gregaria, by ESI-Qq-TOF mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 266:237-242(1999).
CC -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: MIDGUT.
CC -!- MASS SPECTROMETRY: MW=1493.79; METHOD=Electrospray.
CC -!- SIMILARITY: SIMILAR TO THE COCKROACH LEMTRP 3, A TACHYKININ-
CC RELATED PEPTIDE ALSO CONFINED TO THE MIDGUT.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 14 14 AMIDATION.
FT SEQUENCE 14 AA; 1496 MW; CA4C578C0169FC72 CRC64;

Query Match 18.2%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.le+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 KAVP 15
Db 5 KAVP 8

RESULT 3
COOT_SARBU
ID COOT_SARBU STANDARD; PRT; 19 AA.
AC Q09148;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE NEB-colloostatin (Folliculostatin).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE.
RX MEDLINE=95188911; PubMed=7883009;
RA Bylemans D., Proost P., Samijn B., Borovsky D., Grauwels L.,
RA Huybrechts R., van Damme J., van Beeumen J., de Loof A.;
RT "Neb-colloostatin, a second folliculostatin of the grey fleshfly,
RT Neobellieria bullata.";
RL Eur. J. Biochem. 228:45-49(1995).
CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. IT INHIBITS YOLK SYNTHESIS SO
CC INHIBITING THE SUBSEQUENT YOLK DEPOSITION IN PREVITELLOGENIC
CC FOLLICLES.
CC -!- SIMILARITY: TO THE NONHELICAL REGIONS OF THE COLLAGEN FAMILY.
CC -!- CAUTION: NEB-COLLOOSTATIN MAY BE PROTEOLYTICALLY CLEAVED FROM
CC PIR; S69153; S69153.
DR PIR; S69153; S69153.
SQ SEQUENCE 19 AA; 1880 MW; 41B6AF5F0CEB8251 CRC64;

Query Match 18.2%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 LPVP 10
Db 7 LPVP 10

RESULT 4
YOA4 KLEAE
ID YOA4 KLEAE STANDARD; PRT; 20 AA.
AC P56506;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yoaH (Fragment).
GN YOA4.
OS Klebsiella aerogenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=28451;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89056707; PubMed=3057324;
RA Goncharoff P., Nichols B.P.;
RT "Evolution of aminobenzoate synthases: nucleotide sequences of
RT Salmonella typhimurium and Klebsiella aerogenes pabB.";
RL Mol. Biol. Evol. 5:531-548(1988).
RN [2]
RP IDENTIFICATION.
RX MEDLINE=98248213; PubMed=9588799;
RA Rudd K.E., Humphery-Smith I., Wasinger V.C., Bairoch A.;

RT "Low molecular weight proteins: a challenge for post-genomic
 RL research.",
 CC -1- SIMILARITY: BELONGS TO THE UPF0181 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M22078; -; NOT ANNOTATED_CDS.
 DR HAMAP; MF_00507; -; I.
 DR InterPro; IPR005371; UPF0181.
 DR Pfam; PF03701; UPF0181; 1.
 KW Hypothetical protein.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2270 MW; E8AF6425DD9BC88 CRC64;
 Query Match 18.2%; Score 4; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 QKAV 14
 Db 14 QKAV 17
 RESULT 5
 NPB_BOVIN
 ID_NPB_BOVIN STANDARD; PRT; 8 AA.
 AC P15507;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuropeptide B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
 RT "Isolation, sequencing, synthesis, and pharmacological
 RT characterization of two brain neuropeptides that modulate the action
 RT of morphine."
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
 CC -1- FUNCTION: MODULATES THE ACTION OF MORPHINE.
 DR PIR; B24749; B24749.
 KW Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;
 Query Match 13.6%; Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 PQR 17
 Db 5 PQR 7
 RESULT 6
 FAR4_PENMO
 ID_FAR4_PENMO STANDARD; PRT; 9 AA.
 AC P83319;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FRRFamide-like neuropeptide FLP4 (SQPSMRLRF-amide).
 OC Penaeus monodon (Penaeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OX NCBI_TaxID=6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RA MDLINE=21956277; PubMed11959015;
 RA Sithigorngul P., Pupum J., Krungkasem C., Longyant S.,
 RA Chaivichangkur P., Sithigorngul W., Petsom A.;
 RT "Seven novel FRRFamide-like neuropeptide sequences from the eyestalk
 RT of the giant tiger prawn Penaeus monodon."
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FRRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 9
 SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;
 Query Match 13.6%; Score 3; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SQP 4
 Db 1 SQP 3
 RESULT 7
 BPP_VIPAS
 ID_BPP_VIPAS STANDARD; PRT; 10 AA.
 AC P31351;
 DT 01-JUN-1993 (Rel. 26, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide (Angiotensin-converting
 DE enzyme inhibitor).
 OS Vipera aspis (Aspic viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Vipera.
 OX NCBI_TaxID=9706;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom; PubMed=2169439;
 RA Komori Y., Sugihara H.;
 RT "Characterization of a new inhibitor for angiotensin converting
 RT enzyme from the venom of Vipera aspis aspis."
 RL Int. J. Biochem. 22:767-771(1990).
 CC -1- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; A60377; XASNPC.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD RES 1
 SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;
 Query Match 13.6%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 PKV 6
 Db 6 PKV 8

```

RESULT 8
UPA8 HUMAN
ID UPA8 HUMAN STANDARD; PRT; 10 AA.
AC P30094;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 34) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE.
RC TISSUE=Plasma;
RA MEDLINE=93092937; PubMed=1459097;
RX Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7.2, ITS MW IS: 16 kDa.
CC SWISS-2DPAGE; P30094; HUMAN.
DR NON_TER 10 10
FT VARIANT 4 4 S -> H.
FT NON_TER 1 1 /FTID=VAR_000003.
FT SEQUENCE 10 AA; 977 MW; 2EA6E0C77AE325B8 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVP 15
DB 8 AVP 10

RESULT 9
LMT1 LOCMI
ID LMT1 LOCMI STANDARD; PRT; 12 AA.
AC P22395;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Locustamytotropin 1 (LOM-MT-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]_
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90341077; PubMed=1974346;
RA Schoofs L., Holman G.M., Hayes T.K., Tips A., Nachman R.J.,
RA Vandesande F., de Loof A.;
RT "Isolation, identification and synthesis of locustamytotropin
RT (LOM-MT), a novel biologically active insect peptide.";
RL Peptides 11:427-433(1990).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A43975;
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 12 12 AMIDATION.
FT SEQUENCE 12 AA; 1213 MW; D766C927226DDDD CRC64;

Query Match 13.6%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;

QY 13 AVP 15
DB 8 AVP 10

RESULT 10
TM2A METMA
ID TM2A METMA STANDARD; PRT; 12 AA.
AC P80652;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit
DE (EC 2.1.1.86) (N5-methyltetrahydromethanopterin--coenzyme M
DE methyltransferase 28 kDa subunit) (Fragment).
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]_
RP SEQUENCE.
RC STRAIN=Goel / Goel / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=96370840; PubMed=8774736;
RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;
RT "Sodium ion translocation by N5-methyltetrahydromethanopterin:
RT coenzyme M methyltransferase from Methanosarcina mazei Goel
RT reconstituted in ether lipid liposomes.";
RL Eur. J. Biochem. 239:857-864(1996).
CC -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN
CC METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND
CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-
CC TETRAHYDROMETHANOPTERIN.
CC -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
CC (methylthio)ethanesulfonate.
CC -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
KW Transferase; Methyltransferase; Transmembrane; Methanogenesis.
FT NON_TER 12 12
FT SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;

Query Match 13.6%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
DB 7 VLP 9

RESULT 11
EP65 HUMAN
ID EP65 HUMAN STANDARD; PRT; 13 AA.
AC P54953;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Erythrocyte 65 kDa protein (P65) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE.
RX MEDLINE=90004678; PubMed=2507249;
RA Hart G.W., Haltiwanger R.S., Holt G.D., Kelly W.G.;
RT "Nucleoplasmic and cytoplasmic glycoproteins.";
RL Ciba Found. Symp. 145:102-118(1989).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC GO; GO:0005737; C:cytoplasm; NAS.
DR GO;
KW Glycoprotein.

```

```

FT  NON TER      1      1      O-LINKED (GLCNAC).
FT  CARBOHYD     2      13
FT  NON TER     13
SQ  SEQUENCE    13 AA; 1300 MW; DOB873344C61A776 CRC64;

Query Match      13.6%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SQP 4
Db      5 SQP 7

RESULT 12
FIBB RABIT
ID  FIBB RABIT  STANDARD;      PRT;      13 AA.
AC  P14478;
DT  01-JAN-1990 (Rel. 13, Created)
DT  01-JAN-1990 (Rel. 13, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Fibrinogen beta chain [contains: Fibrinopeptide B] (Fragment).
GN  FGB.
OS  Oryctolagus cuniculus (Rabbit).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX  NCBI_TaxID=9986;
RN  [1]
RP  SEQUENCE.
RA  Blomback B., Blomback M., Grondahl N.J.;
RT  "Studies on fibrinopeptides from mammals.";
RL  Acta Chem. Scand. 19:1789-1791(1965).
CC  -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC  POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC  AGGREGATION.
CC  -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC  (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC  -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC  THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC  CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC  RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR  InterPro: IPE002181; Fibrinogen C.
DR  PROSITE: PS00514; FIBRINAG_C_DOMAIN; PARTIAL.
KW  Blood coagulation; Plasma; Sulfation.
FT  PEPTIDE      1      13
FT  MOD RES      4      4
FT  NON TER     13      13
SQ  SEQUENCE    13 AA; 1493 MW; 9417F3B76337CB1A CRC64;

Query Match      13.6%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 VLP 8
Db      8 VLP 10

RESULT 13
HPAL RANES
ID  HPAL RANES  STANDARD;      PRT;      13 AA.
AC  P32415;
DT  01-OCT-1993 (Rel. 27, Created)
DT  01-OCT-1993 (Rel. 27, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Hemolytic protein A1 (Fragment).
OS  Rana esculenta (Edible frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX  NCBI_TaxID=8401;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Skin secretion;
RX  MEDLINE=97175050; PubMed=9022710;

```

```

RX  MEDLINE=90198965; PubMed=2317508;
RA  Siamaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,
RA  Barria D., Bossa F.;
RT  "Purification and characterization of bioactive peptides from skin
RT  extracts of Rana esculenta.";
RL  Biochim. Biophys. Acta 1033:318-323(1990).
CC  -!- FUNCTION: Shows hemolytic activity.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Skin.
DR  PIR; S09018; S09018.
KW  Amphibian defense peptide; Amidation; Hemolysis.
FT  MOD RES      13      13
FT  NON TER     13      13
SQ  SEQUENCE    13 AA; 1390 MW; C6BA768B9DFE587D CRC64;

Query Match      13.6%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LSQ 3
Db      9 LSQ 11

RESULT 14
PEDI HYDAT
ID  PEDI HYDAT  STANDARD;      PRT;      13 AA.
AC  P80578;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  01-OCT-1996 (Rel. 34, Last annotation update)
DE  Pedin.
OS  Hydra attenuata (Hydra) (Hydra vulgaris).
OC  Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC  Hydridae; Hydra.
OX  NCBI_TaxID=6087;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=96232307; PubMed=8674432;
RA  Hoffmeister S.A.H.;
RT  "Isolation and characterization of two new morphogenetically active
RT  peptides from Hydra vulgaris.";
RL  Development 122:1941-1948(1996).
CC  -!- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT
CC  DEVELOPMENT.
KW  Morphogen.
SQ  SEQUENCE    13 AA; 1512 MW; 6F52666E3F37632CB CRC64;

Query Match      13.6%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 VLP 8
Db      7 VLP 9

RESULT 15
TEME RANTE
ID  TEME RANTE  STANDARD;      PRT;      13 AA.
AC  P56920;
DT  30-MAY-2000 (Rel. 39, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Temporin E.
OS  Rana temporaria (European common frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX  NCBI_TaxID=8407;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Skin secretion;
RX  MEDLINE=97175050; PubMed=9022710;

```

```

RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13
FT SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db |||
1 VLP 3

RESULT 16
TEMP_RANTE STANDARD; PRT; 13 AA.
AC P56921;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin F.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
CC GRAM-POSITIVE BACTERIA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13
FT SEQUENCE 13 AA; 1370 MW; 2653612B9DECC338 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
Db |||
7 KVL 9

RESULT 17
CAT2_FASHE STANDARD; PRT; 14 AA.
AC P80342;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cathepsin L2 (EC 3.4.22.15) (Fragment).
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fasciolidae; Fasciola.

```

```

OX NCBI_TaxID=6192;
RN [1]
RP SEQUENCE.
RX MEDLINE=94307282; PubMed=8033913;
RA Dowd A.J., Smith A.M., McGonicle S., Dalton J.P.;
RT "Purification and characterisation of a second cathepsin L proteinase
RT secreted by the parasitic trematode Fasciola hepatica.";
RL Eur. J. Biochem. 223:191-98(1994).
CC -!- FUNCTION: THIOL PROTEASE THAT ASSISTS THE PARASITE IN BURROWING
CC THROUGH THE GUT WALL AND LIVER OF ITS MAMMALIAN HOST.
CC -!- CATALYTIC ACTIVITY: Specificity close to that of papain. As
CC compared to cathepsin B, cathepsin L exhibits higher activity
CC towards protein substrates, but has little activity on Z-Arg-Arg-
CC NHec, and no peptidyl-dipeptidase activity.
CC -!- SUBUNIT: DIMER OF A HEAVY AND A LIGHT CHAIN LINKED BY DISULFIDE
CC BONDS.
CC -!- SUBCELLULAR LOCATION: Lysosomal.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR PIR; S45655; S45655.
DR MEROPS; C01.033; .
DR Interpro; IPR000169; SHprot_acsite.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; PARTIAL.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; PARTIAL.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; PARTIAL.
KW Hydrolase; Thiol protease; Lysosome.
FT NON_TER 14
FT SEQUENCE 14 AA; 1605 MW; 9CAEAB74E9DA110A CRC64;

Query Match 13.6%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVP 15
Db |||
1 AVP 3

RESULT 18
MAST_VESBA STANDARD; PRT; 14 AA.
ID AC P21654;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mastoparan B.
OS Vespa basalis (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7444;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=91174755; PubMed=2006909;
RA Lo C.-L., Hwang L.-L.;
RT "Structure and biological activities of a new mastoparan isolated
RT from the venom of the hornet Vespa basalis.";
RL Biochem. J. 274:453-456(1991).
CC -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
DR PIR; S14336; S14336
KW Mast cell degranulation; Amidation.
FT MOD_RES 14
FT SEQUENCE 14 AA; 1613 MW; D35944CA193A19A2 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
Db |||
12 KVL 14

```

```

RESULT 19
MAST_VESOR
ID MAST_VESOR STANDARD; PRT; 14 AA.
AC P17238;
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mastoparan (Histamine releasing peptide I) (HR-I).
OS Vespa orientalis (Oriental hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
CX NCBI_TaxID=7447;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Miroshnikov A.I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,
RA Rozyanov B.V., Gushchin I.S.;
RT "Structure and properties of histamine releasing peptides from the
RT venom of Vespa orientalis hornet.";
RL Bioorg. Khim. 7:1467-1477(1981).
CC -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
CC PIR; JN0389; JN0389.
CC Mast cell degranulation; Amidation.
KW MOD RES 14 14 AMIDATION.
FT SEQUENCE 14 AA; 1494 MW; C84F9ECA026B00DD CRC64;
SQ
Query Match 13.6%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
DB 12 KVL 14

RESULT 20
TAT_HV128
ID TAT_HV128 STANDARD; PRT; 14 AA.
AC P12509;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
GN TAT.
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
CX NCBI_TaxID=11705;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86235450; PubMed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
RT at risk for AIDS."
RL Science 232:1548-1553(1986).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -!- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J03653; AAA44685.1; -.
CC HIV; J03653; TATSVY1.
CC TRANSCRIPTION regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC NON TER 1 1
CC SEQUENCE 14 AA; 1453 MW; 37CC737BF82D7AA8 CRC64;
SQ
Query Match 13.6%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4
DB 3 SQP 5

RESULT 21
TAT_HV128
ID TAT_HV128 STANDARD; PRT; 14 AA.
AC P12511;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
GN TAT.
OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
CX NCBI_TaxID=11681;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88281278; PubMed=3395517;
RA Yourho J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
RA Gallo R.C.;
RT "Nucleotide sequence analysis of the env gene of a new Zairian
RT isolate of HIV-1."
RL AIDS Res. Hum. Retroviruses 4:165-173(1988).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
CC ZAIREAN MALE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J03653; AAA44685.1; -.
CC HIV; J03653; TATSVY1.
CC TRANSCRIPTION regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC NON TER 1 1
CC SEQUENCE 14 AA; 1453 MW; 37CC737BF82D7AA8 CRC64;
SQ
Query Match 13.6%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4
DB 3 SQP 5

RESULT 22

```

CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

CC EMBL; M12507; AAB12991.1; -.
 CC HIV; M12507; TATSVWJ2.
 CC TRANSCRIPTION regulation; Activator; RNA-binding; Nuclear protein;
 CC AIDS.
 CC NON TER 1 1
 CC SEQUENCE 14 AA; 1467 MW; 37CC737BF82D7AA8 CRC64;
 CC
 CC Query Match 13.6%; Score 3; DB 1; Length 14;
 CC Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4
 DB 3 SQP 5

RESULT 21
 TAT_HV128

CC ID TAT_HV128 STANDARD; PRT; 14 AA.
 CC AC P12511;
 CC DT 01-OCT-1989 (Rel. 12, Created)
 CC DT 01-OCT-1989 (Rel. 12, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE TAT protein (Transactivating regulatory protein) (Fragment).
 CC GN TAT.
 CC OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
 CC OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 CC CX NCBI_TaxID=11681;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=88281278; PubMed=3395517;
 CC RA Yourho J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
 CC RA Gallo R.C.;
 CC RT "Nucleotide sequence analysis of the env gene of a new Zairian
 CC isolate of HIV-1."
 CC RL AIDS Res. Hum. Retroviruses 4:165-173(1988).
 CC CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 CC PROMOTER.
 CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
 CC -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
 CC ZAIREAN MALE.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; J03653; AAA44685.1; -.
 CC HIV; J03653; TATSVY1.

CC TRANSCRIPTION regulation; Activator; RNA-binding; Nuclear protein;
 CC AIDS.
 CC NON TER 1 1
 CC SEQUENCE 14 AA; 1453 MW; 37CC737BF82D7AA8 CRC64;
 CC
 CC Query Match 13.6%; Score 3; DB 1; Length 14;
 CC Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4
 DB 3 SQP 5

RESULT 22

```

UC15_MAIZE
ID UC15_MAIZE STANDARD; PRT; 14 AA.
AC P80621;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 245)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005 (1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.8, ITS MW IS: 35.7 kDa.
DR Maize-2DPAGE; P80621; COLEOPTILE.
DR MaizeDB; 123947; -.
FT NON_TER 1
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1396 MW; C68949275F404CD2 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
Db |||
5 LPV 7

RESULT 23
APP3 MALPA STANDARD; PRT; 15 AA.
ID APP3 MALPA STANDARD; PRT; 15 AA.
AC P83137;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antifungal protein 3 (CW-3) (Fragment).
OS Malva parviflora (Little mallow) (Cheeseweed).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Malvoideae; Malva.
OX NCBI_TaxID=145753;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Seed;
RX MEDLINE=21199399; PubMed=11302747;
RA Wang X., Bunkers G.J., Walters M.R., Thoma R.S.;
RT "Purification and characterization of three antifungal proteins from
RT cheeseweed (Malva parviflora).";
RL Biochem. Biophys. Res. Commun. 282:1224-1228 (2001).
CC -!- FUNCTION: Possesses antifungal activity against P.infestans but
CC not F.graminearum.
CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC concentration.
DR GO; GO:0003799; P:antifungal peptide activity; IDA.
DR GO; GO:0007275; P:development; NAS.
KW Fungicide; Antibiotic.
FT NON_TER 15
FT NON_TER 15
SQ SEQUENCE 15 AA; 2016 MW; 01D9CA069F1A52B2B CRC64;

Query Match 13.6%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 15 PQR 17
Db |||
4 PQR 6

RESULT 24
IRBP_CRISP STANDARD; PRT; 15 AA.
ID IRBP_CRISP STANDARD; PRT; 15 AA.
AC P12665;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Interphotoreceptor retinoid-binding protein (IRBP) (Interstitial
DE retinol-binding protein) (Fragment).
GN RBP3.
OS Cricetidae sp. (Hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae.
OX NCBI_TaxID=36483;
RN [1]
RP SEQUENCE.
RX MEDLINE=86301171; PubMed=3743780;
RA Fong S.L., Cook R.G., Alvarez R.A., Liou G.I., Landers R.A.,
RA Bridges C.D.B.;
RT "N-terminal sequence homologies in interstitial retinol-binding
RT proteins from 10 vertebrate species.";
RL FEBS Lett. 205:309-312 (1986).
CC -!- FUNCTION: IRBP SHUTTLES 11-CIS AND ALL TRANS RETINOIDS BETWEEN
CC THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL
CC PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
CC -!- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES
CC THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT
CC EPITHELIUM CELLS.
DR PIR; G24417; G24417.
KW Vitamin A; Transport.
FT NON_TER 15
FT NON_TER 15
SQ SEQUENCE 15 AA; 1752 MW; C51A8780C85DEC1E CRC64;

Query Match 13.6%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 PIQ 22
Db |||
2 PIQ 4

RESULT 25
MCA2_RHOOP STANDARD; PRT; 15 AA.
ID MCA2_RHOOP STANDARD; PRT; 15 AA.
AC P56870;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative maleylacetate reductase II (EC 1.3.1.32) (Fragment).
OS Rhodococcus opacus (Nocardia opaca).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaeae; Rhodococcus.
OX NCBI_TaxID=37919;
RN [1]
RP SEQUENCE.
RC STRAIN=ICP;
RX MEDLINE=98324954; PubMed=9657989;
RA Seibert V., Kourbatova E.M., Golovleva L.A., Schloemann M.;
RT "Characterization of a maleylacetate reductase encoding region from
RT Rhodococcus opacus ICP.";
RL J. Bacteriol. 180:3503-3508 (1998).
CC -!- CATALYTIC ACTIVITY: 3-oxoadipate + NAD(P) (+) = 2-maleylacetate +
CC NAD(P)H.
CC -!- PATHWAY: 3-chlorocatechol degradation (beta-ketoadipate pathway).
CC THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC
CC AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL
CC PRODUCTS AND AS INDUSTRIAL EFFLUENT.

```


CC -1- SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL DEHYDROGENASE
 CC FAMILY.
 DR InterPro: IPE001670; Fe-ADH.
 DR PROSITE: PS00913; ADH_IRON_1; PARTIAL.
 DR PROSITE: PS00960; ADH_IRON_2; PARTIAL.
 KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1884 MW; 58DA90DD038F025E CRC64;

Query Match 13.6%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
 ||||
 Db 9 PQR 11

RESULT 26
 RBS_PHYPA STANDARD; PRT; 15 AA.
 AC P80657;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ribulose biphosphate carboxylase small chain (EC 4.1.1.39) (RuBisCO
 DE small subunit) (Fragment).
 GN RBSCS.
 OS Physcomitrella patens (Moss).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 CC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 RN NCBI_TaxID=3218;
 [1]
 RP SEQUENCE.

CC TISSUE=Protonema;
 CC MEDLINE=97275459; PubMed=9129336;
 RA Kasten B., Buck F., Nuske J., Reski R.;
 RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
 RT plastid enzymes";
 RL Planta 201:261-272 (1997).
 CC -1- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic
 CC carbon dioxide fixation, as well as the oxidative fragmentation of
 CC the pentose substrate in the photorespiration process. Both
 CC reactions occur simultaneously and in competition at the same
 CC active site.
 CC -1- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) = 2 3-
 CC phospho-D-glycerate.
 CC -1- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) =
 CC 3-phospho-D-glycerate + 2-phosphoglycolate.
 CC -1- SUBUNIT: 8 large chains + 8 small chains.
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC -1- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
 KW Photosynthesis; Carbon dioxide fixation; Photorespiration;
 KW Lyase; Oxidoreductase; Monooxygenase; Chloroplast.
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1801 MW; 28B9E7AC4AED6CE0 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPK 5
 ||||
 Db 9 QPK 11

RESULT 27
 UC29_MAIZE STANDARD; PRT; 15 AA.
 ID UC29_MAIZE
 AC P80635;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 45)
 DE (Fragment).
 ZEa Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.

CC TISSUE=Coleoptile;
 CC RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 CC Parnollet J.-C., Zivy M., de Vienne D.;
 CC "The maize two dimensional gel protein database: towards an integrated
 CC genome analysis program";
 CC Theor. Appl. Genet. 93:997-1005 (1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.9, ITS MW IS: 37.6 kDa.
 CC Maize-2DPAGE: P80635; COLEOPTILE.
 DR MaizeDB; 123960; -. 1
 DR NON_TER 15
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1679 MW; 3D53086B16018BC1 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVP 10
 ||||
 Db 4 PVP 6

RESULT 28
 AF2S_MALPA STANDARD; PRT; 16 AA.
 ID AF2S_MALPA
 AC P83142;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Antifungal protein 2 small subunit (CW-2) (Fragment).
 OS Malva parviflora (Little mallow) (Cheeseweed).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosid II; Malvales; Malvaceae; Malvoideae; Malva.
 OX NCBI_TaxID=145753;
 [1]
 RN SEQUENCE, AND FUNCTION.
 RP TISSUE=Seed;
 CC MEDLINE=20568734; PubMed=11118343;
 RX Wang X., Bunkers G.J.;
 RA "Potent heterologous antifungal proteins from cheeseweed (Malva
 RA parviflora).";
 RT Biochem. Biophys. Res. Commun. 279:669-673 (2000).
 RL -1- FUNCTION: Possesses antifungal activity against P.infestans but
 CC not P.graminearum.
 CC -1- SUBUNIT: Heterodimer of a large and a small subunit.
 CC -1- MISCELLANEOUS: Antimicrobial activity is not affected by salt
 CC concentration.
 CC GO: GO:0003799; F:Antifungal peptide activity; IDA.
 KW Fungicide; Antibiotic.
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 2027 MW; 9998D9EB8FB7EE65 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PQX 12
 ||||
 Db 10 PQX 12

RESULT 29

BOL1_MEGPE
ID A45K_MYCBO STANDARD; PRT; 17 AA.
AC P80069;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 45/47 kDa antigen (Fragment).
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE.
RC STRAIN=BCG / Paris 1173 P2;
RX MEDLINE=93138802; PubMed=8423100;
RA Romain F., Laqueyrie A., Militzer P., Pescher P., Chavarot P.,
RA Lagranderie M., Auregan G., Gheorghiu M., Marchal G.A.;
RT "Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen
complex, an immunodominant target for antibody response after
immunization with living bacteria.";
RL Infect. Immun. 61:742-750(1993).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: TO M.LEPRAE NL43, AND M.TUBERCULOSIS MPT32.
DR PIR; A49237; A49237.
KW Antigen.

FT NON TER 17

SQ SEQUENCE 17 AA; 1521 MW; 4492CC389D9D9893 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVP 10

Db 7 PVP 9

RESULT 30

BOL1_MEGPE
ID BOL1_MEGPE STANDARD; PRT; 17 AA.
AC P10521;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bombolitin I.
OS Megabombus pennsylvanicus (American common bumblebee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=28643;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=85105003; PubMed=2578459;
RA Argiolas A., Pisano J.J.;
RT "Bombolitins, a new class of mast cell degranulating peptides from
the venom of the bumblebee Megabombus pennsylvanicus.";
RL J. Biol. Chem. 260:1437-1444(1985).
CC -!- FUNCTION: Mast cell degranulating peptide.
DR PIR; A22595; A22595
KW Mast cell degranulation.

SQ SEQUENCE 17 AA; 1836 MW; D5FA46F44B876602 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVL 7

Db 12 KVL 14

RESULT 31

BOL2_MEGPE
ID BOL2_MEGPE STANDARD; PRT; 17 AA.
AC P07493;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bombolitin II.
OS Megabombus pennsylvanicus (American common bumblebee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=28643;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=85105003; PubMed=2578459;
RA Argiolas A., Pisano J.J.;
RT "Bombolitins, a new class of mast cell degranulating peptides from
the venom of the bumblebee Megabombus pennsylvanicus.";
RL J. Biol. Chem. 260:1437-1444(1985).
CC -!- FUNCTION: Mast cell degranulating peptide.
DR PIR; B22595; B22595.
KW Mast cell degranulation.

SQ SEQUENCE 17 AA; 1806 MW; C52026F14BD76602 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVL 7

Db 12 KVL 14

RESULT 32

BOL3_MEGPE
ID BOL3_MEGPE STANDARD; PRT; 17 AA.
AC P07494;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bombolitin III.
OS Megabombus pennsylvanicus (American common bumblebee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=28643;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=85105003; PubMed=2578459;
RA Argiolas A., Pisano J.J.;
RT "Bombolitins, a new class of mast cell degranulating peptides from
the venom of the bumblebee Megabombus pennsylvanicus.";
RL J. Biol. Chem. 260:1437-1444(1985).
CC -!- FUNCTION: Mast cell degranulating peptide.
DR PIR; C22595; C22595.
KW Mast cell degranulation.

SQ SEQUENCE 17 AA; 1862 MW; D5FA46F14BC85B02 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVL 7

Db 12 KVL 14

RESULT 33

BOL4_MEGPE
ID BOL4_MEGPE STANDARD; PRT; 17 AA.

AC P07495;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bombolitin IV.
 OS Megabombus pennsylvanicus (American common bumblebee).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
 OC Apidae; Bombus.
 CX NCBI_TaxID=28643;
 RN [1]
 RN SEQUENCE.
 RP TISSUE=Venom;
 RC MEDLINE=85105003; PubMed=2578459;
 RA Argiolas A., Pisano J.J.;
 RT "Bombolittins, a new class of mast cell degranulating peptides from
 RT the venom of the bumblebee Megabombus pennsylvanicus.";
 RL J. Biol. Chem. 260:1437-1444(1985).
 CC -|- FUNCTION: Mast cell degranulating peptide.
 DR PIR: D22595; D22595.
 KW Mast cell degranulation.
 SQ SEQUENCE 17 AA; 1873 MW; A34A43514BCFDFB6 CRC64;
 Query Match 13.6%; Score 3; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 KVL 7
 DB 12 KVL 14

RESULT 34
 H2B3_ICTPU STANDARD; PRT; 17 AA.
 AC P81904;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Histone H2B-3 (Antibacterial histone-like protein 3) (HLP-3)
 DE (Fragment).
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Ictaluridae; Ictalurus.
 CX NCBI_TaxID=7998;
 RN [1]
 RN SEQUENCE, AND FUNCTION.
 RP TISSUE=Skin;
 RC MEDLINE=98309109; PubMed=9645227;
 RA Robinette D., Wada S., Arroll T., Levy M.G., Miller W.L., Noga E.J.;
 RT "Antimicrobial activity in the skin of the channel catfish Ictalurus
 RT punctatus: characterization of broad-spectrum histone-like
 RT antimicrobial proteins.";
 RL Cell. Mol. Life Sci. 54:467-475(1998).
 CC -|- FUNCTION: Has antimicrobial activity. Possesses strong activity
 CC against saprolegnia, the most common fungal infection in fish.
 CC -|- SUBUNIT: The nucleosome is an octamer containing two molecules
 CC each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
 CC bp of DNA.
 CC -|- SUBCELLULAR LOCATION: Nuclear.
 CC -|- MASS SPECTROMETRY: MW=13506; METHOD=MALDI.
 CC -|- SIMILARITY: Belongs to the histone H2B family.
 DR InterPro: IPR000558; Histone H2B.
 DR PROSITE: PS00357; HISTONE H2B; PARTIAL.
 KW Nuclear protein; Chromosomal protein; Nucleosome core; DNA-binding;
 KW Antibiotic; Fungicide.
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 1795 MW; 44FB8D966FD2F377 CRC64;
 Query Match 13.6%; Score 3; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAV 14
 DB 14 KAV 16

RESULT 35
 LPW_CORGL STANDARD; PRT; 17 AA.
 ID AC P06556;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trp operon leader peptide.
 GN TRPL OR GCL3028.1.
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 CX NCBI_TaxID=1718;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP RX MEDLINE=87117512; PubMed=3808947;
 RA Matsui K., Sano K., Ohtsubo E.;
 RT "Complete nucleotide and deduced amino acid sequences of the
 RT Brevibacterium lactofermentum tryptophan operon.";
 RL Nucleic Acids Res. 14:10113-10114(1986).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP RX MEDLINE=88032866; PubMed=3667535;
 RA Matsui K., Miwa K., Sano K.;
 RT "Two single-base-pair substitutions causing desensitization to
 RT tryptophan feedback inhibition of anthranilate synthase and enhanced
 RT expression of tryptophan genes of Brevibacterium lactofermentum.";
 RL J. Bacteriol. 169:5330-5332(1987).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP RX MEDLINE=87277409; PubMed=3609747;
 RA Sano K., Matsui K.;
 RT "Structure and function of the trp operon control regions of
 RT Brevibacterium lactofermentum, a glutamic-acid-producing bacterium.";
 RL Gene 53:191-200(1987).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP RC STRAIN=ATCC 13059 / AS019;
 RX MEDLINE=91088299; PubMed=2263476;
 RA Heery D.M., Dunican L.K.;
 RT "Nucleotide sequence of the Corynebacterium glutamicum trpE gene.";
 RL Nucleic Acids Res. 18:7138-7138(1990).
 RN [5]
 RN SEQUENCE FROM N.A.
 RP RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -|- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
 CC OF TRYPTOPHAN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; X04960; CAA28622.1; -;
 DR EMBL; M17892; AAB59110.1; -;
 DR EMBL; M16663; -; NOT_ANNOTATED_CDS.
 DR EMBL; X55994; CAA39466.1; -;
 DR EMBL; AP005283; -; NOT_ANNOTATED_CDS.
 DR PIR; A29834; A29834.
 KW Tryptophan biosynthesis; Leader peptide; Complete proteome.
 SQ SEQUENCE 17 AA; 2112 MW; 74C7E7924DAAE56B CRC64;

Query Match 13.6%; Score 3; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQ 3
 DB 6 LSQ 8

RESULT 36

UP34_UPEMJ STANDARD; PRT; 17 AA.
 AC P82041;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Uperin 3.4.
 OS Uperoleia mjobergii (Australian toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104954;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "New antibiotic uperin peptides from the dorsal glands of the
 Australian toadlet Uperoleia mjobergii.";
 RL Aust. J. Chem. 49:1325-1331(1996).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=1735; METHOD=FAB.
 KW Amphibian defense peptide; Amidation.
 FT MOD RES 17 17
 SQ SEQUENCE 17 AA; 1737 MW; 6F61B4834375DE1B CRC64;

Query Match 13.6%; Score 3; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAV 14
 DB 8 KAV 10

RESULT 37

UP35_UPEMJ STANDARD; PRT; 17 AA.
 AC P82042;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Uperin 3.5.
 OS Uperoleia mjobergii (Australian toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104954;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "New antibiotic uperin peptides from the dorsal glands of the
 Australian toadlet Uperoleia mjobergii.";
 RL Aust. J. Chem. 49:1325-1331(1996).
 CC -!- FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,
 L.INNOCUA, M.LUTEUS, S.AUREUS, P.MULIOCI, S.EPIDERMIS AND
 S.UBERIS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=1779; METHOD=FAB.
 KW Amphibian defense peptide; Antibiotic; Amidation.

FT MOD RES 17 17
 SQ SEQUENCE 17 AA; 1781 MW; 6F61E483436AD67B CRC64;

Query Match 13.6%; Score 3; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAV 14
 DB 8 KAV 10

RESULT 38

ALI3_CARMA STANDARD; PRT; 18 AA.
 AC P81816;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 13.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD RES 18 18
 SQ SEQUENCE 18 AA; 2225 MW; 3531112C8160AE27 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKV 6
 DB 11 PKV 13

RESULT 39

ALI2_CVDPO STANDARD; PRT; 18 AA.
 AC P82153;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiastatin 2.
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 18 18
 AMIDATION.

SQ SEQUENCE 18 AA; 2169 MW; 8E66679C0CDF175C CRC64;

Query Match 13.6%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
Db 11 LPV 13

RESULT 40

D7A1 ACASC STANDARD; PRT; 18 AA.

ID D7A1 ACASC STANDARD; PRT; 18 AA.

AC P83402;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) (Antiquitin 1) (fragment).

DE (fragment).

OS Acanthopagrus schlegelii (Black porgy).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;

OC Sparidae; Acanthopagrus.

OX NCBI_TaxID=72011;

OX

RN

RP SEQUENCE, ACTIVITY, COFACTOR, AND SUBUNIT.

RC TISSUE=Liver;

RX MEDLINE=21956475; PubMed=11959129;

RA Tang W.-K., Cheng C.H.K., Fong W.-P.;

RT "First purification of the antiquitin protein and demonstration of its enzymatic activity.";

RL FEBS Lett. 516:183-186 (2002).

CC -1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.

CC -1- SUBUNIT: Homotetramer.

CC -1- MISCELLANEOUS: Optimal pH is 9-10. The Km for acetaldehyde is 2.0 mM and Vmax is 1.3 micromol/min x mg enzyme.

CC -1- SIMILARITY: Belongs to the aldehyde dehydrogenase family.

DR GO; GO:0004029; F:aldehyde dehydrogenase (NAD+) activity; IDA.

DR GO; GO:0006081; P:aldehyde metabolism; IDA.

DR InterPro; IPR002086; Aldehyde dehydr.

DR PROSITE; PS00070; ALDEHYDE DEHYDR. CYS; PARTIAL.

DR PROSITE; PS00687; ALDEHYDE DEHYDR. GLU; PARTIAL.

KW Oxidoreductase; NAD.

KW

FT NON TER 18

FT NON TER 18

SQ SEQUENCE 18 AA; 2059 MW; BFF8C3EF1A9B4047 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPK 5
Db 7 QPK 9

RESULT 41

DRPH UCAPU STANDARD; PRT; 18 AA.

ID DRPH UCAPU STANDARD; PRT; 18 AA.

AC P08871;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Pigment-dispersing hormone (PDH) (Light adapting distal retinal pigment hormone) (DRPH).

DE

OS Uca pugnator (Atlantic sand fiddler crab) (Celluca pugnator).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

OC Eubrachyura; Ocypodoidea; Ocypodidae; Ocypodinae; Uca complex; Caluca.

OC

OX NCBI_TaxID=6772;

RN

RP SEQUENCE.

RA Rao K.R., Riehm J.P., Zahnow C.A., Kleinholz L.H., Tarr G.E., Johnson L., Norton S., Landau M., Semmes O.J., Sattelberg R.M., Jorenbey W.H., Hintz M.F.;

RA "Characterization of a pigment-dispersing hormone in eyestalks of the fiddler crab Uca pugnator.";

RT Proc. Natl. Acad. Sci. U.S.A. 82:5319-5322 (1985).

RL

RN

RP

RP SEQUENCE.

RX MEDLINE=93230895; PubMed=8472537;

RA Lochr J., Klein J., Webster S.G., Dirksen H.;

RA "Quantification, immunoaffinity purification and sequence analysis of a pigment-dispersing hormone of the shore crab, Carcinus maenas (L.).";

RT Comp. Biochem. Physiol. 104B:699-706 (1993).

CC -1- FUNCTION: CAUSES THE MIGRATION OF THE DISTAL RETINAL PIGMENT INTO THE PROXIMAL END OF THE PIGMENT CHROMATOPHORE CELLS AND THUS DECREASES THE AMOUNT OF LIGHT ENTERING THE RETINULAS.

CC -1- SIMILARITY: TO THE PDH OF OTHER ARTHROPODS.

DR PIR; A25144; DRUFPD.

KW Hormone; Amidation.

FT DOMAIN 6 9 IMPORTANT FOR DRPH ACTIVITY.

FT MOD RES 18 18 AMIDATION.

FT MOD RES 18 18

SQ SEQUENCE 18 AA; 1928 MW; 25D5C8D016F544E CRC64;

Query Match 13.6%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKV 6
Db 12 PKV 14

RESULT 42

LCIN LAMGL STANDARD; PRT; 18 AA.

ID LCIN LAMGL STANDARD; PRT; 18 AA.

AC P83315;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Lactophorin (Whey protein) (fragment).

OS Lama glama (Llama).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.

OX NCBI_TaxID=9844;

OX

RN

RP SEQUENCE.

RX MEDLINE=20000588; PubMed=10531593;

RA Kappeler S., Farah Z., Puhon Z.;

RT "Alternative splicing of lactophorin mRNA from lactating mammary gland of the camel (Camelus dromedarius).";

RL J. Dairy Sci. 82:1-10 (1999).

CC -1- SIMILARITY: BELONGS TO THE PP3 / GLYCAM-1 FAMILY.

DR GO; GO:0005576; C:extracellular; ISS.

DR PFam; PF05242; GLYCAM-1; 1.

FT NON TER 18

FT NON TER 18

SQ SEQUENCE 18 AA; 2079 MW; CD59616E5B236AC6 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4
Db 16 SQP 18

RESULT 43

NPA_BOVIN STANDARD; PRT; 18 AA.

ID NPA_BOVIN STANDARD; PRT; 18 AA.

AC P15506;

```

DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine."
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; A24749; A24749.
KW Neuropeptide; Amidation.
FT MOD RES 18 18
SQ SEQUENCE 18 AA; 1921 MW; EC52DAE1P45CFCFB CRC64;

Query Match 13.6%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
DB 15 PQR 17

RESULT 44
FIBR_PIG
ID FIBR_PIG STANDARD; PRT; 19 AA.
AC P14477;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals."
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro; IPR002181; Fibrinogen_C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 19
FT FIBRINOPEPTIDE B.
FT MOD RES 4 4
FT SULFATION.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2200 MW; 09F87E44F4F3863D CRC64;

Query Match 13.6%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4' PKV 6

```

```

Db 12 PKV 14

RESULT 45
IRBP_CAVPO
ID IRBP_CAVPO STANDARD; PRT; 19 AA.
AC P12666;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Interphotoreceptor retinoid-binding protein (IRBP) (Interstitial
DE retinol-binding protein) (Fragment).
GN RBP3.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RX MEDLINE=86301171; PubMed=3743780;
RA Fong S.L., Cook R.G., Alvarez R.A., Liou G.I., Landers R.A.,
RA Bridges C.D.B.;
RT "N-terminal sequence homologies in interstitial retinol-binding
RT proteins from 10 vertebrate species."
RL FEBS Lett. 205:309-312(1986).
CC -!- FUNCTION: IRBP SHUTTLES 11-CIS AND ALL TRANS RETINOLIDS BETWEEN
CC THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL
CC PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
CC -!- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES
CC THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT
CC EPITHELIUM CELLS.
DR PIR; D24417; D24417.
KW Vitamin A; Transport.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2155 MW; 7172B271C85969D5 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
DB 14 KVL 16

RESULT 46
ABP_PIG
ID ABP_PIG STANDARD; PRT; 20 AA.
AC Q9TRC7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amiloride-sensitive amine oxidase [copper-containing] (EC 1.4.3.6)
DE (diamine oxidase) (DAO) (Amiloride-binding protein) (ABP)
DE (Histaminase) (PK-DAO) (Fragment).
GN ABP1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=94193685; PubMed=8144586;
RA Novotny W.F., Chassande O., Baker M., Lazdunski M., Barbry P.;
RT "Diamine oxidase is the amiloride-binding protein and is inhibited by
RT amiloride analogues."
RL J. Biol. Chem. 269:9921-9925(1994).
CC -!- FUNCTION: Catalyzes the degradation of compounds such as
CC putrescine, histamine, spermine, and spermidine, substances
CC involved in allergic and immune responses, cell proliferation,
CC tissue differentiation, tumor formation, and possibly apoptosis.

```

```

CC      (By similarity).
CC      -|- CATALYTIC ACTIVITY: RCH(2)NH(2) + H(2)O + O(2) = RCHO + NH(3) +
CC      H(2)O(2).
CC      -|- COFACTOR: Binds 1 copper ion and 1 topaquinone per subunit (By
CC      similarity).
CC      -|- SUBUNIT: HOMODIMER; Disulfide-linked (By similarity).
CC      -|- SUBCELLULAR LOCATION: Extracellular (By similarity).
CC      -|- PTM: Topaquinone (TPQ) is generated by copper-dependent
CC      autoxidation of a specific tyrosyl residue (By similarity).
CC      -|- SIMILARITY: BELONGS TO THE COPPER/TOPAQUINONE OXIDASE FAMILY.
DR      PIR; B54410.
DR      GlycoSuiteDB; O9TRC7.
DR      InterPro; IPR000269; CUNH oxidase.
DR      PROSITE; PS01164; COPPER_AMINE_OXID_1; PARTIAL.
DR      PROSITE; PS01165; COPPER_AMINE_OXID_2; PARTIAL.
KW      Oxidoreductase; Copper; Heparin-binding; TPQ.
FT      NON_TER 20
FT      NON_TER 20
SQ      SEQUENCE 20 AA; 1898 MW; 4A0E3133B0B2D69F CRC64;

Query Match      13.6%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 KAV 14
      |||
Db      18 KAV 20

RESULT 47
AF2L_MALPA
ID      AF2L_MALPA STANDARD; PRT; 20 AA.
AC      P83143;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Antifungal protein 2 large subunit (CW-2) (Fragment).
OS      Malva parviflora [Little mallow] (Cheeseweed).
OC      Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eurosids II; Malvales; Malvaceae; Malvoideae; Malva.
OX      NCBI_TaxID=145753;
RN      [1]
RP      SEQUENCE AND FUNCTION.
RC      TISSUE=Seed.
RX      MEDLINE=20568734; PubMed=11118343;
RA      Wang X., Bunkers G.J.;
RT      "Potent heterologous antifungal proteins from cheeseweed (Malva
RT      parviflora).";
RL      Biochem. Biophys. Res. Commun. 279:669-673(2000).
CC      -|- FUNCTION: Possesses antifungal activity against P.infestans but
CC      not F.graminearum.
CC      -|- SUBUNIT: Heterodimer of a large and a small subunit.
CC      -|- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC      concentration.
CC      GO: GO:0003799; F:antifungal peptide activity; IDA.
DR      GO; GO:0003799; F:antifungal peptide activity; IDA.
DR      Fungicide; Antibiotic.
FT      NON_TER 20
FT      NON_TER 20
SQ      SEQUENCE 20 AA; 2603 MW; 6E766A5E342036DA CRC64;

Query Match      13.6%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 PQR 17
      |||
Db      4 PQR 6

RESULT 48
BIP_PHAVU
ID      BIP_PHAVU STANDARD; PRT; 20 AA.
AC      P80589;
DT      01-DEC-1992 (Rel. 24, Created)

```

```

DT      01-DEC-1992 (Rel. 24, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Luminal binding protein (78 kDa glucose-regulated protein homolog)
DE      (GRP 78) (Fragment).
OS      Phaseolus vulgaris (Kidney bean) (French bean).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX      NCBI_TaxID=3885;
RN      [1]
RP      SEQUENCE.
RC      STRAIN=cv. Greensleeves; TISSUE=Cotyledon;
RX      MEDLINE=94221064; PubMed=1344885;
RA      D'Amico L., Valsasina B., Daminati M.G., Fabbrini M.S., Nitti G.,
RA      Bollini R., Ceriotti A., Vitale A.;
RT      "Bean homologs of the mammalian glucose-regulated proteins: induction
RT      by tunicamycin and interaction with newly synthesized seed storage
RT      proteins in the endoplasmic reticulum.";
RL      Plant J. 2:443-455(1992).
CC      -|- FUNCTION: PROBABLY PLAYS A ROLE IN FACILITATING THE ASSEMBLY OF
CC      MULTIMERIC PROTEIN COMPLEXES INSIDE THE ER.
CC      -|- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC      -|- INDUCTION: By tunicamycin.
CC      -|- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR      InterPro; IPR001023; Hsp70.
DR      PROSITE; PS00297; HSP70_1; PARTIAL.
DR      PROSITE; PS00329; HSP70_2; PARTIAL.
DR      PROSITE; PS01036; HSP70_3; PARTIAL.
KW      ATP-binding; Endoplasmic reticulum.
FT      UNSURE 4 4 OR T.
FT      UNSURE 18 18 OR T.
FT      NON_TER 20
FT      NON_TER 20
SQ      SEQUENCE 20 AA; 2147 MW; 809D43AF21A21476 CRC64;

Query Match      13.6%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KVL 7
      |||
Db      5 KVL 7

RESULT 49
CATI_FASHE
ID      CATI_FASHE STANDARD; PRT; 20 AA.
AC      Q09093;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Cathepsin L1 (EC 3.4.22.15) (Fragment).
OS      Fasciola hepatica (Liver fluke).
OC      Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC      Echinostomida; Echinostomata; Fasciolioidea; Fasciolidae; Fasciola.
OX      NCBI_TaxID=6192;
RN      [1]
RP      SEQUENCE.
RC      MEDLINE=94158959; PubMed=8114809;
RA      Smith A.M., Dowd A.J., McGonigle S., Keegan P.S., Brennan G.,
RA      Trudgett A., Dalton J.P.;
RT      "Purification of a cathepsin L-like proteinase secreted by adult
RT      Fasciola hepatica.";
RL      Mol. Biochem. Parasitol. 62:1-8(1993).
CC      -|- FUNCTION: THIOI PROTEASE THAT ASSISTS THE PARASITE IN BURROWING
CC      THROUGH THE GUT WALL AND LIVER OF ITS MAMMALIAN HOST.
CC      -|- CATALYTIC ACTIVITY: Specificity close to that of papain. As
CC      compared to cathepsin B, cathepsin L exhibits higher activity
CC      towards protein substrates, but has little activity on Z-Arg-Arg-
CC      NHMeC, and no peptidyl-dipeptidase activity.
CC      -|- SUBUNIT: DIMER OF A HEAVY AND A LIGHT CHAIN LINKED BY DISULFIDE
CC      BONDS.
CC      -|- SUBCELLULAR LOCATION: Lysosomal.
CC      -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.

```

```

DR PIR; S68785;
DR MEROPS; COL033;
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000169; SHprot acsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PROSITE; PS00139; THIOLESTERASE_CYS; PARTIAL.
DR PROSITE; PS00639; THIOLESTERASE_HIS; PARTIAL.
DR PROSITE; PS00640; THIOLESTERASE_ASN; PARTIAL.
DR Hydrolase; Thiol protease; Lysosome.
KW NON TER 20
SQ SEQUENCE 20 AA; 2174 MW; 97CDEDB33055BCAE CRC64;

Query Match 13.6%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVP 15
DB 1 AVP 3

RESULT 50
ID CD4 SHEEP STANDARD; PRT; 20 AA.
AC P05542;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/Leu-3)
DE (Fragment).
DN CD4.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=86166694; PubMed=3082751;
RA Classon B.J., Tsagaratos J., Kirsbaum L., Maddox J., McKay C.R.,
RA Brandon M., McKenzie I.F.C., Walker I.D.;
RT "The L3T4 antigen in mouse and the sheep equivalent are
RT immunoglobulin-like."
RL Immunogenetics 23:129-132(1986).
CC -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION.
CC -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
DR PIR; B47642;
DR GO; GO:0042101; C:T-cell receptor complex; ISS.
DR GO; GO:0015026; F:coreceptor activity; ISS.
DR GO; GO:0042289; F:MHC class II protein binding activity; ISS.
DR GO; GO:0006955; P:immune response; ISS.
DR GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . ; ISS.
DR GO; GO:0030217; P:T-cell differentiation; ISS.
DR GO; GO:0045058; P:T-cell selection; ISS.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; ISS.
KW Immunoglobulin domain; T-cell; Immune response.
KW NON TER 20
SQ SEQUENCE 20 AA; 1928 MW; 421F09570FEA97EE CRC64;

Query Match 13.6%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAV 14
DB 1 KAV 3

RESULT 51
FIBB_ELEMA
ID FIBB_ELEMA STANDARD; PRT; 20 AA.

```

```

AC P14538;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Elephas maximus (Indian elephant).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Proboscidea; Elephantidae; Elephas.
OX NCBI_TaxID=9783;
RN [1]
RP SEQUENCE.
RA O'Neil P.B., Doolittle R.F.;
RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL Syst. Zool. 22:590-595(1973).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro; IPR002181; Fibrinogen_C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 20 FIBRINOPEPTIDE B.
FT MOD RES 4 4 SULFATION.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2107 MW; B4F52B959933273 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVP 15
DB 12 AVP 14

RESULT 52
H2B1 ICTPU STANDARD; PRT; 20 AA.
AC P81903;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histone H2B-1 (Antibacterial histone-like protein 1) (HLP-1)
DE (Fragment).
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Skin;
RX MEDLINE=98309109; PubMed=9645227;
RA Robinette D., Wada S., Arroll T., Levy M.G., Miller W.L., Noga E.J.;
RT "Antimicrobial activity in the skin of the channel catfish Ictalurus
RT punctatus: characterization of broad-spectrum histone-like
RT antimicrobial proteins.";
RL Cell. Mol. Life Sci. 54:467-475(1998).
CC -!- FUNCTION: Has broad-spectrum antimicrobial and antibacterial
CC activity. It is important in the antimicrobial defenses of fish
CC skin and possesses strong activity against saprolegnia, the most
CC common fungal infection in fish. It is also inhibitory to fish
CC bacterial pathogens, such as aeromonas hydrophila, vibrio
CC alginolyticus and E.coli D31.
CC -!- SUBUNIT: The nucleosome is an octamer containing two molecules
CC each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
CC Bp of DNA.

```



```

CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- MASS SPECTROMETRY: MW=13459; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the histone H2B family.
DR InterPro; IPR000558; Histone_H2B.
DR PROSITE; PS00357; HISTONE_H2B; PARTIAL.
KW Nuclear protein; Chromosomal protein; Nucleosome core; DNA-binding;
KW Antibiotic; Fungicide.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2033 MW; C13B4A04FB9D966F CRC64;

Query Match 13.6%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 KAV 14
Db 14 KAV 16

RESULT 53
OAR_PROPHY STANDARD; PRT; 20 AA.
AC PI4803;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Octopamine receptor (Octopamine binding protein) (Fragment).
OS Plectin pyrals (North American firefly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia;
OC Cantharidea; Lampyridae; Photinus.
OX NCBI_TaxID=7054;
RN [1]
RP SEQUENCE.
RC TISSUE=Light organ;
RX MEDLINE=90092510; PubMed=2513233;
RA Nathanson J.A., Kantham L., Hunnicutt E.J.;
RT "Isolation and N-terminal amino acid sequence of an octopamine ligand
RL binding protein.";
RL FEBS Lett. 259:117-120(1989).
CC -!- FUNCTION: PUTATIVE RECEPTOR FOR OCTOPAMINE. OCTOPAMINE (OA) IS A
CC NEUROTRANSMITTER, NEUROHORMONE, AND NEUROMODULATOR IN
CC INVERTEBRATES. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC PROTEINS WHICH ACTIVATE ADENYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC PIR; S28779; S28779.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1; PARTIAL.
KW G-protein coupled receptor.
FT UNSURE 2 2
FT UNSURE 9 9
FT UNSURE 19 19
FT NON_TER 20
SQ SEQUENCE 20 AA; 2500 MW; ACBC81A11BE8D4AB CRC64;

Query Match 13.6%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSQ 3
Db 5 LSQ 7

RESULT 54
DCMS_PSECH STANDARD; PRT; 4 AA.
AC PI9918;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO

```

```

DE dehydrogenase subunit S) (CO-DH S) (Fragment).
GN CUTS.
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydohydrogenic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC acceptor.
CC -!- COFACTOR: BINDS TWO 2FE-2S CLUSTERS.
CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
CC PIR; P10146; P10146.
DR Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S.
FT NON_TER 4
SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 KA 13
Db 3 KA 4

RESULT 55
FFKA_ATEL STANDARD; PRT; 4 AA.
AC P58705;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antho-KAamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actinidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92028852; PubMed=1681803;
RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a
RT novel neuropeptide from sea anemones.";
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-KAamide and Antho-RKamide.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron-specific.
DR PIR; JQ1273; JQ1273.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 L-3-PHENYLLACTYL.
FT MOD_RES 4 4 AMIDATION.
FT NON_TER 4
SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

```

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KA 13
DB 3 KA 4

RESULT 56
BPP7 BOTIN STANDARD; PRT; 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it. It acts as an indirect hypotensive agent.
DR PIR; G37196; G37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QK 12
DB 1 QK 2

RESULT 57
PCT PERAM STANDARD; PRT; 5 AA.
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES=P.americana;

RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569(1981).
RN [3]
RP SEQUENCE.
RC SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A., Watson W.H., III, Hunt D.F., Griffin P.R., Alexander J.E., Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).
RN [4]
RP SEQUENCE.
RC SPECIES=C.maenas;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangier J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72(1986).
CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY. MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN THE CRAB PERICARDIAL ORGANS.
DR PIR; A01644; HOROHA.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LP 8
DB 3 LP 4

RESULT 58
ACPH RABIT STANDARD; PRT; 6 AA.
AC P25154;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase) (APH) (Acylaminoacyl-peptidase) (Fragment).
GN APEH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=92222120; PubMed=1807161;
RA Krishna R.G., Chin C.C.Q., Wolf F.;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after unblocking with N-acylaminoacyl-peptide hydrolase.";
RL Anal. Biochem. 199:45-50(1991).
CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS. IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid + peptide.
CC -!- SUBUNIT: Homotetramer.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
DR PIR; A49792; A49792.
DR MEROPS; S09.004; -.
DR InterPro; IPR002471; Prol_endopep_ser.

```

DR PROSITE; PS00708; PRO ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD_RES 1 1 ACETYLATION.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 775 MW; 6732DC40B16F000 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VL 7
Db 5 VL 6

RESULT 59
EIO1_LITRU STANDARD; PRT; 6 AA.
AC P82096;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 6 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VP 10
Db 2 VP 3

RESULT 60
TRP1_PSEPU STANDARD; PRT; 6 AA.
AC P36414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE TRPBA operon transcriptional activator (Fragment).
GN TRP1.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PPG1 C1S;
RX MEDLINE=89335826; PubMed=2503057;
RA Eberly L., Crawford I.P.;
RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
RT putida.";
RL Blochmire 71:521-531(1989).
CC -1- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING

```

```

CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRP1 BINDS UPSTREAM OF THE
CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X13299; CAA31660.1; -.
CC InterPro; IPR000847; HTH_LYSR.
CC PROSITE; PS00044; HTH_LYSR FAMILY; PARTIAL.
CC Tryptophan biosynthesis; Transcription regulation; Activator;
KW DNA-binding.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LP 8
Db 5 LP 6

RESULT 61
CARP_MYTED STANDARD; PRT; 7 AA.
AC P10420;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Catch-relaxing peptide (CARP).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=88052022; PubMed=3676797;
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA Muneoka Y.;
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
RL Brain Res. 422:374-376(1987).
CC -1- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)
CC AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS
CC RETRACTOR MUSCLE.
CC PIR; A29342; EQWUCR.
KW Hormone; Amidation.
FT MOD_RES 7 7
SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 MP 20
Db 2 MP 3

RESULT 62
LANC_CARUI STANDARD; PRT; 7 AA.
ID LANC_CARUI
AC P36960;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)

```

```

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lantibiotic carnocin UI49 (Fragment).
OS Carnobacterium sp. (strain UI49).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Carnobacterium.
OX NCBI_TaxID=35782;
RN [1]
RP SEQUENCE
RX MEDLINE=92321768; PubMed=1622206;
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from
RT a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -!- FUNCTION: LANTHONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
KW Antibiotic; Bacteriocin; Lantibiotic.
FT NON TER 7
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 5 QP 6

RESULT 63
TPFY_PACDA
ID_TPFY_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-1 (pdt-1)
OS Pachymedusa dactylos (Giant mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
RP PRO-7.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Shaw C.;
RT "Pachymedusa dactylos trypsinogen-like protein (pdt-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT cDNA.";
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=WALDI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0045986; P:negative regulation of smooth muscle contractility; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD RES 3
FT MOD RES 3
FT MOD RES 7
FT MOD RES 7
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VP 10
DB 6 VP 7

RESULT 64

```

```

UF04_MOUSE
ID UF04_MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
FT NON TER 7
SQ SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5
DB 1 PK 2

RESULT 65
UN06_PINPS
ID_UN06_PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
FT NON TER 1
FT NON TER 1
FT NON TER 7
SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LP 8
DB 5 LP 6

RESULT 66
AL12_CARMA
ID_AL12_CARMA STANDARD; PRT; 8 AA.
AC P81815;

```

DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 12.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Multigene family.
 SQ SEQUENCE 8 AA; 913 MW; 672879DCB569AB7 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 DM 19
 ||
 Db 2 DM 3

RESULT 67
 AL18 CARMA STANDARD; PRT; 8 AA.
 ID AL18 CARMA STANDARD; PRT; 8 AA.
 AC P81821;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 18.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Multigene family.
 FT MOD RES 8 AMIDATION (POTENTIAL).
 SQ SEQUENCE 8 AA; 919 MW; C82879D5AB569AB5 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 DM 19
 ||
 Db 2 DM 3

RESULT 68
 ALL6_CYPDPO STANDARD; PRT; 8 AA.
 ID ALL6_CYPDPO STANDARD; PRT; 8 AA.
 AC P82157;

DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiastatin 6.
 OS Cydia pomonella (Coddling moth).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LP 8
 ||
 Db 1 LP 2

RESULT 69
 B44K_PORGI STANDARD; PRT; 8 AA.
 ID B44K_PORGI STANDARD; PRT; 8 AA.
 AC P81836;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 44 kDa immunogenic protein (fragment).
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OX NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=VPB 3492;
 RX MEDLINE=20198497; PubMed=10731616;
 RA Norris J.M., Love D.N.;
 RT "Serum antibody responses of cats to soluble whole cell antigens of
 RT feline Porphyromonas gingivalis.";
 RL Vet. Microbiol. 73:37-49(2000).
 CC -!- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
 KW Antigen.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 989 MW; 9554540326CB476D CRC64;

Query Match 9.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QK 12
 ||
 Db 4 QK 5

RESULT 70
 CAD1_ENTFA STANDARD; PRT; 8 AA.
 ID CAD1_ENTFA STANDARD; PRT; 8 AA.
 AC P13288;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CAD1.

```

OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN SEQUENCE.
RX MEDLINE=85051889; PubMed=6437872;
RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,
RT "Isolation and structure of the bacterial sex pheromone, cAD1, that
RT induces plasmid transfer in Streptococcus faecalis.";
RL FEBS Lett. 178:97-100(1984).
CC -!- FUNCTION: cAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID PAD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match          9.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VL 7
DB 5 VL 6

RESULT 71
CLP_THICU          STANDARD;          PRT;          8 AA.
AC P80488;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Thiolithothroph-specific protein (Fragment).
OS Thiolithothroph cuprinus.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Thiomonas.
OX NCBI_TaxID=36860;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 5494;
RA Marin I., Amato A.M., Jerez C.A., Amils R., Abad J.P.;
RL Submitted (SEP-1995) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
CC CHEMOLITHOTROPHICALLY.
FT NON_TER 8
SQ SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;

Query Match          9.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PV 9
DB 2 PV 3

RESULT 72
COW2_CONFU          STANDARD;          PRT;          8 AA.
AC P58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=99388839; PubMed=10461743;

```

```

RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2
FT MOD_RES 4
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match          9.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VL 7
DB 3 VL 4

RESULT 73
CPD1_ENTFA          STANDARD;          PRT;          8 AA.
ID CPD1_ENTFA
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone cPD1.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, cPD1.";
RL Science 226:849-850(1984).
CC -!- FUNCTION: cPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOICIN PLASMID PPD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match          9.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LS 2
DB 6 LS 7

RESULT 74
FUSS_FUSSO          STANDARD;          PRT;          8 AA.
AC P81010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Allergen Fus s i3596* (Fragment).
OS Fusarium solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocnemycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=70791;
RN [1]
RP SEQUENCE.
RC STRAIN=IARI 3596; TISSUE=Mycelium;
RA Verma J., Gangal S.V.;
RL Submitted (JUL-1997) to the SWISS-PROT data bank.
KW Allergen.

```

FT NON TER 8 8
 SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;
 Query Match 9.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VP 10
 ||
 Db 7 VP 8

RESULT 75
 PP3 PERAM
 ID_PP3 PERAM STANDARD; PRT; 8 AA.
 AC P82618;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-3 (Pea-PK-3) (EXPRU-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;
 OC Blattellidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Retrocerebral complex;
 RX MEDLINE=99212469; PubMed=10196736;
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and
 abdominal neurohemal organs of the American cockroach.";
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRlamides in the nervous system of
 the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 (MYOTROPIC ACTIVITY).
 CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
 CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 8 8
 SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VP 10
 ||
 Db 2 VP 3

Search completed: November 25, 2003, 19:28:24
 Job time : 7.87375 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 41.314 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-27

Perfect score: 22

Sequence: 1 LSQPKVLFPQKAVPQRDMPIQ 22

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_nhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriaph.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	5	22.7	20	5	Q9TWX2
2	4	18.2	11	6	Q9TQSO
3	4	18.2	12	6	Q8WNW9
4	4	18.2	17	12	Q6S373
5	4	18.2	18	4	Q16173
6	4	18.2	18	6	Q95MB1
7	4	18.2	19	12	O11338
8	4	18.2	19	13	Q9PRT0
9	4	18.2	20	2	Q8KUT9
10	4	18.2	20	5	Q9TWF4
11	4	18.2	20	15	Q9INA9
12	3	13.6	7	2	O50556
13	3	13.6	8	2	O45615
14	3	13.6	8	2	O56759
15	3	13.6	8	4	Q9UHK1
16	3	13.6	8	6	Q9TRX8

17	3	13.6	9	2	P72345	P72345 pseudomonas
18	3	13.6	9	2	P82568	P82568 streptococc
19	3	13.6	9	3	Q9P8E5	Q9P8E5 kluyveromyc
20	3	13.6	9	12	Q84333	Q84333 simian viru
21	3	13.6	9	15	Q64972	Q64972 avian rous-
22	3	13.6	10	2	Q9R5N2	Q9R5N2 clostridium
23	3	13.6	10	2	Q9R5N1	Q9R5N1 clostridium
24	3	13.6	10	2	Q9R5N3	Q9R5N3 clostridium
25	3	13.6	10	5	Q26093	Q26093 pisaster oc
26	3	13.6	10	5	P82223	P82223 bombyx mori
27	3	13.6	10	5	P82224	P82224 bombyx mori
28	3	13.6	10	8	Q8MBR7	Q8MBR7 chalcophoru
29	3	13.6	10	8	Q95D53	Q95D53 magnolia me
30	3	13.6	10	11	Q9JLI5	Q9JLI5 mus musculu
31	3	13.6	10	11	Q9BSU5	Q9BSU5 mus musculu
32	3	13.6	10	11	Q8CJE0	Q8CJE0 rattus norv
33	3	13.6	10	12	Q39957	Q39957 hepatitis g
34	3	13.6	10	13	Q9TWX9	Q9TWX9 eptaretus
35	3	13.6	10	13	Q8JFE7	Q8JFE7 ficedula al
36	3	13.6	10	13	Q8JF33	Q8JF33 ficedula hy
37	3	13.6	11	2	Q9EUZ3	Q9EUZ3 escherichia
38	3	13.6	11	12	Q86864	Q86864 lymphocytic
39	3	13.6	12	2	Q932U8	Q932U8 acinetobact
40	3	13.6	12	2	Q52112	Q52112 acinetobact
41	3	13.6	12	2	Q8GMV1	Q8GMV1 acinetobact
42	3	13.6	12	2	Q8GMT8	Q8GMT8 acinetobact
43	3	13.6	12	2	Q8GML2	Q8GML2 acinetobact
44	3	13.6	12	2	Q8GBY8	Q8GBY8 planktochri
45	3	13.6	12	4	Q9H4F4	Q9H4F4 homo sapien
46	3	13.6	12	4	Q96P98	Q96P98 homo sapien
47	3	13.6	12	8	Q31851	Q31851 arabidopsis
48	3	13.6	12	10	Q8SAS2	Q8SAS2 pinus sylve
49	3	13.6	12	10	Q8SAS3	Q8SAS3 pinus sylve
50	3	13.6	12	10	P82441	P82441 nicotiana t
51	3	13.6	12	12	Q81339	Q81339 barley stri
52	3	13.6	12	13	Q902L3	Q902L3 xenopus lae
53	3	13.6	13	2	Q31295	Q31295 buchnera ap
54	3	13.6	13	6	Q8WNS4	Q8WNS4 bos taurus
55	3	13.6	13	8	Q9THS0	Q9THS0 bryopsis sp
56	3	13.6	13	11	Q88176	Q88176 mus musculu
57	3	13.6	13	11	Q9QVK6	Q9QVK6 rattus sp.
58	3	13.6	13	12	Q81761	Q81761 hepatitis c
59	3	13.6	13	12	Q81794	Q81794 hepatitis c
60	3	13.6	13	12	Q81784	Q81784 hepatitis c
61	3	13.6	13	12	Q81778	Q81778 hepatitis c
62	3	13.6	13	12	Q81787	Q81787 hepatitis c
63	3	13.6	13	12	Q81775	Q81775 hepatitis c
64	3	13.6	13	12	Q81767	Q81767 hepatitis c
65	3	13.6	13	12	Q81798	Q81798 hepatitis c
66	3	13.6	13	12	Q81774	Q81774 hepatitis c
67	3	13.6	13	12	Q81766	Q81766 hepatitis c
68	3	13.6	13	12	Q81793	Q81793 hepatitis c
69	3	13.6	13	12	Q81768	Q81768 hepatitis c
70	3	13.6	13	12	Q81785	Q81785 hepatitis c
71	3	13.6	13	12	Q81800	Q81800 hepatitis c
72	3	13.6	13	12	Q81765	Q81765 hepatitis c
73	3	13.6	13	12	Q81781	Q81781 hepatitis c
74	3	13.6	13	12	Q81769	Q81769 hepatitis c
75	3	13.6	13	12	Q81773	Q81773 hepatitis c
76	3	13.6	13	12	Q81799	Q81799 hepatitis c
77	3	13.6	13	12	Q9WMG5	Q9WMG5 sigma virus
78	3	13.6	13	12	Q81786	Q81786 hepatitis c
79	3	13.6	13	12	Q81788	Q81788 hepatitis c
80	3	13.6	13	12	Q81763	Q81763 hepatitis c
81	3	13.6	13	12	Q81764	Q81764 hepatitis c
82	3	13.6	13	12	Q81796	Q81796 hepatitis c
83	3	13.6	13	12	Q81791	Q81791 hepatitis c
84	3	13.6	13	12	Q81770	Q81770 hepatitis c
85	3	13.6	13	12	Q81762	Q81762 hepatitis c
86	3	13.6	13	12	Q81790	Q81790 hepatitis c
87	3	13.6	13	12	Q81783	Q81783 hepatitis c
88	3	13.6	13	12	Q81789	Q81789 hepatitis c
89	3	13.6	13	12	Q81797	Q81797 hepatitis c

90 3 13.6 13 12 Q81795 hepatitis c
 91 3 13.6 13 12 Q81782 hepatitis c
 92 3 13.6 13 12 Q81780 hepatitis c
 93 3 13.6 13 12 Q81771 hepatitis c
 94 3 13.6 13 12 Q81779 hepatitis c
 95 3 13.6 13 12 Q81772 hepatitis c
 96 3 13.6 13 12 Q81792 hepatitis c
 97 3 13.6 13 12 Q81777 hepatitis c
 98 3 13.6 13 13 P82882 rana clamit
 99 3 13.6 13 13 P82883 rana clamit
 100 3 13.6 13 13 P82884 rana clamit

ALIGNMENTS

RESULT 1
 Q9TWX2
 ID Q9TWX2 PRELIMINARY; PRT; 20 AA.
 AC Q9TWX2;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Vitronectin-like protein (Fragment).
 OS Physarum polycephalum (Slime mold).
 OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
 OC Physarum.
 OX NCBI_TaxID=5791;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92137326; PubMed=1370938;
 RA Miyazaki K., Hamano T., Hayashi M.;
 RT "Physarum vitronectin-like protein: an Arg-Gly-Asp-dependent cell-
 spreading protein with a distinct NH2-terminal sequence."
 RL Exp. Cell Res. 199:106-110(1992).
 FT NON_TER 1
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2173 MW; 7DA5DAC504E7177F CRC64;

Query Match 22.7%; Score 5; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVFQK 12
 Db 4 PVFQK 8

RESULT 2
 Q9TQSO
 ID Q9TQSO PRELIMINARY; PRT; 11 AA.
 AC Q9TQSO;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE C-KIT (Fragment).
 GN KIT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Olsen H.G., Vage D.I., Lien S., Klungland H.;
 RT "A polymorphism in the bovine c-kit gene."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ243424; CAB60775.1;
 DR EMBL; AJ243060; CAB60774.1;
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1126 MW; DD785FF8A2D2D772 CRC64;

Query Match 18.2%; Score 4; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 KAVP 15
 Db 2 KAVP 5

RESULT 3

Q8WNW9
 ID Q8WNW9 PRELIMINARY; PRT; 12 AA.
 AC Q8WNW9;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Estrogen receptor alpha (Fragment).
 GN ER.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Endometrium;
 RA Ing N.H.;
 RT "Estradiol Stabilizes Estrogen Receptor mRNA in Ovine Endometrium Via
 Discrete Sequence Elements in its 4000 Base Long 3'Untranslated
 Region."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY059388; AAL1379.1;
 FT NON_TER 12
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1301 MW; 419C0B96EA21A1E7 CRC64;

Query Match 18.2%; Score 4; DB 6; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAVP 15
 Db 8 KAVP 11

RESULT 4

Q65373
 ID Q65373 PRELIMINARY; PRT; 17 AA.
 AC Q65373;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
 DE ORF 2 minigene.
 OS Orgyia pseudotsugata single capsid nuclear polyhedrosis virus
 OS (OpsNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=10450;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93286576; PubMed=8389803;
 RA Russell R.L., Rohmann G.F.;
 RT "Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia
 pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."
 RL J. Gen. Virol. 74:1191-1195(1993).
 DR EMBL; D13375; BAA02640.1;
 SQ SEQUENCE 17 AA; 1892 MW; BFEC2A959495FE6A CRC64;

Query Match 18.2%; Score 4; DB 12; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9

```

Db          2 VLPV 5
|||||
PRELIMINARY;      PRT;      18 AA.

RESULT 5
Q16173
ID Q16173      PRELIMINARY;      PRT;      18 AA.
AC Q16173;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE Dystrophin protein (Fragment).
GN DYSTROPHIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94258162; PubMed=8199594;
RA Wilton S.D.; Chandler D.C.; Makulas B.A.; Laing N.G.;
RT "Identification of a point mutation and germinal mosaicism in a
RT Duchenne muscular dystrophy family.";
RL Hum. Mutat. 3:133-140(1994).
DR EMBL; S71486; AAD14085.1; -.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2159 MW; C33D41084760ED5E CRC64;

Query Match      18.2%; Score 4; DB 4; Length 18;
Best Local Similarity 100.0%; Pred.No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          11 QKAV 14
|||||
PRELIMINARY;      PRT;      18 AA.

RESULT 6
Q95MB1
ID Q95MB1      PRELIMINARY;      PRT;      18 AA.
AC Q95MB1;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Desmocollin 2 (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21314992; PubMed=11421942;
RA Shubitowski D.M.; Venta P.J.; Douglass C.L.; Zhou R.-X.; Ewart S.L.;
RT "Polymorphism identification within 50 equine gene-specific sequence
RT tagged sites.";
RL Anim. Genet. 32:78-78(2001).
DR EMBL; AY008781; AAG39473.1; -.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1992 MW; B67FE953ECF19196 CRC64;

Query Match      18.2%; Score 4; DB 6; Length 18;
Best Local Similarity 100.0%; Pred.No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          3 QPKV 6
|||||
PRELIMINARY;      PRT;      19 AA.

RESULT 7
O11338
ID O11338      PRELIMINARY;      PRT;      19 AA.

```

```

AC O11338;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE H1-7-1 protein (Fragment).
GN H1-7-1.
OS Molluscum contagiosum virus subtype 1 (MCV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
RN [1]
RP SEQUENCE FROM N.A.
RA Moratilla M.; Agromayor M.; Nunez A.; Funes J.M.; Varas A.J.;
RA Lopez-Esteban J.L.; Esteban M.; Martin-Gallardo A.;
RT "A Random DNA Sequencing, Computer-Based Approach for the Generation
RT of a Gene Map of Molluscum Contagiosum Virus.";
RL Virus Genes 0:0-0(1997).
DR EMBL; U86916; AAB57971.1; -.
DR InterPro; IPR004900; Pox_P35.
DR Pfam; PF03213; Pox_P35; 1.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2018 MW; 1ECAF8E98F95ED65 CRC64;

Query Match      18.2%; Score 4; DB 12; Length 19;
Best Local Similarity 100.0%; Pred.No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 VLPV 9
|||||
PRELIMINARY;      PRT;      19 AA.

RESULT 8
Q9PRT0
ID Q9PRT0      PRELIMINARY;      PRT;      19 AA.
AC Q9PRT0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE 23A7 antigen (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=95332492; PubMed=7608337;
RA Denburg J.L.; Caldwell R.T.; Marner J.M.;
RT "Developmental changes in epitope accessibility as an indicator of
RT multiple states of an immunoglobulin-like neural cell adhesion
RT molecule.";
RL J. Comp. Neurol. 354:533-550(1995).
SQ SEQUENCE 19 AA; 2051 MW; 83E67BEE484EBD03 CRC64;

Query Match      18.2%; Score 4; DB 13; Length 19;
Best Local Similarity 100.0%; Pred.No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LSQP 4
|||||
PRELIMINARY;      PRT;      20 AA.

RESULT 9
Q8KUI9
ID Q8KUI9      PRELIMINARY;      PRT;      20 AA.
AC Q8KUI9;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Nitrogen regulatory protein P-II (Fragment).
OS Neisseria meningitidis.

```

```

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C11;
RC MEDLINE=22040572; PubMed=12045242;
RA Comanducci M., Bambini S., Brunelli B., Adu-Bobie J., Arico B.,
RA Capecechi B., Giuliani M.M., Nasignani V., Santini L., Savino S.,
RA Granoff D.M., Caugant D.A., Pizzo M., Rappuoli R., Mora M.;
RT "Nada, a novel vaccine candidate of Neisseria meningitidis.";
RL J. Exp. Med. 195:1445-1454(2002).
DR EMBL: AF452480; AAM53107.1; -.
DR InterPro: IPR002187; PII_glnb.
DR Pfam: PF00543; P-II; 1.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2165 MW; 5CB529B59D995B5C CRC64;

Query Match 18.2%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
DB 1 VLPV 4

RESULT 10
Q9TWP4
ID Q9TWP4 PRELIMINARY; PRT; 20 AA.
AC Q9TWP4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Vitronectin homolog (Fragment).
OS Physarum polycephalum (Slime mold).
OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
OC Physarum.
OX NCBI_TaxID=5791;
RN [1]
RP SEQUENCE.
RX MEDLINE=94221676; PubMed=8168157;
RA Miyazaki K., Miyata T., Sawada H., Matuda S., Hayashi M.;
RT "Physarum vitronectin-like protein has extensive homology to
RT dihydrolipoamide acetyltransferase.";
RL Cell Struct. Funct. 18:323-331(1993).
SQ SEQUENCE 20 AA; 2116 MW; EDE10130972831EA CRC64;

Query Match 18.2%; Score 4; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVPQ 16
DB 1 AVPQ 4

RESULT 11
Q9INA9
ID Q9INA9 PRELIMINARY; PRT; 20 AA.
AC Q9INA9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag protein (Fragment).
DR GAG.
GN Human immunodeficiency virus 1.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DRCM23;
RX MEDLINE=99260287; PubMed=10331444;

```

```

RA Mokili J.L., Wade C.M., Burns S.M., Cutting W.A., Bopopi J.M.,
RA Green S.D., Peutherer J.F., Simmonds P.;
RT "Genetic heterogeneity of HIV type 1 subtypes in Kimpese, rural
RT Democratic Republic of Congo.";
RL AIDS Res. Hum. Retroviruses 15:655-664(1999).
DR EMBL: AF144840; AAF69066.1; -.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2271 MW; B39B8CB9B53ABCF8 CRC64;

Query Match 18.2%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QKAV 14
DB 15 QKAV 18

RESULT 12
O50556
ID O50556 PRELIMINARY; PRT; 7 AA.
AC O50556;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE GlyA (Fragment).
GN GlyA.
OS Actinobacillus actinomycetemcomitans (Haemophilus
OS actinomycetemcomitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33384;
RX MEDLINE=96355846; PubMed=8751884;
RA Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
RA Kraig E.;
RT "cis Elements and trans factors are both important in strain-specific
RT regulation of the leukotoxin gene in Actinobacillus
RT actinomycetemcomitans.";
RL Infect. Immun. 64:3451-3460(1996).
DR EMBL: U51862; AAB88721.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
DB 3 LPV 5

RESULT 13
Q45615
ID Q45615 PRELIMINARY; PRT; 8 AA.
AC Q45615;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GutB protein (Fragment).
GN GUTB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=94253000; PubMed=8195086;
RA Ye R., Wong S.L.;
RT "Transcriptional regulation of the Bacillus subtilis glucitol

```

```

RT dehydrogenase gene.";
RL J. Bacteriol. 176:3314-3320(1994).
DR EMBL: L16626; AAA20875.1; -.
DT NON_TER 8
SQ SEQUENCE 8 AA; 927 MW; F56C772D1A1F1A6 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VPQ 11
Db 5 VPQ 7

RESULT 14
Q56759
ID Q56759 PRELIMINARY; PRT; 8 AA.
AC Q56759;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Haloacid dehalogenase (Fragment).
GN DHLB.
OS Xanthobacter autotrophicus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hyphomicrobiaceae; Xanthobacter.
OX NCBI_TaxID=280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GJ10, and CV. M50;
RX MEDLINE=95173113; PubMed=7868610;
RA Van der Ploeg J., Willemse M., van Hall G., Janssen D.B.;
RT "Adaptation of Xanthobacter autotrophicus GJ10 to bromoacetate due to
RT activation and mobilization of the haloacetate dehalogenase gene by
RT insertion element IS1247."
RL J. Bacteriol. 177:1348-1356(1995).
DR EMBL: X84038; CAA58857.1; -.
DT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 922 MW; F3A9D2D2CDD33056 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAV 14
Db 3 KAV 5

RESULT 15
Q9UHK1
ID Q9UHK1 PRELIMINARY; PRT; 8 AA.
AC Q9UHK1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Alpha-1-antitrypsin M-variant (Fragment).
GN A.A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ambrose H.J., Chambers S., Mieli-Vergani G., Robertson N.H.,
RA Newton C.R., Ferrie R.M.;
RT "Molecular characterisation of a new alpha-1-antitrypsin M variant
RT allele, Mwhitsable: implications for DNA-based diagnosis.";
RL Diagn. Mol. Pathol. 0:0-0(2000).
DR EMBL: AF159454; AAF15128.1; -.
DT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 922 MW; F3A9D2D2CDD33056 CRC64;

```

```

SQ SEQUENCE 8 AA; 838 MW; 84A732CDD331F2CD CRC64;

Query Match 13.6%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAV 14
Db 4 KAV 6

RESULT 16
Q9TRX8
ID Q9TRX8 PRELIMINARY; PRT; 8 AA.
AC Q9TRX8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Osteopontin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91282766; PubMed=1676261;
RA Prince C.W., Dickie D., Krumdieck C.L.;
RT "Osteopontin, a substrate for transglutaminase and factor XIII
RT activity.";
RL Biochem. Biophys. Res. Commun. 177:1205-1210(1991).
DT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 920 MW; 05DAFAF76322D767 CRC64;

Query Match 13.6%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
Db 1 LPV 3

RESULT 17
P72345
ID P72345 PRELIMINARY; PRT; 9 AA.
AC P72345;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE TabA (Fragment).
GN TABA.
OS Pseudomonas syringae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=317;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR2R;
RX MEDLINE=93167809; PubMed=7679566;
RA Barta T.M., Kinscherf T.G., Uchytel T.F., Willis D.K.;
RT "DNA sequence and transcriptional analysis of the tbaA gene required
RT for tabtoxin biosynthesis by Pseudomonas syringae.";
RL Appl. Environ. Microbiol. 59:458-466(1993).
DT NON_TER 9
FT NON_TER 9
SQ SEQUENCE FROM N.A.
RC STRAIN=BR2R;
RX Kinscherf T.G., Willis D.K.;
RT "Sequence analysis of the tabtoxin biosynthetic region.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF519896; AAB25381.2; -.
DT NON_TER 9
FT NON_TER 9

```

SQ SEQUENCE 9 AA; 1037 MW; 2B34D9D5BB05B047 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 MPI 21

Db |||

1 MPI 3

RESULT 18

ID P82568

AC P82568 PRELIMINARY; PRT; 9 AA.

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE Unknown protein from 2D-page (Fragment).

OS Streptococcus pyogenes.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1314;

RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RC STRAIN=JRS4;

RA Hogan D.A., Du P., Stevenson T.I., Whittom M., Kilby G.W., Rogers J.,

RA VanBogelen R.A.;

RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes

RT proteins.";

RL Submitted (MAY-2000) to the SWISS-PROT data bank.

CC -1- MASS SPECTROMETRY; MW=22592.04; METHOD=ELECTROSPRAY.

FT NON_TER 1 1

FT NON_TER 9 9

SQ SEQUENCE 9 AA; 1069 MW; 2A771042CB1AB2D7 CRC64;

Query Match

Best Local Similarity 100.0%; Score 3; DB 2; Length 9;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9

Db |||

1 LPV 3

RESULT 19

ID Q9P8E5

AC Q9P8E5 PRELIMINARY; PRT; 9 AA.

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE HIS4 protein (Fragment).

GN HIS4.

OS Kluyveromyces fragilis (Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

OX NCBI_TaxID=28985;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NRRL-Y1140;

RA MEDLINE=99448382; PubMed=10518937;

RA Lamas-Maciel M., Esperanza Cerdan E., Freire-Picos M.A.;

RT "Kluyveromyces fragilis HIS4 transcriptional regulation: similarities

RT and differences to Saccharomyces cerevisiae HIS4 gene.";

RL FEBS Lett. 458:72-76(1999).

DR EMBL; AT238494; CAB87125.1; -.

FT NON_TER 9 9

SQ SEQUENCE 9 AA; 1015 MW; 5770D2D772D2D767 CRC64;

Query Match

Best Local Similarity 100.0%; Score 3; DB 3; Length 9;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9

Db |||

2 LPV 4

RESULT 20

Q84333

ID Q84333 PRELIMINARY; PRT; 9 AA.

AC Q84333;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE (Defective variant in 1449) with monkey alu-type insert

DE (Fragment).

OS Simian virus 40 (SV40).

OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.

OX NCBI_TaxID=10633;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=81054804; PubMed=6254029;

RA Dhruva B.R., Shenk T., Subramanian K.N.;

RT "Integration in vivo into Simian virus 40 DNA of a sequence that

RT resembles a certain family of genomic interspersed repeated

RT sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 77:4514-4518(1980).

DR EMBL; K01001; AAA47875.1; -.

FT NON_TER 9 9

SQ SEQUENCE 9 AA; 1133 MW; 802204044732C33A CRC64;

Query Match

Best Local Similarity 100.0%; Score 3; DB 12; Length 9;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7

Db |||

3 KVL 5

RESULT 21

Q64972

ID Q64972 PRELIMINARY; PRT; 9 AA.

AC Q64972;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Rous associated virus type 1 (RAV-1) mil protein, 3' end, and env

DE protein (Fragment).

OS Avian rous-associated virus type 1.

OC Viruses; Retroviridae; Retroviridae; Alpharetrovirus.

OX NCBI_TaxID=11950;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89037349; PubMed=2846875;

RA Marx M., Cribanti P., Eychene A., Bechade C., Laugier D.,

RA Ghysdael J., Pessac B., Calothy G.;

RT "Activation and transduction of c-mil sequences in chicken neuroretina

RT cells induced to proliferate by infection with avian lymphomatosis

RT virus.";

RL J. Virol. 62:4627-4633(1988).

DR EMBL; M25399; AAA42548.1; -.

FT NON_TER 1 1

SQ SEQUENCE 9 AA; 1033 MW; 83AED7673411B5A1 CRC64;

Query Match

Best Local Similarity 100.0%; Score 3; DB 15; Length 9;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9

Db |||

6 LPV 8

RESULT 22
Q9RSN2 ID Q9RSN2 PRELIMINARY; PRT; 10 AA.
AC Q9RSN2;
DE 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Neurotoxin type A HN+ 57 kDa SUBUNIT-SAMPLE 2 (Fragment).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE.
RX MEDLINE=92143938; PubMed=1781887;
RA Somers E., DasGupta B.R.;
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or without hemagglutinating activity: do they share common amino acid sequences and genes?";
RL J. Protein Chem. 10:415-425(1991).
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1225 MW; EC3DE932D366C1BA CRC64;

Query Match 13.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db 7 VLP 9

RESULT 23
Q9RSN1 ID Q9RSN1 PRELIMINARY; PRT; 10 AA.
AC Q9RSN1;
DE 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Neurotoxin type A HN+ 57 kDa subunit (Fragment).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE.
RX MEDLINE=92143938; PubMed=1781887;
RA Somers E., DasGupta B.R.;
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or without hemagglutinating activity: do they share common amino acid sequences and genes?";
RL J. Protein Chem. 10:415-425(1991).
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1172 MW; E5DAE932D416C1BA CRC64;

Query Match 13.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db 7 VLP 9

RESULT 24
Q9RSN3 ID Q9RSN3 PRELIMINARY; PRT; 10 AA.
AC Q9RSN3;
DE 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Neurotoxin type B HN+ 57 kDa subunit (Fragment).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE.
RX MEDLINE=92143938; PubMed=1781887;
RA Somers E., DasGupta B.R.;
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or without hemagglutinating activity: do they share common amino acid sequences and genes?";
RL J. Protein Chem. 10:415-425(1991).
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1221 MW; C3DBE932D416C1B2 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db 7 VLP 9

RESULT 25
Q26093 ID Q26093 PRELIMINARY; PRT; 10 AA.
AC Q26093;
DE 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE H2B (10 AA) (Fragment).
OS Pisaster ochraceus (Sea star).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Forcipulatacea; Forcipulatida; Asterialidae; Pisaster.
OX NCBI_TaxID=7612;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SpERM;
RA Howell A.M., Cool D., Hewitt J., Ydenberg B., Smith M.J., Honda B.M.;
RT "Organization and Unusual Expression of Histone Genes in the Sea Star
J. Mol. Evol. 25:29-36(1987).
RL J. Mol. Evol. 25:29-36(1987).
DR EMBL; X05620; CAA29107.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 10 AA; 1126 MW; DD780681BB5321B2 CRC64;

Query Match 13.6%; Score 3; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAV 14
Db 1 KAV 3

RESULT 26
P82223 ID P82223 PRELIMINARY; PRT; 10 AA.
AC P82223;
DE 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE.

```

RC STRAIN-XINHANG X KEMING; TISSUE=Body wall, and Fat body;
RX MEDLINE=21177481; PubMed=11280994;
RA Zhong B.X.;
RT "Protein database for several tissues derived from five instar of
   silkworm.";
RL I Chuan Hsueh Pao 28:217-224(2001).
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1054 MW; D0F722C325B1F1B2 CRC64;

Query Match      13.6%; Score 3; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
DB 7 KVL 9

RESULT 27
P82224
ID P82224 PRELIMINARY; PRT; 10 AA.
AC P82224;
DT 01-OCT-2001 (TRENBLrel. 18, Created)
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TRENBLrel. 18, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE.
RC STRAIN-XINHANG X KEMING; TISSUE=Body wall, and Fat body;
RX MEDLINE=21177481; PubMed=11280994;
RA Zhong B.X.;
RT "Protein database for several tissues derived from five instar of
   silkworm.";
RL I Chuan Hsueh Pao 28:217-224(2001).
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1064 MW; D77CBF25B1F1B2CD CRC64;

Query Match      13.6%; Score 3; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
DB 8 KVL 10

RESULT 28
Q8WB7
ID Q8WB7 PRELIMINARY; PRT; 10 AA.
AC Q8WB7;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN COI.
OS Chaitophorus leucomelas.
OC Chaitophoridae.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
OC Aphidoidea; Drepanosiphidae; Chaitophorus.
OX NCBI_TaxID=136351;
RN [1]
RP SEQUENCE FROM N.A.
RA Shingleton A.W., Stern D.L.;
RT "Molecular phylogenetic evidence for multiple origins of ant mutualism
   within the aphid genus Chaitophorus.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF444288; AAL38565.1; -.

```

```

KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1194 MW; 6E553D5042D7672B CRC64;

Query Match      13.6%; Score 3; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
DB 4 LPV 6

RESULT 29
Q95DS3
ID Q95DS3 PRELIMINARY; PRT; 10 AA.
AC Q95DS3;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Rbcl protein (Fragment).
GN RbCL.
OS Magnolia mexicana.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Magnoliales; Magnoliaceae; Magnolia.
OX NCBI_TaxID=111569;
RN [1]
RP SEQUENCE FROM N.A.
RA Azuma H., Garcia-Franco J.G., Rico-Gray V., Thien L.B.;
RT "Molecular phylogeny of Magnoliaceae.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
KW EMBL; AB055580; BAB69572.1; -.
DR Chloroplast.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1091 MW; 344DEA21AB01A327 CRC64;

Query Match      13.6%; Score 3; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAV 14
DB 8 KAV 10

RESULT 30
Q9JLI5
ID Q9JLI5 PRELIMINARY; PRT; 10 AA.
AC Q9JLI5;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE Melanocortin type 1 receptor MCLR (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6;
RX MEDLINE=20090876; PubMed=10623832;
RA Adachi S., Morii E., Kim D.-K., Ogiwara H., Jippo T., Ito A., Lee Y.M.,
RA Kitamura Y.;
RT "Involvement of mi-transcription factor in expression of alpha-
   melanocyte-stimulating hormone receptor in cultured mast cells of
   mice.";
RL J. Immunol. 164:855-860(2000).
RL EMBL; AF176016; AAF37323.1; -.
DR KW Receptor.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1148 MW; 95B58A26C76B06C1 CRC64;

```

Query Match 13.6%; Score 3; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 POK 12
 ||||
 6 POK 8

RESULT 31

Q9ESU5 PRELIMINARY; PRT; 10 AA.
 AC Q9ESU5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Fas death receptor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/He;
 RX MEDLINE=20127858; PubMed=10660538;
 RA Munsch D., Watanabe-Fukunaga R., Bourdon J.C., Nagata S., May E.,
 RA Yoshish-Rouch E., Reisdorf P.;
 RT "Human and mouse Fas (APO-1/CD95) death receptor genes each contain a
 RT p53-responsive element that is activated by p53 mutants unable to
 RT induce apoptosis.";
 RL J. Biol. Chem. 275:3867-3872(2000).
 DR EMBL; AF282865; AAGO2410.1; -.
 KW Receptor.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1242 MW; 22145E32CDC37043 CRC64;

Query Match 13.6%; Score 3; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
 ||||
 7 VLP 9

RESULT 32

Q8CJEO PRELIMINARY; PRT; 10 AA.
 AC Q8CJEO;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Resistin (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Nohira T., Hisatomi H.;
 RA "Rattus norvegicus resistin DNA, intron2.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB093559; BAC21195.1; -.
 FT NON TER 1 1
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1079 MW; 34EA46D326DDC777 CRC64;

Query Match 13.6%; Score 3; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QKA 13

Db ||||
 6 QKA 8

RESULT 33

C39957 PRELIMINARY; PRT; 10 AA.
 AC C39957;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE E1 protein (Fragment).
 OS Hepatitis GB virus C.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC GBV-C/HGV group
 OX NCBI_TaxID=39839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bd inburgh haemophilic;
 RX MEDLINE=97368412; PubMed=9225026;
 RA Smith D.B., Cuccanu N., Davidson F., Jarvis L.M., Mokili J.L.,
 RA Hamid S., Ludlam C.A., Simmonds P.;
 RT "Discrimination of hepatitis G virus/GBV-C geographical variants by
 RT analysis of the 5' non-coding region.";
 RL J. Gen. Virol. 78:1533-1542(1997).
 DR EMBL; AF003175; AAC57986.1; -.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1067 MW; CC88FE2727273772 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVP 15
 ||||
 2 AVP 4

RESULT 34

Q9TWX9 PRELIMINARY; PRT; 10 AA.
 AC Q9TWX9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE HX=C3 homolog.
 OS Eptatretus burgeri (Inshore hagfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
 OC Myxiniidae; Eptatretinae; Eptatretus.
 OX NCBI_TaxID=7764;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=92091759; PubMed=1727859;
 RA Fujii T., Nakamura T., Sekizawa A., Tomonaga S.;
 RA "Isolation and characterization of a protein from hagfish serum that
 RT is homologous to the third component of the mammalian complement
 RT system.";
 RL J. Immunol. 148:117-123(1992).
 SQ SEQUENCE 10 AA; 968 MW; DB3C186DD042C732 CRC64;

Query Match 13.6%; Score 3; DB 13; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
 ||||
 2 KVL 4

RESULT 35

Q8JFE7 PRELIMINARY; PRT; 10 AA.
 ID Q8JFE7
 AC Q8JFE7;


```

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Myelin proteolipid protein (Fragment).
OS Ficedula albicollis.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=59894;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bc5, and Bc8;
RX MEDLINE=21918460; PubMed=11918793;
RA Primer C.R., Borge T., Lindell J., Saetre G.-P.;
RT "Single-nucleotide polymorphism characterization in species with
RT limited available sequence information: high nucleotide diversity
RT revealed in the avian genome.";
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454217; AAM22903.1; -.
DR EMBL; AF454218; AAM22904.1; -.
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1206 MW; 1FAAC9676732C86B CRC64;

Query Match 13.6%; Score 3; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db |||
5 VLP 7

RESULT 36
Q8JU33 PRELIMINARY; PRT; 10 AA.
ID Q8JU33;
AC Q8JU33;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Myelin proteolipid protein (Fragment).
OS Ficedula hypoleuca.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=46689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Op86;
RX MEDLINE=21918460; PubMed=11918793;
RA Primer C.R., Borge T., Lindell J., Saetre G.-P.;
RT "Single-nucleotide polymorphism characterization in species with
RT limited available sequence information: high nucleotide diversity
RT revealed in the avian genome.";
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454216; AAM22902.1; -.
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1206 MW; 1FAAC9676732C86B CRC64;

Query Match 13.6%; Score 3; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db |||
5 VLP 7

RESULT 37
Q9EUZ3 PRELIMINARY; PRT; 11 AA.
ID Q9EUZ3
AC Q9EUZ3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

```

```

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Ribosome binding factor A (fragment).
GN RBFA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IQ490;
RA Hedegaard J., Kristensen J.E., Nakamura Y., Sperling-Petersen H.U.,
RA Mortensen K.K.;
RT "Sequence of the infB gene from Escherichia coli strain IQ489 and
RT IQ490.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132862; CAC20133.1; -.
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA; 1319 MW; 5B234CFE740879CB CRC64;

Query Match 13.6%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
Db |||
8 PQR 10

RESULT 38
Q86864 PRELIMINARY; PRT; 11 AA.
ID Q86864
AC Q86864;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE LCMV viral protein (Fragment).
GN LCMV VIRAL PROTEIN.
OS Lymphocytic choriomeningitis virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
OX NCBI_TaxID=11623;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95190990; PubMed=7533851;
RA Moskopidhis D., Zinkernagel R.M.;
RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
RT choriomeningitis virus.";
RL J. Virol. 69:2187-2193(1995).
DR EMBL; S75739; AAB33665.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1186 MW; D6235C80D9C45B42 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAV 14
Db |||
2 KAV 4

RESULT 39
Q932U8 PRELIMINARY; PRT; 12 AA.
ID Q932U8
AC Q932U8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Urf-2X protein.
GN URF-2X.
OS Acinetobacter sp.
OC Plasmid pKLH205, and Plasmid pKLH204.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.

```

```

OX NCBI_TaxID=472;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ED45-25; PLASMID=pKLH205, and pKLH204;
RX MEDLINE=21272500; PubMed=11376944;
RA Kholodii G.;
RT "The shuffling function of resolvases.";
RL Gene 269:121-130 (2001).
DR EMBL; AJ251707; CAC39413.1; -.
DR EMBL; AJ250851; CAC39402.1; -.
KW Plasmid.
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred.No.1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4
DB 4 SQP 6

RESULT 40
Q52112
ID Q52112 PRELIMINARY; PRT; 12 AA.
AC Q52112; O08093; O08128; O08132; Q56909;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE URF2X protein (Fragment).
GN URF-2X OR URF2X.
OS Acinetobacter calcoaceticus,
OS Pantoea agglomerans,
OS Alcaligenes sp.,
OS Enterobacter cloacae,
OS Escherichia coli,
OS Yersinia enterocolitica, and
OS mercury resistant bacterium '96 SE13.
OG Plasmid pKLH2. Plasmid pKLH286, Plasmid pKLH210, Plasmid pCL17, and
OG Plasmid pKLH201.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=471, 549, 512, 550, 562, 630, 93601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=A.calcoaceticus; PLASMID=pKLH2;
RX MEDLINE=94134837; PubMed=8302940;
RA Kholodii G.Y., Lomovskaya O.L., Gorlenko Z.M., Mindlin S.Z.,
RA Yurieva O.V., Nikiforov V.G.;
RT "Molecular characterization of an aberrant mercury resistance
RT transposable element from an environmental Acinetobacter strain.";
RL Plasmid 30:303-308 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=P.agglomerans, Alcaligenes sp., E.cloacae, and E.coli;
RX MEDLINE=97303088; PubMed=9159519;
RA Nikiforov V., Kholodii G., Minakhin L., Gorlenko Z., Kalyaeva E.,
RA Mindlin S., Nikiforov V.;
RT "Intercontinental spread of promiscuous mercury-resistance transposons
RT in environmental bacteria.";
RL Mol. Microbiol. 24:321-329 (1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Y.enterocolitica; STRAIN=Various strains;
RX MEDLINE=95273477; PubMed=7753910;
RA Osbourn S.E.V., Turner A.K., Grinstead J.;
RT "Nucleotide sequence within Tn3926 confirms this as a Tn21-like
RT transposable element and provides evidence for the origin of the mer
RT operon carried by plasmid pKLH2.";
RL Plasmid 33:65-69 (1995).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=mercury resistant bacterium '96 SE13;

```

```

RA Holt R.J., Bruce K.D., Strike P.;
RT "Conservation of transposon structures in soil bacteria.";
FEMS Microbiol. Ecol. 0:0-0 (1999).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=A.calcoaceticus; STRAIN=KH14; PLASMID=pKLH201;
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
RA Nikiforov V.G.;
RT "pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF213017; AAA19685.1; -.
DR EMBL; Y08992; CAA70180.1; -.
DR EMBL; Y08993; CAA70193.1; -.
DR EMBL; Y09025; CAA70234.1; -.
DR EMBL; Y10102; CAA71186.1; -.
DR EMBL; X78059; CAA54979.1; -.
DR EMBL; AF134211; AAD34400.1; -.
DR EMBL; AJ251307; CAC80877.1; -.
KW Plasmid.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred.No.1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4
DB 4 SQP 6

RESULT 41
Q8GMV1
ID Q8GMV1 PRELIMINARY; PRT; 12 AA.
AC Q8GMV1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Urf-2X protein.
GN URF-2X.
OS Acinetobacter lwoffii.
OG Plasmid pKLH202.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=28090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TC108;
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
RA Nikiforov V.G.;
RT "pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250245; CAC80792.1; -.
KW Plasmid.
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred.No.1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4
DB 4 SQP 6

RESULT 42
Q8GMT8
ID Q8GMT8 PRELIMINARY; PRT; 12 AA.
AC Q8GMT8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

```

```

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Urf-2X protein.
GN URF-2X.
OS Acinetobacter junii.
OG Plasmid pKLH203.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=40215;
RN [1]_TaxID=40215;
RP SEQUENCE FROM N.A.
RC STRAIN=NC13-1;
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
RA Nikiforov V.G.;
RT "pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250494; CAC80763.1; -.
KW Plasmid.
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SOP 4
DB 4 SOP 6

RESULT 43
QGML2
ID Q8GML2 PRELIMINARY; PRT; 12 AA.
AC Q8GML2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Urf-2X protein.
GN URF-2X.
OS Acinetobacter sp. ED23-35.
OG Plasmid pKLH208.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=109250;
RN [1]_TaxID=109250;
RP SEQUENCE FROM N.A.
RC STRAIN=ED23-35;
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
RA Nikiforov V.G.;
RT "pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251272; CAC80895.1; -.
KW Plasmid.
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SOP 4
DB 4 SOP 6

RESULT 44
QGBY8
ID Q8GBY8 PRELIMINARY; PRT; 12 AA.
AC Q8GBY8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Gas vesicle protein GvpA (Fragment).
GN GvPA.

```

```

OS Planktothrix agardhii.
OC Bacteria; Cyanobacteria; Oscillatoriales; Planktothrix.
OX NCBI_TaxID=54305;
RN [1]_TaxID=54305;
RP SEQUENCE FROM N.A.
RC STRAIN=CYA 29;
RA Beard S.J., Handley B.A., Walsby A.E.;
RT "Spontaneous mutations in gas vesicle genes of Planktothrix spp.
RT affect gas vesicle production and critical pressure.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ494992; CAD41965.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1112 MW; C78F8CAB43DDC6DD CRC64;

Query Match 13.6%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVP 15
DB 8 AVP 10

RESULT 45
Q9H4F4
ID Q9H4F4 PRELIMINARY; PRT; 12 AA.
AC Q9H4F4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Survival interacting protein 1 (Fragment).
GN SIPI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Helmsken C., Wetter A., Rudnik-Schoneborn S., Liehr T., Zerres K.,
RA Wirth B.;
RT "An essential SMN interacting protein (SIPI) is not involved in the
RT phenotypic variability of spinal muscular atrophy (SMA).";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250939; CAC16171.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1455 MW; 6BA6698AD0D72AB4 CRC64;

Query Match 13.6%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 QRD 18
DB 4 QRD 6

RESULT 46
Q96P98
ID Q96P98 PRELIMINARY; PRT; 12 AA.
AC Q96P98;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CD27-binding protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;
RT "Characterization of TPA-responsive genes in U937 cells using ordered
RT differential display PCR.";

```

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF401214; AAL02171.1; --
 FT NON TER 1
 SQ SEQUENCE 12 AA; 1333 MW; 977A27103ADEA5A1 CRC64;

Query Match 13.6%; Score 3; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
 Db 1 KVL 3

RESULT 47

Q31851 ID Q31851 PRELIMINARY; PRT; 12 AA.
 AC Q31851;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Glyceroldehyde-3-phosphate dehydrogenase (Fragment).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia; TISSUE=Leaf;
 RX MEDLINE=94187724; PubMed=8139555;
 RA Conley T.R., Park S.-C., Kwon H.-B., Peng H.-S., Shih M.-C.;
 RT "Characterization of cis-acting elements in light regulation of the
 RT nuclear gene encoding the A subunit of chloroplast isozymes
 RT Glyceraldehyde-3-phosphate dehydrogenase from Arabidopsis thaliana.";
 RL Mol. Cell. Biol. 14:2525-2533 (1994).
 DR EMBL; L14743; AAA31640.1; --
 KW Chloroplast.
 FT NON TER 12
 SQ SEQUENCE 12 AA; 1263 MW; 81BA4C7D4BD5B9D1 CRC64;

Query Match 13.6%; Score 3; DB 8; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKV 6
 Db 9 PKV 11

RESULT 48

Q8SA52 ID Q8SA52 PRELIMINARY; PRT; 12 AA.
 AC Q8SA52;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative fructokinase (Fragment).
 OS Pinus sylvestris (Scots pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=3349;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=plus tree Ell101;
 RX MEDLINE=21660210; PubMed=11801746;
 RA Dvornyk V., Sirvio A., Mikkonen M., Savolainen O.;
 RT "Low Nucleotide Diversity at the pall Locus in the Widely Distributed
 RT Pinus sylvestris.";
 RL Mol. Biol. Evol. 19:179-188 (2002).
 DR EMBL; AF359120; AAL74388.1; --
 KW Kinase.

FT NON TER 1
 SQ SEQUENCE 12 AA; 1228 MW; C6FE739330A72DDD CRC64;

Query Match 13.6%; Score 3; DB 10; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
 Db 9 KVL 11

RESULT 49

Q8SAS3 ID Q8SAS3 PRELIMINARY; PRT; 12 AA.
 AC Q8SAS3;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative fructokinase (Fragment).
 OS Pinus sylvestris (Scots pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=3349;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=plus tree B635C;
 RX MEDLINE=21660210; PubMed=11801746;
 RA Dvornyk V., Sirvio A., Mikkonen M., Savolainen O.;
 RT "Low Nucleotide Diversity at the pall Locus in the Widely Distributed
 RT Pinus sylvestris.";
 RL Mol. Biol. Evol. 19:179-188 (2002).
 DR EMBL; AF359119; AAL74387.1; --
 KW Kinase.
 FT NON TER 1
 SQ SEQUENCE 12 AA; 1198 MW; C6E9EC9330A72DDD CRC64;

Query Match 13.6%; Score 3; DB 10; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
 Db 9 KVL 11

RESULT 50

P82441 ID P82441 PRELIMINARY; PRT; 12 AA.
 AC P82441;
 DT 01-JUN-2000 (TREMBlrel. 14, Created)
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE 26 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
 OC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojtaszek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture.";
 RL Planta 200:0-0 (2000).
 CC -!- SUBCELLULAR LOCATION: CELL WALL.
 CC -!- TISSUE SPECIFICITY: XYLEM.
 KW Cell wall.
 FT NON TER 12
 SQ SEQUENCE 12 AA; 1234 MW; 340012240872C9D7 CRC64;

Query Match 13.6%; Score 3; DB 10; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVP 10
 ||||
 Db 8 PVP 10

RESULT 51

ID Q83139 PRELIMINARY; PRT; 12 AA.
 AC Q83139;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE (Strain CV17) genomic RNA-gamma, 5' leader.
 OS Barley stripe mosaic virus (BSMV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hordeivirus.
 CX NCBI_TaxID=12327;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV17;
 RX MEDLINE=91062385; PubMed=2247462;
 RA Petty I.T., Edwards M.C., Jackson A.O.;
 RT "Systemic movement of an RNA plant virus determined by a point
 RT substitution in a 5' leader sequence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8894-8897(1990).
 DR EMBL; M38633; AAA75527.1; -.
 SQ SEQUENCE 12 AA; 1416 MW; 36A281207BC05047 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 MPI 21
 ||||
 Db 4 MPI 6

RESULT 52

ID Q90ZL3 PRELIMINARY; PRT; 12 AA.
 AC Q90ZL3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Casein kinase 2 alpha subunit (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodidae; Xenopus.
 CX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilhelm V., Neckelman G., Allende C.C., Allende J.E.;
 RT "The Genomic Structure of Two Protein Kinase CK2 alpha Genes of
 RT xenopus laevis and Features of the Putative Promoter Region.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY032954; AAK50341.1; -.
 KW Kinase.
 FT NON_TER
 SQ SEQUENCE 12 AA; 1320 MW; D005098DFD15A772 CRC64;

Query Match 13.6%; Score 3; DB 13; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVP 10
 ||||
 Db 4 PVP 6

RESULT 53

ID O31295 PRELIMINARY; PRT; 13 AA.
 AC O31295;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 2-isopropylmalate synthase (EC 4.1.3.12) (Fragment).
 GN LEUA.
 OS Buchnera aphidicola.
 OC Plasmid pBtcl.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 CX NCBI_TaxID=9;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97386415; PubMed=9244264;
 RA Van Ham R.C.H.J., Moya A., Latorre A.;
 RT "Putative origin of plasmids carrying the genes involved in leucine
 RT biosynthesis in Buchnera aphidicola (endosymbiont of aphids).";
 RL J. Bacteriol. 179:4768-4777(1997).
 DR EMBL; Y11966; CAA72696.1; -.
 KW Lyase; Plasmid.
 FT NON_TER
 SQ SEQUENCE 13 AA; 1487 MW; 1BD1D3E72A9E2050 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PKV 6
 ||||
 Db 3 PKV 5

RESULT 54

ID Q8WNS4 PRELIMINARY; PRT; 13 AA.
 AC Q8WNS4;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE X-linked zinc finger protein (Fragment).
 GN ZFX.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 CX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Poloumienko A., Blecher S.;
 RT "Comparison between intron-exon structures in ZFX and ZFY genes.";
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF032363; AAL58189.1; -.
 FT NON_TER
 SQ SEQUENCE 13 AA; 1366 MW; C32F1B202464DDDD CRC64;

Query Match 13.6%; Score 3; DB 6; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 MPI 21
 ||||
 Db 1 MPI 3

RESULT 55

ID Q9THS0 PRELIMINARY; PRT; 13 AA.
 AC Q9THS0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

```
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE PbsH (Fragment).
GN PbsH.
OS Bryopsis sp. B.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpales;
OC Bryopsidaceae; Bryopsis.
OX NCBI_TaxID=103785;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96-15-06;
RA Krellwitz E.C.; Kowalik K.V.; Manos P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
RT Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT Chloroplast psbB Operon.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF170406; AAD56944.1; -.
KW Chloroplast.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1351 MW; 2C316AF02E93A338 CRC64;

Query Match 13.6%; Score 3; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 MPI 21
DB 1 MPI 3

RESULT 56
O88176
ID O88176 PRELIMINARY; PRT; 13 AA.
AC O88176;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN NCAM1 OR NCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb-c; TISSUE=Liver;
RX MEDLINE=98250618; PubMed=9592442;
RA Kawahigashi H.; Harada Y.; Asano A.; Nakamura M.;
RT "A cis-acting regulatory element that affects the alternative splicing
RT of a muscle-specific exon in the mouse NCAM gene.";
RL Biochim. Biophys. Acta 1397:305-315(1998).
DR EMBL; AB001873; BAA31275.1; -.
DR MGD; MGI:97281; Ncam1.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 13.6%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
DB 4 LPV 6

RESULT 57
Q9QVK6
ID Q9QVK6 PRELIMINARY; PRT; 13 AA.
AC Q9QVK6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
```

```
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Phosphoglycerate mutase P29 (EC 2.7.5.3) (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE
RX MEDLINE=91373341; PubMed=1832670;
RA Hoppner W.; Beckert L.; Buck F.; Seitz H.J.;
RT "Is the p29 protein involved in the rapid regulation of
RT phosphoenolpyruvate carboxykinase (GTP)?";
RL J. Biol. Chem. 266:17257-17260(1991).
SQ SEQUENCE 13 AA; 1456 MW; 39099D8CBA6D2D7 CRC64;

Query Match 13.6%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
DB 5 LPV 7

RESULT 58
O81761
ID O81761 PRELIMINARY; PRT; 13 AA.
AC O81761;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D3;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J.; Purcell R.H.; Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84842; AAA45679.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
DB 7 PQR 9

RESULT 59
O81794
ID O81794 PRELIMINARY; PRT; 13 AA.
AC O81794;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
```

```
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=IND5;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84854; AAA45701.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein. 13 13
FT NON_TER
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
Db |||
7 PQR 9

RESULT 60
Q81784 PRELIMINARY; PRT; 13 AA.
ID Q81784;
AC Q81784;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
RC SEQUENCE FROM N.A.
RP STRAIN=Z1;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84845; AAA45701.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein. 13 13
FT NON_TER
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
Db |||
7 PQR 9

RESULT 61
Q81778 PRELIMINARY; PRT; 13 AA.
ID Q81778;
AC Q81778;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=SW3;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84850; AAA45695.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein. 13 13
FT NON_TER
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 15 PQR 17
Db 7 PQR 9

RESULT 63
Q81775
ID Q81775 PRELIMINARY; PRT; 13 AA.
AC Q81775;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SA7;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84852; AAA45693.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
Db 7 PQR 9

RESULT 64
Q81767
ID Q81767 PRELIMINARY; PRT; 13 AA.
AC Q81767;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HK5;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84849; AAA45685.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.

FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
Db 7 PQR 9

RESULT 65
Q81798
ID Q81798 PRELIMINARY; PRT; 13 AA.
AC Q81798;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SA11;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84858; AAA45715.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
Db 7 PQR 9

RESULT 66
Q81774
ID Q81774 PRELIMINARY; PRT; 13 AA.
AC Q81774;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SA1;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A


```

CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84860; AAA45692.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
DB 7 PQR 9

RESULT 67
Q81766 PRELIMINARY; PRT; 13 AA.
AC Q81766;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HK2;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84827; AAA45684.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA; 1571 MW; 464D1DE1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
DB 7 PQR 9

RESULT 68
Q81793 PRELIMINARY; PRT; 13 AA.
AC Q81793;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=IND3;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84861; AAA45710.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
DB 7 PQR 9

RESULT 69
Q81768 PRELIMINARY; PRT; 13 AA.
ID Q81768
AC Q81768;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P10;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84855; AAA45686.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
DB 7 PQR 9

RESULT 70
Q81785 PRELIMINARY; PRT; 13 AA.
ID Q81785
AC Q81785;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

```

```
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
RX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z4;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84848; AAA45702.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON TER
FT NON TER
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PQR 17
Db 7 PQR 9

RESULT 71
Q81800 PRELIMINARY; PRT; 13 AA.
AC Q81800;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
RX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US11;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84865; AAA45717.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON TER
FT NON TER
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PQR 17
Db 7 PQR 9

RESULT 72
Q81765 PRELIMINARY; PRT; 13 AA.
AC Q81765;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
RX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DR4;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84859; AAA45683.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON TER
FT NON TER
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PQR 17
Db 7 PQR 9

RESULT 73
Q81781 PRELIMINARY; PRT; 13 AA.
AC Q81781;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
RX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T9;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84846; AAA45698.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON TER
FT NON TER
SQ SEQUENCE 13 AA; 1557 MW; 464CF7E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PQR 17
Db 7 PQR 9
```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
|||
Db 7 PQR 9

RESULT 74

Q81769 Q81769 PRELIMINARY; PRT; 13 AA.
AC Q81769;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P8;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84856; AAA45687.1; --
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1559 MW; 465365E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
|||
Db 7 PQR 9

RESULT 75

Q81773 Q81773 PRELIMINARY; PRT; 13 AA.
AC Q81773;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S9;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84838; AAA45691.1; --
DR InterPro; IPR002522; HCV_capsid.

DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
|||
Db 7 PQR 9

Search completed: November 25, 2003, 19:34:06
Job time : 42.314 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 56.1512 Seconds
(without alignments)
62.189 Million cell updates/sec

Title: US-09-641-801-27

Perfect score: 22

Sequence: 1 LSQPKVLPVQKAVQRDMPIQ 22

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A_Geneseq_19Jun03.*

1:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	50.0	14	23 AAU83308	Antiviral composi
2	11	50.0	16	23 AAU83331	Antiviral composi
3	11	50.0	19	23 AAU83340	Antiviral composi
4	10	45.5	10	23 AAU83287	Antiviral composi
5	10	45.5	14	23 AAU83311	Antiviral composi
6	10	45.5	17	23 AAU83334	Antiviral composi
7	9	40.9	9	22 AAE07191	Colostrinin peptid
8	9	40.9	10	22 AAE07201	Modified colostrin
9	9	40.9	10	23 AAU83291	Antiviral composi

10	9	40.9	14	23 AAU83313	Antiviral composi
11	9	40.9	16	23 AAU83329	Antiviral composi
12	8	36.4	19	23 AAU83292	Antiviral composi
13	8	36.4	13	23 AAU83301	Antiviral composi
14	8	36.4	13	23 AAU83303	Antiviral composi
15	8	36.4	13	23 AAU83304	Antiviral composi
16	8	36.4	13	23 AAU83306	Antiviral composi
17	8	36.4	13	23 AAU83307	Antiviral composi
18	8	36.4	14	23 AAU83310	Antiviral composi
19	8	36.4	14	23 AAU83315	Antiviral composi
20	8	36.4	14	23 AAU83317	Antiviral composi
21	8	36.4	14	23 AAU83318	Antiviral composi
22	8	36.4	14	23 AAU83320	Antiviral composi
23	8	36.4	15	23 AAU83321	Antiviral composi
24	8	36.4	15	23 AAU83322	Antiviral composi
25	8	36.4	15	23 AAU83323	Antiviral composi
26	8	36.4	15	23 AAU83324	Antiviral composi
27	8	36.4	15	23 AAU83326	Antiviral composi
28	8	36.4	15	23 AAU83332	Antiviral composi
29	8	36.4	16	23 AAU83330	Antiviral composi
30	8	36.4	16	23 AAU83333	Antiviral composi
31	8	36.4	16	23 AAU83336	Antiviral composi
32	8	36.4	16	23 AAU83337	Antiviral composi
33	8	36.4	16	23 AAU83339	Antiviral composi
34	8	36.4	17	23 AAU83338	Antiviral composi
35	8	36.4	19	23 AAU83341	Antiviral composi
36	7	31.8	7	17 AAU04273	Milk derived anti-
37	7	31.8	8	23 AAU83284	Angiotensin conver
38	7	31.8	11	23 AAU83295	Angiotensin conver
39	7	31.8	12	23 AAU83312	Hypotensive polype
40	7	31.8	13	23 AAU83298	Hypotensive polype
41	7	31.8	13	23 AAU83314	Antiviral composi
42	7	31.8	14	23 AAU83325	Antiviral composi
43	7	31.8	14	23 AAU83328	Antiviral composi
44	6	27.3	6	17 AAR95892	Angiotensin conver
45	6	27.3	7	17 AAR95891	Angiotensin conver
46	6	27.3	8	15 AAR58331	Hypotensive polype
47	6	27.3	8	15 AAR58338	Hypotensive polype
48	6	27.3	9	23 AAR58328	Antiviral composi
49	6	27.3	9	23 AAR58329	Antiviral composi
50	6	27.3	10	23 AAR58329	Antiviral composi
51	6	27.3	10	23 AAR58329	Antiviral composi
52	6	27.3	11	23 AAR58296	Antiviral composi
53	6	27.3	14	16 AAR80311	Antiviral composi
54	6	27.3	14	16 AAR80314	Bovine casein isop
55	6	27.3	14	19 AAW49705	Synthetic peptide
56	6	27.3	15	16 AAR80352	Casein consensus f
57	6	27.3	15	16 AAR80355	Protein polymeric
58	6	27.3	15	19 AAW49740	Glutamine donor pe
59	6	27.3	15	23 AAU83319	Antiviral composi
60	6	27.3	16	23 AAU83335	Antiviral composi
61	6	27.3	18	15 AAR58332	Hypotensive polype
62	5	22.7	8	23 AAU83285	Antiviral composi
63	5	22.7	9	23 ABG67718	Human ADPI tryptic
64	5	22.7	10	18 AAW25911	Beta-2-microglobul
65	5	22.7	10	22 ABB56257	Vascular dementia-
66	5	22.7	10	22 AAU68209	Human Breast cance
67	5	22.7	10	22 AAU68513	Human Expression r
68	5	22.7	10	23 ABG32209	Sheep colostrinin
69	5	22.7	10	23 ABB84035	Transglutaminase i
70	5	22.7	12	23 AAU83300	Antiviral composi
71	5	22.7	13	22 AAM98483	Human peptide #175
72	5	22.7	13	22 AAM98484	Human peptide #175
73	5	22.7	13	23 AAU83309	Antiviral composi
74	5	22.7	14	19 AAW49741	Glutamine donor pe
75	5	22.7	14	23 AAU83316	Antiviral composi
76	5	22.7	15	16 AAR58353	Protein polymeric
77	5	22.7	15	18 AAW25904	Beta-2-microglobul
78	5	22.7	15	21 AAB15819	Human chemokine de
79	5	22.7	15	23 AAU83327	Antiviral composi
80	5	22.7	16	18 AAW25409	p53bp2 SH3 domain
81	5	22.7	18	19 AAW69068	Neuronal NOS bindi
82	5	22.7	19	20 AAY17233	Casein antimicrobi

83 C.albicans enclase
84 Transglutaminase i
85 Chymotrypsin inhib
86 Chymotrypsin inhib
87 Antiviral composi
88 Antiviral composi
89 Hypotensive polype
90 Proline-rich SH3 b
91 Beta-2-microglobul
92 Beta-2-microglobul
93 H11 binding site c
94 H11 binding site c
95 Human ADPI tryptic
96 Tumour necrosis fa
97 Hepatitis C virus
98 Alpha-4beta-1 inte
99 HIV A02 super moti
100 HIV A03 motif tat
A localisation dom

ALIGNMENTS

RESULT 1
AAU83308
ID AAU83308 standard; Peptide; 14 AA.

XX AC AAU83308;

XX DT 23-APR-2002 (first entry)

XX DE Antiviral composition peptide-A, fragment #26.

XX KW Virucide; Immunostimulant; interleukin-8; viral infection;

XX KW monocyte chemotactic protein 1; immune system.

XX OS Synthetic.

XX PN US2002004579-A1.

XX PD 10-JAN-2002.

XX PF 17-JAN-2001; 2001US-0764017.

XX PR 22-OCT-1996; 96US-0735236.

XX PR 25-JUN-1999; 99US-0344095.

XX PA (ADVI-) ADVANCED VIRAL RES CORP.

XX PI Friedland B, Hirschman SZ, Taraporewala IB;

XX DR WPI; 2002-163727/21.

XX PT New peptides compositions, useful for treating viral infections and
stimulating the immune system -

XX PS Disclosure; Page 7; 37pp; English.

XX CC The invention relates to a new peptide composition comprising a specified
peptide sequence. The composition comprises nucleotide-peptide comprising
a peptide linked through a serine residue and diphosphodiester to a
nucleotide; or peptides with about 31 amino acid residues capable of
stimulating production of interleukin-8 in cultured cells; or peptides
with about 31 amino acid residues capable of stimulating production of
monocyte chemotactic protein 1 in cultured cells. The peptides are useful
for treating viral infections and stimulating the immune system.
AAU83282-AAU83401 represent peptides used in the composition of the
invention.

XX SQ Sequence 14 AA;

Query Match 50.0%; Score 11; DB 23; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00015;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 KVLVPVQKAVP 15
Db 1 KVLVPVQKAVP 11

RESULT 2

AAU83331
ID AAU83331 standard; Peptide; 16 AA.

XX AC AAU83331;

XX DT 23-APR-2002 (first entry)

XX DE Antiviral composition peptide-A, fragment #49.

XX KW Virucide; Immunostimulant; interleukin-8; viral infection;

XX KW monocyte chemotactic protein 1; immune system.

XX OS Synthetic.

XX PN US2002004579-A1.

XX PD 10-JAN-2002.

XX PF 17-JAN-2001; 2001US-0764017.

XX PR 22-OCT-1996; 96US-0735236.

XX PR 25-JUN-1999; 99US-0344095.

XX PA (ADVI-) ADVANCED VIRAL RES CORP.

XX PI Friedland B, Hirschman SZ, Taraporewala IB;

XX DR WPI; 2002-163727/21.

XX PT New peptides compositions, useful for treating viral infections and
stimulating the immune system -

XX PS Disclosure; Page 8; 37pp; English.

XX CC The invention relates to a new peptide composition comprising a specified
peptide sequence. The composition comprises nucleotide-peptide comprising
a peptide linked through a serine residue and diphosphodiester to a
nucleotide; or peptides with about 31 amino acid residues capable of
stimulating production of interleukin-8 in cultured cells; or peptides
with about 31 amino acid residues capable of stimulating production of
monocyte chemotactic protein 1 in cultured cells. The peptides are useful
for treating viral infections and stimulating the immune system.
AAU83282-AAU83401 represent peptides used in the composition of the
invention.

XX SQ Sequence 16 AA;

Query Match 50.0%; Score 11; DB 23; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVPVQKAVP 15

Db 1 KVLVPVQKAVP 11

RESULT 3

AAU83340
ID AAU83340 standard; Peptide; 19 AA.

XX AC AAU83340;

XX DT 23-APR-2002 (first entry)

XX DE Antiviral composition peptide-A, fragment #58.

XX Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX Synthetic.
 OS
 XX US2002004579-A1.
 XX 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX
 PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX WPI; 2002-163727/21.
 XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX Disclosure; Page 8; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 SQ Sequence 19 AA;
 Query Match 50.0%; Score 11; DB 23; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.0002;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 KVLVPVQKAVP 15
 DB 1 KVLVPVQKAVP 11
 RESULT 4
 AAU83287
 ID AAU83287 standard; Peptide; 10 AA.
 XX
 AC AAU83287;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #5.
 XX
 KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX Synthetic.
 OS
 XX US2002004579-A1.
 XX 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 PA (ADVI-) ADVANCED VIRAL RES CORP.

XX Friedland B, Hirschman SZ, Taraporewala IB;
 XX WPI; 2002-163727/21.
 XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX Disclosure; Page 7; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 SQ Sequence 10 AA;
 Query Match 45.5%; Score 10; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 KVLVPVQKAV 14
 DB 1 KVLVPVQKAV 10
 RESULT 5
 AAU83311
 ID AAU83311 standard; Peptide; 14 AA.
 XX
 AC AAU83311;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #29.
 XX
 KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX Synthetic.
 OS
 XX US2002004579-A1.
 XX 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX
 PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX WPI; 2002-163727/21.
 XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX Disclosure; Page 7; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells; or peptides
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of

CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.

SQ Sequence 14 AA;

Query Match 45.5%; Score 10; DB 23; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPVPQKAVP 15
 |||||
 Db 1 VLPVPQKAVP 10

RESULT 6

AAU83334
 ID AAU83334 standard; Peptide; 17 AA.

XX AC AAU83334;

XX DT 23-APR-2002 (first entry)

XX DE Antiviral composition peptide-A, fragment #52.

XX KW Virucide; Immunostimulant; interleukin-8; viral infection;
 XX KW monocyte chemotactic protein 1; immune system.

XX OS Synthetic.

XX PN US2002004579-A1.

XX PD 10-JAN-2002.

XX PF 17-JAN-2001; 2001US-0764017.

XX PR 22-OCT-1996; 96US-0735236.

XX PR 25-JUN-1999; 99US-0344095.

XX PA (ADVI-) ADVANCED VIRAL RES CORP.

XX PI Friedland B, Hirschman SZ, Tataporewala IB;

XX DR WPI; 2002-163727/21.

XX PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -

XX PS Disclosure; Page 8; 37pp; English.

XX CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.

SQ Sequence 17 AA;

Query Match 45.5%; Score 10; DB 23; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPVPQKAVP 15
 |||||
 Db 1 VLPVPQKAVP 10

RESULT 8

RESULT 7

AAE07191

ID AAE07191 standard; peptide; 9 AA.

XX AC AAE07191;

XX DT 06-NOV-2001 (first entry)

XX DE Colostrinin peptide 7.

XX KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 XX KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 XX KW central nervous system disorder; neurodegenerative disorder; weight loss;
 XX KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 XX KW acquired immunological deficiency; neurological disorder; dementia;
 XX KW antiviral.

XX OS Unidentified.

XX PN WO200155199-A1.

XX PD 02-AUG-2001.

XX PF 26-JAN-2001; 2001WO-GB00329.

XX PR 26-JAN-2000; 2000GB-0001825.

XX PA (REGE-) REGEN THERAPEUTICS PLC.

XX PI Georgiades JA;

XX DR WPI; 2001-488775/53.

XX PT Peptide useful as an inter alia in the treatment of e.g. disorders of
 PT the immune system and the central nervous system comprises ten
 PT amino-terminal amino acid sequence derived from peptides present in
 PT colostrinin -

XX PS Claim 1; Page 15; 40pp; English.

XX CC The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improve the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is colostrinin peptide 7 related to the invention.
 CC Colostrinin peptide 7 corresponds to position 182-200 of beta-caesin.

SQ Sequence 9 AA;

Query Match 40.9%; Score 9; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPKVLPVPQ 11
 |||||
 Db 1 QPKVLPVPQ 9

AAE07201
 ID AAE07201 standard; peptide; 10 AA.
 XX
 AC AAE07201;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Modified colostrinin cyclic peptide #7.
 XX
 KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl; this residue forms a cyclic
 FT linkage with Gln found at the C-terminal end"
 XX
 PN WO200155199-A1.
 XX
 XX 02-AUG-2001.
 XX
 PF 26-JAN-2001; 2001WO-GB00329.
 XX
 PR 26-JAN-2000; 2000GB-0001825.
 XX
 PA (REG-) REGEN THERAPEUTICS PLC.
 XX
 PI Georgiades JA;
 XX
 DR WPI; 2001-488775/53.
 XX
 XX Peptide useful as an inter alia in the treatment of e.g. disorders of
 PT the immune system and the central nervous system comprises ten
 PT amino-terminal amino acid sequence derived from peptides present in
 PT colostrinin -
 XX
 PS Example 2; Page 9; 40pp; English.
 XX
 CC The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is modified colostrinin cyclic peptide #7 related to
 CC the invention.
 XX
 XX Sequence 10 AA;
 XX
 SQ Query Match 40.9%; Score 9; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 3 QPKVLPVPQ 11
 |||||||

Db 2 QPKVLPVPQ 10
 RESULT 9
 AAU83291
 ID AAU83291 standard; Peptide; 10 AA.
 XX
 AC AAU83291;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #9.
 XX
 KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX
 OS Synthetic.
 XX
 PN US2002004579-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX
 PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX
 DR WPI; 2002-163727/21.
 XX
 XX New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 PT
 PS Disclosure; Page 7; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 SQ Sequence 10 AA;
 XX
 XX Query Match 40.9%; Score 9; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 7 LPVPQKAVP 15
 |||||||
 Db 1 LPVPQKAVP 9
 RESULT 10
 AAU83313
 ID AAU83313 standard; Peptide; 14 AA.
 XX
 AC AAU83313;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #31.
 XX
 KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX

OS Synthetic.
 PN US2002004579-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX
 PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX
 DR WPI; 2002-163727/21.
 XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 PS Disclosure; Page 8; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 SQ Sequence 14 AA;
 Query Match 40.9%; Score 9; DB 23; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 LPVPQKAVP 15
 Db |||||
 1 LPVPQKAVP 9
 RESULT 11
 AAU83329
 ID AAU83329 standard; Peptide; 16 AA.
 XX
 AC AAU83329;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #47.
 XX
 KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX
 OS Synthetic.
 XX
 PN US2002004579-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX
 PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX
 DR WPI; 2002-163727/21.

XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 PS Disclosure; Page 8; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 SQ Sequence 16 AA;
 Query Match 40.9%; Score 9; DB 23; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 LPVPQKAVP 15
 Db |||||
 1 LPVPQKAVP 9
 RESULT 12
 AAU83292
 ID AAU83292 standard; Peptide; 9 AA.
 XX
 AC AAU83292;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #10.
 XX
 KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX
 OS Synthetic.
 XX
 PN US2002004579-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX
 PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX
 DR WPI; 2002-163727/21.
 XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 PS Disclosure; Page 7; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.

```

XX SQ Sequence 9 AA;
Query Match 36.4%; Score 8; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQRDMPIQ 22
Db |||||||
2 PQRDMPIQ 9

RESULT 13
AAU83301
ID AAU83301 standard; Peptide; 13 AA.
XX AC AAU83301;
XX XX
DT 23-APR-2002 (first entry)
XX XX
DE Antiviral composition peptide-A, fragment #19.
XX XX
KW Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX OS Synthetic.
XX XX
XX US2002004579-A1.
XX PN
XX 10-JAN-2002.
XX PD
XX PF 17-JAN-2001; 2001US-0764017.
XX XX
XX PR 22-OCT-1996; 96US-0735236.
XX PR 25-JUN-1999; 99US-0344095.
XX XX
XX PA (ADVI-) ADVANCED VIRAL RES CORP.
XX XX
XX PI Friedland B, Hirschman SZ, Taraporewala IB;
XX XX
XX DR WPI; 2002-163727/21.
XX XX
XX PT New peptides compositions, useful for treating viral infections and
XX PT stimulating the immune system -
XX XX
XX PS Disclosure; Page 7; 37pp; English.
XX XX
XX CC The invention relates to a new peptide composition comprising a specified
XX CC peptide sequence. The composition comprises nucleotide-peptide comprising
XX CC a peptide linked through a serine residue and diphosphodiester to a
XX CC nucleotide; or peptides with about 31 amino acid residues capable of
XX CC stimulating production of interleukin-8 in cultured cells; or peptides
XX CC with about 31 amino acid residues capable of stimulating production of
XX CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
XX CC for treating viral infections and stimulating the immune system.
XX CC AAU83282-AAU83401 represent peptides used in the composition of the
XX CC invention.
XX SQ Sequence 13 AA;
Query Match 36.4%; Score 8; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQRDMPIQ 22
Db |||||||
6 PQRDMPIQ 13

RESULT 15
AAU83304
ID AAU83304 standard; Peptide; 13 AA.
XX AC
XX AC AAU83304;
XX XX
DT 23-APR-2002 (first entry)
XX XX
DE Antiviral composition peptide-A, fragment #22.
XX XX
KW Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX XX
XX OS Synthetic.
XX XX
XX US2002004579-A1.
XX PN
XX PD 10-JAN-2002.
XX XX
XX PF 17-JAN-2001; 2001US-0764017.
XX XX
XX PR 22-OCT-1996; 96US-0735236.
XX PR 25-JUN-1999; 99US-0344095.
XX XX
XX PA (ADVI-) ADVANCED VIRAL RES CORP.
XX XX
XX PI Friedland B, Hirschman SZ, Taraporewala IB;
XX XX
XX DR WPI; 2002-163727/21.
XX XX
XX PT New peptides compositions, useful for treating viral infections and
XX PT stimulating the immune system -
XX XX
XX PS Disclosure; Page 7; 37pp; English.
XX XX
XX CC The invention relates to a new peptide composition comprising a specified
XX CC peptide sequence. The composition comprises nucleotide-peptide comprising
XX CC a peptide linked through a serine residue and diphosphodiester to a
XX CC nucleotide; or peptides with about 31 amino acid residues capable of
XX CC stimulating production of interleukin-8 in cultured cells; or peptides
XX CC with about 31 amino acid residues capable of stimulating production of
XX CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
XX CC for treating viral infections and stimulating the immune system.
XX CC AAU83282-AAU83401 represent peptides used in the composition of the
XX CC invention.
XX SQ Sequence 13 AA;
Query Match 36.4%; Score 8; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQRDMPIQ 22
Db |||||||
6 PQRDMPIQ 13

RESULT 14
AAU83303
ID AAU83303 standard; Peptide; 13 AA.
XX XX

```

XX 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX (ADVI-) ADVANCED VIRAL RES CORP.
 XX Friedland B, Hirschman SZ, Taraporewala IB;
 XX WPI; 2002-163727/21.
 XX
 XX New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 PT Disclosure; Page 7; 37pp; English.
 PS
 XX The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells; or peptides
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 36.4%; Score 8; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 PQRDMPIQ 22
 DB 4 PQRDMPIQ 11
 RESULT 16
 AAU83306
 ID AAU83306 standard; Peptide; 13 AA.
 AC AAU83306;
 XX
 XX 23-APR-2002 (first entry)
 DE Antiviral composition peptide-A, fragment #24.
 XX Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX Synthetic.
 OS
 XX US2002004579-A1.
 PN 10-JAN-2002.
 XX
 XX 17-JAN-2001; 2001US-0764017.
 PF
 XX 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX (ADVI-) ADVANCED VIRAL RES CORP.
 PA Friedland B, Hirschman SZ, Taraporewala IB;
 XX WPI; 2002-163727/21.
 XX
 XX New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 PT Disclosure; Page 7; 37pp; English.
 PS
 XX The invention relates to a new peptide composition comprising a specified

CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 36.4%; Score 8; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 PQRDMPIQ 22
 DB 3 PQRDMPIQ 10
 RESULT 17
 AAU83307
 ID AAU83307 standard; Peptide; 13 AA.
 XX
 XX AAU83307;
 AC
 XX
 XX 23-APR-2002 (first entry)
 DT Antiviral composition peptide-A, fragment #25.
 DE Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX Synthetic.
 OS
 XX US2002004579-A1.
 PN 10-JAN-2002.
 XX
 XX 17-JAN-2001; 2001US-0764017.
 PF
 XX 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX (ADVI-) ADVANCED VIRAL RES CORP.
 PA Friedland B, Hirschman SZ, Taraporewala IB;
 XX WPI; 2002-163727/21.
 XX
 XX New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 PT Disclosure; Page 7; 37pp; English.
 PS
 XX The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 36.4%; Score 8; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      15 PORDMPIQ 22
DB      4 PORDMPIQ 11

RESULT 18
AAU83310
ID AAU83310 standard; Peptide; 14 AA.
XX
AC AAU83310;
XX
DT 23-APR-2002 (first entry)
XX
DE Antiviral composition peptide-A, fragment #28.
XX
KW Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX
OS Synthetic.
XX
FN US2002004579-A1.
XX
PD 10-JAN-2002.
XX
PF 17-JAN-2001; 2001US-0764017.
XX
PR 22-OCT-1996; 96US-0735236.
PR 25-JUN-1999; 99US-0344095.
XX
PA (ADVI-) ADVANCED VIRAL RES CORP.
XX
PI Friedland B, Hirschman SZ, Taraporewala IB;
XX
DR WPI; 2002-163727/21.
XX
PT New peptides compositions, useful for treating viral infections and
PT stimulating the immune system -
XX
PS Disclosure; Page 8; 37pp; English.
XX
CC The invention relates to a new peptide composition comprising a specified
CC peptide sequence. The composition comprises nucleotide-peptide comprising
CC a peptide linked through a serine residue and diphosphodiester to a
CC nucleotide; or peptides with about 31 amino acid residues capable of
CC stimulating production of interleukin-8 in cultured cells; or peptides
CC with about 31 amino acid residues capable of stimulating production of
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC for treating viral infections and stimulating the immune system.
CC AAU83282-AAU83401 represent peptides used in the composition of the
CC invention.
XX
SQ Sequence 14 AA;

Query Match      36.4%; Score 8; DB 23; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 PORDMPIQ 22
DB      4 PORDMPIQ 12

RESULT 20
AAU83317
ID AAU83317 standard; Peptide; 14 AA.
XX
AC AAU83317;
XX
DT 23-APR-2002 (first entry)
XX
DE Antiviral composition peptide-A, fragment #35.
XX
KW Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX
OS Synthetic.
XX
FN US2002004579-A1.
XX
PD 10-JAN-2002.
XX
PF 17-JAN-2001; 2001US-0764017.
XX
PR 22-OCT-1996; 96US-0735236.
PR 25-JUN-1999; 99US-0344095.
XX
PA (ADVI-) ADVANCED VIRAL RES CORP.
XX
PI Friedland B, Hirschman SZ, Taraporewala IB;

```

XX WPI; 2002-163727/21.
 XX
 XX New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 XX Disclosure; Page 8; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 36.4%; Score 8; DB 23; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 PQRDMPDPIQ 22
 Db |||||||
 3 PQRDMPDPIQ 10
 RESULT 21
 AAU83318
 ID AAU83318 standard; Peptide; 14 AA.
 AC
 AAU83318;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #36.
 XX
 KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX
 OS Synthetic.
 XX
 US2002004579-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX
 PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX
 WPI; 2002-163727/21.
 XX
 XX New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 XX Disclosure; Page 8; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.

CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 36.4%; Score 8; DB 23; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 PQRDMPDPIQ 22
 Db |||||||
 3 PQRDMPDPIQ 10
 RESULT 22
 AAU83320
 ID AAU83320 standard; Peptide; 14 AA.
 AC
 AAU83320;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #38.
 XX
 KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX
 OS Synthetic.
 XX
 US2002004579-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX
 PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX
 WPI; 2002-163727/21.
 XX
 XX New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 XX Disclosure; Page 8; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 36.4%; Score 8; DB 23; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 PQRDMPDPIQ 22
 Db |||||||
 1 PQRDMPDPIQ 8
 RESULT 23
 AAU83321

ID AAU83321 standard; Peptide; 15 AA.
 XX AC AAU83321;
 XX DT 23-APR-2002 (first entry)
 XX DE Antiviral composition peptide-A, fragment #39.
 XX DE Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX OS Synthetic.
 XX US2002004579-A1.
 XX PD 10-JAN-2002.
 XX PF 17-JAN-2001; 2001US-0764017.
 XX PR 22-OCT-1996; 96US-0735236.
 XX PR 25-JUN-1999; 99US-0344095.
 XX PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX DR WPI; 2002-163727/21.
 XX New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX Disclosure; Page 8; 37pp; English.
 XX The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX SQ Sequence 15 AA;
 Query Match 36.4%; Score 8; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 PORDMPIQ 22
 DB 7 PORDMPIQ 14
 RESULT 24
 AAU83322
 ID AAU83322 standard; Peptide; 15 AA.
 XX AC AAU83322;
 XX DT 23-APR-2002 (first entry)
 XX DE Antiviral composition peptide-A, fragment #40.
 XX Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX OS Synthetic.
 XX US2002004579-A1.
 XX PD 10-JAN-2002.
 XX PF 17-JAN-2001; 2001US-0764017.
 XX PR 22-OCT-1996; 96US-0735236.
 XX PR 25-JUN-1999; 99US-0344095.
 XX PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX DR WPI; 2002-163727/21.
 XX New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX Disclosure; Page 8; 37pp; English.

XX 17-JAN-2001; 2001US-0764017.
 XX PF 22-OCT-1996; 96US-0735236.
 XX PR 25-JUN-1999; 99US-0344095.
 XX PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX DR WPI; 2002-163727/21.
 XX New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX Disclosure; Page 8; 37pp; English.
 XX The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX SQ Sequence 15 AA;
 Query Match 36.4%; Score 8; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 PVPQKAVP 15
 DB 1 PVPQKAVP 8
 RESULT 25
 AAU83323
 ID AAU83323 standard; Peptide; 15 AA.
 XX AC AAU83323;
 XX DT 23-APR-2002 (first entry)
 XX DE Antiviral composition peptide-A, fragment #41.
 XX Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX OS Synthetic.
 XX US2002004579-A1.
 XX PD 10-JAN-2002.
 XX PF 17-JAN-2001; 2001US-0764017.
 XX PR 22-OCT-1996; 96US-0735236.
 XX PR 25-JUN-1999; 99US-0344095.
 XX PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX DR WPI; 2002-163727/21.
 XX New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX Disclosure; Page 8; 37pp; English.

XX The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX

SQ Sequence 15 AA;

Query Match 36.4%; Score 8; DB 23; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQRDMP1Q 22

Db 7 PQRDMP1Q 14

RESULT 26

AAU83324

ID AAU83324 standard; Peptide; 15 AA.

XX AC

XX AC

DT 23-APR-2002 (first entry)

XX

DE Antiviral composition peptide-A, fragment #42.

XX

KW Virucide; Immunostimulant; interleukin-8; viral infection;

KW monocyte chemotactic protein 1; immune system.

XX

XX Synthetic.

OS

XX US2002004579-A1.

PN

XX 10-JAN-2002.

PD

XX 17-JAN-2001; 2001US-0764017.

PF

XX 22-OCT-1996; 96US-0735236.

PR

XX 25-JUN-1999; 99US-0344095.

PR

XX (ADVI-) ADVANCED VIRAL RES CORP.

XX

PI Friedland B, Hirschman SZ, Taraporewala IB;

XX

DR WPI; 2002-163727/21.

XX

XX New peptides compositions, useful for treating viral infections and

PT stimulating the immune system -

XX

PS Disclosure; Page 8; 37pp; English.

XX

CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX

SQ Sequence 15 AA;

Query Match 36.4%; Score 8; DB 23; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQRDMP1Q 22

Db 5 PQRDMP1Q 12

RESULT 27

AAU83326

ID AAU83326 standard; Peptide; 15 AA.

XX AC

XX AC

DT 23-APR-2002 (first entry)

XX

DE Antiviral composition peptide-A, fragment #44.

XX

KW Virucide; Immunostimulant; interleukin-8; viral infection;

KW monocyte chemotactic protein 1; immune system.

XX

XX Synthetic.

OS

XX US2002004579-A1.

PN

XX 10-JAN-2002.

PD

XX 17-JAN-2001; 2001US-0764017.

PF

XX 22-OCT-1996; 96US-0735236.

PR

XX 25-JUN-1999; 99US-0344095.

PR

XX (ADVI-) ADVANCED VIRAL RES CORP.

XX

PI Friedland B, Hirschman SZ, Taraporewala IB;

XX

XX WPI; 2002-163727/21.

XX

XX New peptides compositions, useful for treating viral infections and

PT stimulating the immune system -

XX

XX Disclosure; Page 8; 37pp; English.

XX

CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX

SQ Sequence 15 AA;

Query Match 36.4%; Score 8; DB 23; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQRDMP1Q 22

Db 4 PQRDMP1Q 11

RESULT 28

AAU83332

ID AAU83332 standard; Peptide; 15 AA.

XX AC

XX AC

DT 23-APR-2002 (first entry)

XX

DE Antiviral composition peptide-A, fragment #50.

XX Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX Synthetic.
 OS US2002004579-A1.
 XX PD 10-JAN-2002.
 XX PF 17-JAN-2001; 2001US-0764017.
 XX PR 22-OCT-1996; 96US-0735236.
 XX PR 25-JUN-1999; 99US-0344095.
 XX PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX DR WPI; 2002-163727/21.
 XX PT New peptides compositions, useful for treating viral infections and stimulating the immune system -
 XX PS Disclosure; Page 8; 37pp; English.
 CC The invention relates to a new peptide composition comprising a specified peptide sequence. The composition comprises nucleotide-peptide comprising a peptide linked through a serine residue and diphosphodiester to a nucleotide; or peptides with about 31 amino acid residues capable of stimulating production of interleukin-8 in cultured cells; or peptides with about 31 amino acid residues capable of stimulating production of monocyte chemotactic protein 1 in cultured cells. The peptides are useful for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the invention.
 XX SQ Sequence 15 AA;
 PT Query Match 36.4%; Score 8; DB 23; Length 15;
 PT Best Local Similarity 100.0%; Pred. No. 0.16;
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 PORDMPIQ 22
 DB 2 PORDMPIQ 9
 RESULT 29
 AAU83330
 ID AAU83330 standard; Peptide; 16 AA.
 XX AC AAU83330;
 XX DT 23-APR-2002 (first entry)
 XX DE Antiviral composition peptide-A, fragment #48.
 XX KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX OS Synthetic.
 OS US2002004579-A1.
 XX PN Friedland B, Hirschman SZ, Taraporewala IB;
 XX PD 10-JAN-2002.
 XX PF 17-JAN-2001; 2001US-0764017.
 XX PR 22-OCT-1996; 96US-0735236.
 XX PR 25-JUN-1999; 99US-0344095.
 XX PA (ADVI-) ADVANCED VIRAL RES CORP.

XX PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX DR WPI; 2002-163727/21.
 XX PT New peptides compositions, useful for treating viral infections and stimulating the immune system -
 XX PS Disclosure; Page 8; 37pp; English.
 CC The invention relates to a new peptide composition comprising a specified peptide sequence. The composition comprises nucleotide-peptide comprising a peptide linked through a serine residue and diphosphodiester to a nucleotide; or peptides with about 31 amino acid residues capable of stimulating production of interleukin-8 in cultured cells; or peptides with about 31 amino acid residues capable of stimulating production of monocyte chemotactic protein 1 in cultured cells. The peptides are useful for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the invention.
 XX SQ Sequence 16 AA;
 PT Query Match 36.4%; Score 8; DB 23; Length 16;
 PT Best Local Similarity 100.0%; Pred. No. 0.17;
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 KVLFPVPQK 12
 DB 1 KVLFPVPQK 8
 RESULT 30
 AAU83333
 ID AAU83333 standard; Peptide; 16 AA.
 XX AC AAU83333;
 XX DT 23-APR-2002 (first entry)
 XX DE Antiviral composition peptide-A, fragment #51.
 XX KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX OS Synthetic.
 OS US2002004579-A1.
 XX PN Friedland B, Hirschman SZ, Taraporewala IB;
 XX PD 10-JAN-2002.
 XX PF 17-JAN-2001; 2001US-0764017.
 XX PR 22-OCT-1996; 96US-0735236.
 XX PR 25-JUN-1999; 99US-0344095.
 XX PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX DR WPI; 2002-163727/21.
 XX PT New peptides compositions, useful for treating viral infections and stimulating the immune system -
 XX PS Disclosure; Page 8; 37pp; English.
 CC The invention relates to a new peptide composition comprising a specified peptide sequence. The composition comprises nucleotide-peptide comprising a peptide linked through a serine residue and diphosphodiester to a nucleotide; or peptides with about 31 amino acid residues capable of stimulating production of interleukin-8 in cultured cells; or peptides with about 31 amino acid residues capable of stimulating production of monocyte chemotactic protein 1 in cultured cells. The peptides are useful for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the invention.

CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.

SQ Sequence 16 AA;

Query Match 36.4%; Score 8; DB 23; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PQDMPPIQ 22

Db 7 PQDMPPIQ 14

RESULT 31

AAU83336
 ID AAU83336 standard; Peptide; 16 AA.

XX AC AAU83336;

XX DT 23-APR-2002 (first entry)

XX DE Antiviral composition peptide-A, fragment #54.

XX KW Virucide; Immunostimulant; interleukin-8; viral infection;

XX KW monocyte chemotactic protein 1; immune system.

XX OS Synthetic.

XX PN US2002004579-A1.

XX PD 10-JAN-2002.

XX PF 17-JAN-2001; 2001US-0764017.

XX PR 22-OCT-1996; 96US-0735236.

XX PR 25-JUN-1999; 99US-0344095.

XX PA (ADVI-) ADVANCED VIRAL RES CORP.

XX PI Friedland B, Hirschman SZ, Taraporewala IB;

XX PX WPI; 2002-163727/21.

XX PT New peptides compositions, useful for treating viral infections and
 stimulating the immune system -

XX PS Disclosure; Page 8; 37pp; English.

XX CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.

SQ Sequence 16 AA;

Query Match 36.4%; Score 8; DB 23; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PQDMPPIQ 22

Db 1 PQDMPPIQ 8

RESULT 32

AAU83337
 ID AAU83337 standard; Peptide; 16 AA.

XX AC AAU83337;

XX DT 23-APR-2002 (first entry)

XX DE Antiviral composition peptide-A, fragment #55.

XX KW Virucide; Immunostimulant; interleukin-8; viral infection;

XX KW monocyte chemotactic protein 1; immune system.

XX OS Synthetic.

XX PN US2002004579-A1.

XX PD 10-JAN-2002.

XX PF 17-JAN-2001; 2001US-0764017.

XX PR 22-OCT-1996; 96US-0735236.

XX PR 25-JUN-1999; 99US-0344095.

XX PA (ADVI-) ADVANCED VIRAL RES CORP.

XX PI Friedland B, Hirschman SZ, Taraporewala IB;

XX PX WPI; 2002-163727/21.

XX PT New peptides compositions, useful for treating viral infections and
 stimulating the immune system -

XX PS Disclosure; Page 8; 37pp; English.

XX CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.

XX SQ Sequence 16 AA;

Query Match 36.4%; Score 8; DB 23; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PQDMPPIQ 22

Db 4 PQDMPPIQ 11

RESULT 33

AAU83339
 ID AAU83339 standard; Peptide; 16 AA.

XX AC AAU83339;

XX DT 23-APR-2002 (first entry)

XX DE Antiviral composition peptide-A, fragment #57.

XX KW Virucide; Immunostimulant; interleukin-8; viral infection;

XX KW monocyte chemotactic protein 1; immune system.

XX OS Synthetic.

XX PN US2002004579-A1.

XX PD 10-JAN-2002.
 XX PF 17-JAN-2001; 2001US-0764017.
 XX PR 22-OCT-1996; 96US-0735236.
 XX PR 25-JUN-1999; 99US-0344095.
 XX PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX DR WPI; 2002-163727/21.
 XX PT New peptides compositions, useful for treating viral infections and
 XX PT stimulating the immune system -
 XX PS Disclosure; Page 8; 37pp; English.
 XX CC The invention relates to a new peptide composition comprising a specified
 XX CC peptide sequence. The composition comprises nucleotide-peptide comprising
 XX CC a peptide linked through a serine residue and diphosphodiester to a
 XX CC nucleotide; or peptides with about 31 amino acid residues capable of
 XX CC stimulating production of interleukin-8 in cultured cells; or peptides
 XX CC with about 31 amino acid residues capable of stimulating production of
 XX CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 XX CC for treating viral infections and stimulating the immune system.
 XX CC AAU83282-AAU83401 represent peptides used in the composition of the
 XX CC invention.
 XX SQ Sequence 16 AA;
 XX Query Match 36.4%; Score 8; DB 23; Length 16;
 XX Best Local Similarity 100.0%; Pred. No. 0.17;
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 15 PORDMPIQ 22
 XX DB |||||||
 XX 3 PORDMPIQ 10
 XX RESULT 34
 XX AAU83338
 XX ID AAU83338 standard; Peptide; 17 AA.
 XX AC AAU83338;
 XX DT 23-APR-2002 (first entry)
 XX DE Antiviral composition peptide-A, fragment #56.
 XX KW Virucide; Immunostimulant; interleukin-8; viral infection;
 XX KW monocyte chemotactic protein 1; immune system.
 XX OS Synthetic.
 XX PN US2002004579-A1.
 XX PD 10-JAN-2002.
 XX PF 17-JAN-2001; 2001US-0764017.
 XX PR 22-OCT-1996; 96US-0735236.
 XX PR 25-JUN-1999; 99US-0344095.
 XX PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX DR WPI; 2002-163727/21.
 XX PT New peptides compositions, useful for treating viral infections and
 XX PT stimulating the immune system -

XX PS Disclosure; Page 8; 37pp; English.
 XX CC The invention relates to a new peptide composition comprising a specified
 XX CC peptide sequence. The composition comprises nucleotide-peptide comprising
 XX CC a peptide linked through a serine residue and diphosphodiester to a
 XX CC nucleotide; or peptides with about 31 amino acid residues capable of
 XX CC stimulating production of interleukin-8 in cultured cells; or peptides
 XX CC with about 31 amino acid residues capable of stimulating production of
 XX CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 XX CC for treating viral infections and stimulating the immune system.
 XX CC AAU83282-AAU83401 represent peptides used in the composition of the
 XX CC invention.
 XX SQ Sequence 17 AA;
 XX Query Match 36.4%; Score 8; DB 23; Length 17;
 XX Best Local Similarity 100.0%; Pred. No. 0.18;
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 15 PORDMPIQ 22
 XX DB |||||||
 XX 7 PORDMPIQ 14
 XX RESULT 35
 XX AAU83341
 XX ID AAU83341 standard; Peptide; 19 AA.
 XX AC AAU83341;
 XX DT 23-APR-2002 (first entry)
 XX DE Antiviral composition peptide-A, fragment #59.
 XX KW Virucide; Immunostimulant; interleukin-8; viral infection;
 XX KW monocyte chemotactic protein 1; immune system.
 XX OS Synthetic.
 XX PN US2002004579-A1.
 XX PD 10-JAN-2002.
 XX PF 17-JAN-2001; 2001US-0764017.
 XX PR 22-OCT-1996; 96US-0735236.
 XX PR 25-JUN-1999; 99US-0344095.
 XX PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX DR WPI; 2002-163727/21.
 XX PT New peptides compositions, useful for treating viral infections and
 XX PT stimulating the immune system -
 XX PS Disclosure; Page 8; 37pp; English.
 XX CC The invention relates to a new peptide composition comprising a specified
 XX CC peptide sequence. The composition comprises nucleotide-peptide comprising
 XX CC a peptide linked through a serine residue and diphosphodiester to a
 XX CC nucleotide; or peptides with about 31 amino acid residues capable of
 XX CC stimulating production of interleukin-8 in cultured cells; or peptides
 XX CC with about 31 amino acid residues capable of stimulating production of
 XX CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 XX CC for treating viral infections and stimulating the immune system.
 XX CC AAU83282-AAU83401 represent peptides used in the composition of the
 XX CC invention.
 XX SQ Sequence 19 AA;

```

Query Match      36.4%; Score 8; DB 23; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 PORDMPIQ 22
      |||||
Db       5 PORDMPIQ 12

RESULT 36
AAU04273
ID      AAU04273 standard; peptide; 7 AA.
XX
AC      AAU04273;
XX
DT      06-JUN-1997 (first entry)
XX
DE      Milk derived anti-hypertensive peptide.
XX
KW      Anti-hypertensive; fermentation; animal milk; Lactobacillus;
KW      microorganism; digestion; protease; reduction; blood pressure.
XX
OS      Mammalian spp.
XX
PN      EP737690-A2.
XX
PD      16-OCT-1996.
XX
PF      10-APR-1996; 96EP-0302522.
XX
PR      10-APR-1995; 95JP-0084247.
XX
PA      (CALV ) CALPIS FOOD IND CO LTD.
XX
PI      Maeno M;
XX
WPI; 1996-457284/46.
XX
XX
PT      Antihypertensive compans. derived from milk - by fermentation or
PT      protease digestion
XX
PS      Claim 1; Page 9; 10pp; English.
XX
CC      The present anti-hypertensive (AH) peptide was prepared by
CC      fermenting an animal milk starting material with a Lactobacillus
CC      microorganism, especially L. helveticus, L. delbrueckii subspecies
CC      bulgaricus or L. acidophilus, or digesting it with a protease at
CC      20-50 degrees C for 3-30 hours, obtaining an eluent by
CC      ultrafiltration and then fractionating the eluent by reverse phase
CC      HPLC. An AH composition comprising the peptide is safe and reduces
CC      blood pressure at low oral doses, e.g. 0.2-10, preferably
CC      1 mg/kg/day or 5-20 ml/kg/day when ingested as a yogurt. The change
CC      in the systolic blood pressure of spontaneously hypertensive rats
CC      treated intragastrically with 1 mg/kg of body weight of the present
CC      AH peptide was minus 24 +/- 7.8 mmHg.
XX
SQ      Sequence 7 AA;

Query Match      31.8%; Score 7; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KVLFPVPQ 11
      |||||
Db       1 KVLFPVPQ 7

RESULT 37
AAU83284
ID      AAU83284 standard; Peptide; 8 AA.
XX
AC      AAU83284;
XX

Query Match      31.8%; Score 7; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 VPQKAVP 15
      |||||
Db       1 VPQKAVP 7

RESULT 38
AAU83295
ID      AAU83295 standard; Peptide; 11 AA.
XX
AC      AAU83295;
XX
DT      23-APR-2002 (first entry)
XX
DE      Antiviral composition peptide-A, fragment #13.
XX
KW      Virucide; Immunostimulant; interleukin-8; viral infection;
KW      monocyte chemotactic protein 1; immune system.
XX
OS      Synthetic.
XX
PN      US2002004579-A1.
XX
PD      10-JAN-2002.
XX
PF      17-JAN-2001; 2001US-0764017.
XX
PR      22-OCT-1996; 96US-0735236.
XX
PA      (ADVI-) ADVANCED VIRAL RES CORP.
XX
PI      Friedland B, Hirschman SZ, Taraporewala IB;
XX
WPI; 2002-163727/21.
XX
XX
PT      New peptides compositions, useful for treating viral infections and
PT      stimulating the immune system -
XX
PS      Disclosure; Page 7; 37pp; English.
XX
CC      The invention relates to a new peptide composition comprising a specified
CC      peptide sequence. The composition comprises nucleotide-peptide comprising
CC      a peptide linked through a serine residue and diphosphodiester to a
CC      nucleotide; or peptides with about 31 amino acid residues capable of
CC      stimulating production of interleukin-8 in cultured cells; or peptides
CC      with about 31 amino acid residues capable of stimulating production of
CC      monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC      for treating viral infections and stimulating the immune system.
CC      AAU83282-AAU83401 represent peptides used in the composition of the
CC      invention.
XX
SQ      Sequence 8 AA;

Query Match      31.8%; Score 7; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 VPQKAVP 15
      |||||
Db       1 VPQKAVP 7

RESULT 39
AAU83295
ID      AAU83295 standard; Peptide; 11 AA.
XX
AC      AAU83295;
XX
DT      23-APR-2002 (first entry)
XX
DE      Antiviral composition peptide-A, fragment #13.
XX
KW      Virucide; Immunostimulant; interleukin-8; viral infection;
KW      monocyte chemotactic protein 1; immune system.
XX
OS      Synthetic.
XX
PN      US2002004579-A1.
XX
PD      10-JAN-2002.
XX
PF      17-JAN-2001; 2001US-0764017.
XX
PR      22-OCT-1996; 96US-0735236.
XX

```


Db	1	VFOKAVP	7	
OS	XX	Synthetic.		
XX	XX	US2002004579-A1.		
XX	XX			
XX	XX	10-JAN-2002.		
XX	XX			
XX	XX	17-JAN-2001; 2001US-0764017.		
XX	XX			
XX	XX	22-OCT-1996; 96US-0735236.		
XX	XX	25-JUN-1999; 99US-0344095.		
XX	XX	(ADVI-) ADVANCED VIRAL RES CORP.		
XX	XX			
XX	XX	Friedland B, Hirschman SZ, Taraporewala IB;		
XX	XX	WPI; 2002-163727/21.		
XX	XX			
XX	XX	New peptides compositions, useful for treating viral infections and stimulating the immune system		
XX	XX	Disclosure; Page 8; 37pp; English.		
XX	XX			
XX	XX	The invention relates to a new peptide composition comprising a specified peptide sequence. The composition comprises nucleotide-peptide comprising a peptide linked through a serine residue and diphosphodiester to a nucleotide; or peptides with about 31 amino acid residues capable of stimulating production of interleukin-8 in cultured cells; or peptides with about 31 amino acid residues capable of stimulating production of monocyte chemotactic protein 1 in cultured cells. The peptides are useful for treating viral infections and stimulating the immune system.		
XX	XX	AAU83282-AAU83401 represent peptides used in the composition of the invention.		
XX	XX			
XX	XX	Sequence 14 AA;		
XX	XX			
XX	XX	Query Match 31.8%; Score 7; DB 23; Length 14;		
XX	XX	Best Local Similarity 100.0%; Pred. No. 1.6;		
XX	XX	Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
XX	XX			
XX	XX	Qy 16 QRDMPQ 22		
XX	XX	Db 1 QRDMPQ 7		
XX	XX			
XX	XX	RESULT 43		
XX	XX	AAU83328		
XX	XX	ID AAU83328 standard; Peptide; 14 AA.		
XX	XX	AC AAU83328;		
XX	XX			
XX	XX	23-APR-2002 (first entry)		
XX	XX			
XX	XX	Antiviral composition peptide-A, fragment #46.		
XX	XX			
XX	XX	Virucide; Immunostimulant; interleukin-8; viral infection;		
XX	XX	monocyte chemotactic protein 1; immune system.		
XX	XX	Synthetic.		
XX	XX			
XX	XX	US2002004579-A1.		
XX	XX			
XX	XX	10-JAN-2002.		
XX	XX			
XX	XX	17-JAN-2001; 2001US-0764017.		
XX	XX			
XX	XX	22-OCT-1996; 96US-0735236.		
XX	XX	25-JUN-1999; 99US-0344095.		
XX	XX	(ADVI-) ADVANCED VIRAL RES CORP.		
XX	XX			
XX	XX	Friedland B, Hirschman SZ, Taraporewala IB;		
XX	XX	WPI; 2002-163727/21.		
XX	XX			
XX	XX	New peptides compositions, useful for treating viral infections and stimulating the immune system		
XX	XX	Disclosure; Page 8; 37pp; English.		
XX	XX			
XX	XX	The invention relates to a new peptide composition comprising a specified peptide sequence. The composition comprises nucleotide-peptide comprising a peptide linked through a serine residue and diphosphodiester to a nucleotide; or peptides with about 31 amino acid residues capable of stimulating production of interleukin-8 in cultured cells; or peptides with about 31 amino acid residues capable of stimulating production of monocyte chemotactic protein 1 in cultured cells. The peptides are useful for treating viral infections and stimulating the immune system.		
XX	XX	AAU83282-AAU83401 represent peptides used in the composition of the invention.		
XX	XX			
XX	XX	Sequence 13 AA;		
XX	XX			
XX	XX	Query Match 31.8%; Score 7; DB 23; Length 13;		
XX	XX	Best Local Similarity 100.0%; Pred. No. 1.5;		
XX	XX	Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
XX	XX			
XX	XX	Qy 16 QRDMPQ 22		
XX	XX	Db 1 QRDMPQ 7		
XX	XX			
XX	XX	RESULT 42		
XX	XX	AAU83325		
XX	XX	ID AAU83325 standard; Peptide; 14 AA.		
XX	XX	AC AAU83325;		
XX	XX			
XX	XX	23-APR-2002 (first entry)		
XX	XX			
XX	XX	Antiviral composition peptide-A, fragment #43.		
XX	XX			
XX	XX	Virucide; Immunostimulant; interleukin-8; viral infection;		
XX	XX	monocyte chemotactic protein 1; immune system.		

```

XX  New peptides compositions, useful for treating viral infections and
PT  stimulating the immune system -
XX
XX  Disclosure; Page 8; 37pp; English.
XX
XX  The invention relates to a new peptide composition comprising a specified
CC  peptide sequence. The composition comprises nucleotide-peptide comprising
CC  a peptide linked through a serine residue and diphosphodiester to a
CC  nucleotide; or peptides with about 31 amino acid residues capable of
CC  stimulating production of interleukin-8 in cultured cells; or peptides
CC  with about 31 amino acid residues capable of stimulating production of
CC  monocyte chemoattractant protein 1 in cultured cells. The peptides are useful
CC  for treating viral infections and stimulating the immune system.
CC  AAU93282-AAU83401 represent peptides used in the composition of the
CC  invention.
XX
SQ  Sequence 14 AA;
    Query Match      31.8%; Score 7; DB 23; Length 14;
    Best Local Similarity 100.0%; Pred. No. 1.6;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  16 QRDMPIQ 22
    |||||
    4 QRDMPIQ 10

Db
RESULT 44
AAR95892
ID  AAR95892 standard; peptide; 6 AA.
XX
AC  AAR95892;
XX
DT  18-NOV-1996 (first entry)
XX
DE  Angiotensin converting enzyme inhibitor #2.
XX
KW  Angiotensin converting enzyme; inhibitor; ACE; hypotensive; health food;
KW  animal milk; drug; proteinase; carboxypeptidase.
XX
OS  Synthetic.
XX
PN  JP08099994-A.
XX
PD  16-APR-1996.
XX
PF  28-APR-1995; 95JP-0105262.
XX
PR  02-AUG-1994; 94JP-0181653.
XX
PA  (CALV ) CALPIS SHOKUHIN KOGYO KK.
XX
DR  WPI; 1996-246958/25.
XX
PT  New ACE-inhibiting peptide derived from animal milk - useful as
PT  hypotensive drug or health food component
XX
PS  Claim 1; Page 6; 7pp; Japanese.
XX
DE  Angiotensin converting enzyme inhibitor #2.
XX
KW  Angiotensin converting enzyme; inhibitor; ACE; hypotensive; health food;
KW  animal milk; drug; proteinase; carboxypeptidase.
XX
OS  Synthetic.
XX
PN  JP08099994-A.
XX
PD  16-APR-1996.
XX
PF  28-APR-1995; 95JP-0105262.
XX
PR  02-AUG-1994; 94JP-0181653.
XX
PA  (CALV ) CALPIS SHOKUHIN KOGYO KK.
XX
DR  WPI; 1996-246958/25.
XX
PT  New ACE-inhibiting peptide derived from animal milk - useful as
PT  hypotensive drug or health food component
XX
PS  Claim 1; Page 6; 7pp; Japanese.
XX
CC  AAR95891 and AAR95892 represent angiotensin converting enzyme (ACE)
CC  inhibitors. These sequences have hypotensive activity, and can be used
CC  in drugs and health foods. These sequences are prepared by treating
CC  animal milk with a proteinase and then a carboxypeptidase. These
CC  peptides are highly safe, and can be easily prepared at low cost.
XX
SQ  Sequence 6 AA;
    Query Match      27.3%; Score 6; DB 17; Length 6;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 KVLFPV 10
    |||||
    2 KVLFPV 7

Db
RESULT 46
AAR58331
ID  AAR58331 standard; peptide; 8 AA.
XX
AC  AAR58331;
XX
DT  22-SEP-1994 (first entry)
XX
DE  Hypotensive polypeptide.
XX
KW  Hypotensive; antioxidant; calcium absorption; salt; food;
KW  pharmaceuticals; physiologically active agents.
XX
OS  Lactobacillus helveticus.
XX
PN  JP06041191-A.
XX
PD  15-FEB-1994.
XX
PF  03-MAR-1993; 93JP-0043047.

```

```

Db      1 KVLFPV 6
      |||||
RESULT 45
AAR95891
ID  AAR95891 standard; peptide; 7 AA.
XX
AC  AAR95891;
XX
DT  18-NOV-1996 (first entry)
XX
DE  Angiotensin converting enzyme inhibitor #1.
XX
KW  Angiotensin converting enzyme; inhibitor; ACE; hypotensive; health food;
KW  animal milk; drug; proteinase; carboxypeptidase.
XX
OS  Synthetic.
XX
PN  JP08099994-A.
XX
PD  16-APR-1996.
XX
PF  28-APR-1995; 95JP-0105262.
XX
PR  02-AUG-1994; 94JP-0181653.
XX
PA  (CALV ) CALPIS SHOKUHIN KOGYO KK.
XX
DR  WPI; 1996-246958/25.
XX
PT  New ACE-inhibiting peptide derived from animal milk - useful as
PT  hypotensive drug or health food component
XX
PS  Claim 1; Page 6; 7pp; Japanese.
XX
CC  AAR95891 and AAR95892 represent angiotensin converting enzyme (ACE)
CC  inhibitors. These sequences have hypotensive activity, and can be used
CC  in drugs and health foods. These sequences are prepared by treating
CC  animal milk with a proteinase and then a carboxypeptidase. These
CC  peptides are highly safe, and can be easily prepared at low cost.
XX
SQ  Sequence 7 AA;
    Query Match      27.3%; Score 6; DB 17; Length 7;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 KVLFPV 10
    |||||
    2 KVLFPV 7

Db
RESULT 46
AAR58331
ID  AAR58331 standard; peptide; 8 AA.
XX
AC  AAR58331;
XX
DT  22-SEP-1994 (first entry)
XX
DE  Hypotensive polypeptide.
XX
KW  Hypotensive; antioxidant; calcium absorption; salt; food;
KW  pharmaceuticals; physiologically active agents.
XX
OS  Lactobacillus helveticus.
XX
PN  JP06041191-A.
XX
PD  15-FEB-1994.
XX
PF  03-MAR-1993; 93JP-0043047.

```

```

XX PR 04-MAR-1992; 92JP-0047340.
XX PA (CALV ) CALPIS SHOKUHIN KOGYO KK.
XX DR WPI; 1994-089332/11.
XX
XX New polypeptide - used in physiologically active agents having
XX PT e.g. hypotensive antioxidative and calcium absorption promoting
XX PT activity
XX
XX PS Claim 1-2; Page 8; 10pp; Japanese.
XX
XX Sequences (AAR58319-341) are used in conjunction with
XX CC physiologically active agents showing a property such as
XX CC hypotensive activity, calcium absorption promoting activity and
XX CC antioxidative activity. The peptides are non-toxic and can be
XX CC used in physiologically active agents.
XX
XX SQ Sequence 8 AA;
XX
XX Query Match 27.3%; Score 6; DB 15; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 5 KVLFPV 10
XX DB 2 KVLFPV 7
XX
XX RESULT 47
XX AAR58338
XX ID AAR58338 standard; peptide; 8 AA.
XX AC AAR58338;
XX
XX DT 22-SEP-1994 (first entry)
XX DE Hypotensive polypeptide.
XX
XX KW Hypotensive; antioxidative; calcium absorption; salt; food;
XX KW pharmaceuticals; physiologically active agents.
XX
XX OS Lactobacillus helveticus.
XX
XX PN JP06041191-A.
XX PD 15-FEB-1994.
XX PF 03-MAR-1993; 93JP-0043047.
XX PR 04-MAR-1992; 92JP-0047340.
XX
XX PA (CALV ) CALPIS SHOKUHIN KOGYO KK.
XX DR WPI; 1994-089332/11.
XX
XX New polypeptide - used in physiologically active agents having
XX PT e.g. hypotensive antioxidative and calcium absorption promoting
XX PT activity
XX
XX PS Claim 1-2; Page 9; 10pp; Japanese.
XX
XX Sequences (AAR58319-341) are used in conjunction with
XX CC physiologically active agents showing a property such as
XX CC hypotensive activity, calcium absorption promoting activity and
XX CC antioxidative activity. The peptides are non-toxic and can be
XX CC used in physiologically active agents.
XX
XX SQ Sequence 8 AA;
XX
XX Query Match 27.3%; Score 6; DB 15; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;

```

```

XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 17 RDWPIQ 22
XX DB 1 RDWPIQ 6
XX
XX RESULT 48
XX AAU83288
XX ID AAU83288 standard; Peptide; 9 AA.
XX AC AAU83288;
XX
XX DT 23-APR-2002 (first entry)
XX DE Antiviral composition peptide-A, fragment #6.
XX KW Virucide; immunostimulant; interleukin-8; viral infection;
XX KW monocyte chemotactic protein 1; immune system.
XX
XX OS Synthetic.
XX
XX PN US2002004579-A1.
XX PD 10-JAN-2002.
XX
XX PF 17-JAN-2001; 2001US-0764017.
XX PR 22-OCT-1996; 96US-0735236.
XX PR 25-JUN-1999; 99US-0344095.
XX
XX PA (ADVI-) ADVANCED VIRAL RES CORP.
XX
XX PI Friedland B, Hirschman SZ, Taraporewala IB;
XX DR WPI; 2002-163727/21.
XX
XX PT New peptides compositions, useful for treating viral infections and
XX PT stimulating the immune system -
XX
XX PS Disclosure; Page 7; 37pp; English.
XX
XX CC The invention relates to a new peptide composition comprising a specified
XX CC peptide sequence. The composition comprises nucleotide-peptide comprising
XX CC a peptide linked through a serine residue and diphosphodiester to a
XX CC nucleotide; or peptides with about 31 amino acid residues capable of
XX CC stimulating production of interleukin-8 in cultured cells; or peptides
XX CC with about 31 amino acid residues capable of stimulating production of
XX CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
XX CC for treating viral infections and stimulating the immune system.
XX CC AAU83282-AAU83401 represent peptides used in the composition of the
XX CC invention.
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 27.3%; Score 6; DB 23; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 10 PQKAVP 15
XX DB 1 PQKAVP 6
XX
XX RESULT 49
XX AAU83289
XX ID AAU83289 standard; Peptide; 9 AA.
XX AC AAU83289;
XX
XX DT 23-APR-2002 (first entry)
XX DE Antiviral composition peptide-A, fragment #7.

```

```

XX Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX Synthetic.
XX US2002004579-A1.
XX 10-JAN-2002.
XX 17-JAN-2001; 2001US-0764017.
XX 22-OCT-1996; 96US-0735236.
XX 25-JUN-1999; 99US-0344095.
XX (ADVI-) ADVANCED VIRAL RES CORP.
XX Friedland B, Hirschman SZ, Taraporewala IB;
XX WPI; 2002-163727/21.
XX New peptides compositions, useful for treating viral infections and
XX stimulating the immune system -
XX Disclosure; Page 7; 37pp; English.
XX The invention relates to a new peptide composition comprising a specified
XX peptide sequence. The composition comprises nucleotide-peptide comprising
XX a peptide linked through a serine residue and diphosphodiester to a
XX nucleotide; or peptides with about 31 amino acid residues capable of
XX stimulating production of interleukin-8 in cultured cells; or peptides
XX with about 31 amino acid residues capable of stimulating production of
XX monocyte chemotactic protein 1 in cultured cells. The peptides are useful
XX for treating viral infections and stimulating the immune system.
XX AAU83282-AAU83401 represent peptides used in the composition of the
XX invention.
XX Sequence 9 AA;
XX Query Match 27.3%; Score 6; DB 23; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 10 POKAVP 15
XX Db 1 POKAVP 6
XX RESULT 50
XX AAU83293
XX ID AAU83293 standard; Peptide; 10 AA.
XX AC AAU83293;
XX 23-APR-2002 (first entry)
XX Antiviral composition peptide-A, fragment #11.
XX Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX Synthetic.
XX US2002004579-A1.
XX 10-JAN-2002.
XX 17-JAN-2001; 2001US-0764017.
XX 22-OCT-1996; 96US-0735236.
XX 25-JUN-1999; 99US-0344095.
XX (ADVI-) ADVANCED VIRAL RES CORP.
XX Friedland B, Hirschman SZ, Taraporewala IB;
XX WPI; 2002-163727/21.
XX New peptides compositions, useful for treating viral infections and
XX stimulating the immune system -
XX Disclosure; Page 7; 37pp; English.
XX The invention relates to a new peptide composition comprising a specified
XX peptide sequence. The composition comprises nucleotide-peptide comprising
XX a peptide linked through a serine residue and diphosphodiester to a
XX nucleotide; or peptides with about 31 amino acid residues capable of
XX stimulating production of interleukin-8 in cultured cells; or peptides
XX with about 31 amino acid residues capable of stimulating production of
XX monocyte chemotactic protein 1 in cultured cells. The peptides are useful
XX for treating viral infections and stimulating the immune system.
XX AAU83282-AAU83401 represent peptides used in the composition of the
XX invention.
XX Sequence 10 AA;
XX Query Match 27.3%; Score 6; DB 23; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 12;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 10 POKAVP 15
XX Db 1 POKAVP 6
XX RESULT 51
XX AAU83294
XX ID AAU83294 standard; Peptide; 10 AA.
XX AC AAU83294;
XX 23-APR-2002 (first entry)
XX Antiviral composition peptide-A, fragment #12.
XX Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX Synthetic.
XX US2002004579-A1.
XX 10-JAN-2002.
XX 17-JAN-2001; 2001US-0764017.
XX 22-OCT-1996; 96US-0735236.
XX 25-JUN-1999; 99US-0344095.
XX (ADVI-) ADVANCED VIRAL RES CORP.
XX Friedland B, Hirschman SZ, Taraporewala IB;
XX WPI; 2002-163727/21.
XX New peptides compositions, useful for treating viral infections and
XX stimulating the immune system -
XX Disclosure; Page 7; 37pp; English.
XX The invention relates to a new peptide composition comprising a specified
XX peptide sequence. The composition comprises nucleotide-peptide comprising
XX a peptide linked through a serine residue and diphosphodiester to a
XX nucleotide; or peptides with about 31 amino acid residues capable of
XX stimulating production of interleukin-8 in cultured cells; or peptides
XX with about 31 amino acid residues capable of stimulating production of
XX monocyte chemotactic protein 1 in cultured cells. The peptides are useful
XX for treating viral infections and stimulating the immune system.
XX AAU83282-AAU83401 represent peptides used in the composition of the
XX invention.
XX Sequence 10 AA;
XX Query Match 27.3%; Score 6; DB 23; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 12;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 10 POKAVP 15
XX Db 1 POKAVP 6
XX RESULT 51
XX AAU83294
XX ID AAU83294 standard; Peptide; 10 AA.
XX AC AAU83294;
XX 23-APR-2002 (first entry)
XX Antiviral composition peptide-A, fragment #12.
XX Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX Synthetic.
XX US2002004579-A1.
XX 10-JAN-2002.
XX 17-JAN-2001; 2001US-0764017.
XX 22-OCT-1996; 96US-0735236.
XX 25-JUN-1999; 99US-0344095.
XX (ADVI-) ADVANCED VIRAL RES CORP.
XX Friedland B, Hirschman SZ, Taraporewala IB;
XX WPI; 2002-163727/21.
XX New peptides compositions, useful for treating viral infections and
XX stimulating the immune system -
XX Disclosure; Page 7; 37pp; English.
XX The invention relates to a new peptide composition comprising a specified
XX peptide sequence. The composition comprises nucleotide-peptide comprising
XX a peptide linked through a serine residue and diphosphodiester to a
XX nucleotide; or peptides with about 31 amino acid residues capable of
XX stimulating production of interleukin-8 in cultured cells; or peptides
XX with about 31 amino acid residues capable of stimulating production of
XX monocyte chemotactic protein 1 in cultured cells. The peptides are useful
XX for treating viral infections and stimulating the immune system.
XX AAU83282-AAU83401 represent peptides used in the composition of the
XX invention.

```


CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.

SQ Sequence 10 AA;

Query Match 27.3%; Score 6; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PQKAVP 15
 |||||
 Db 1 PQKAVP 6

RESULT 52
 AAU83296
 ID AAU83296 standard; Peptide; 11 AA.

XX AC AAU83296;

XX 23-APR-2002 (first entry)

XX Antiviral composition peptide-A, fragment #14.

KW Viricide; Immunosimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.

XX Synthetic.

XX US2002004579-A1.

XX 10-JAN-2002.

XX 17-JAN-2001; 2001US-0764017.

XX 22-OCT-1996; 96US-0735236.

XX 25-JUN-1999; 99US-0344095.

XX (ADVI-) ADVANCED VIRAL RES CORP.

XX Friedland B, Hirschman SZ, Taraporewala IB;

XX WPI; 2002-163727/21.

XX New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -

XX Disclosure; Page 7; 37pp; English.

XX The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.

XX Sequence 11 AA;

Query Match 27.3%; Score 6; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PQKAVP 15
 |||||
 Db 1 PQKAVP 6

RESULT 53
 AAR80311
 ID AAR80311 standard; peptide; 14 AA.

XX AC AAR80311;

XX 17-APR-1996 (first entry)

XX Bovine casein isopeptide substrate consensus sequence.

KW Pendant group; repeating unit; enzyme recognition site; sealant; elastin;
 KW enzymatic cross-linking; biocompatible material; structural integrity;
 KW medical adhesive; wound closure; tissue repair.

XX Synthetic.

XX WO9523611-A1.

XX 08-SEP-1995.

XX 03-MAR-1995; 95WO-US02728.

XX 03-MAR-1994; 94US-0205518.

XX (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

XX Cappello J;

XX WPI; 1995-320413/41.

XX Protein polymers comprising repeating units and sequences - capable
 PT of enzyme-catalysed covalent bond formation useful as a
 PT biocompatible material for wound closure and tissue repair

XX Disclosure; Page 16; 138pp; English.

XX The sequence of the isopeptide substrate motif from bovine casein. The
 CC sequence corresponds to residues 162-175 of the protein. The motif can
 CC be used in a novel polymer comprising two spaced enzyme recognition site
 CC and may contain repetitive units of 3-8 amino acids with at least two
 CC pendant groups. The polymers contg. the multimeric repeat sequence can
 CC be used as substrates for enzymatic cross-linking. The polymers can be
 CC used in biological systems where in situ formation of a biocompatible
 CC material with structural integrity is required e.g. as medical adhesives
 CC and sealants or for wound closure or tissue repair.

XX Sequence 14 AA;

Query Match 27.3%; Score 6; DB 16; Length 14;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLVPV 10
 |||||
 Db 8 KVLVPV 13

RESULT 54
 AAR80314
 ID AAR80314 standard; peptide; 14 AA.

XX AC AAR80314;

XX 17-APR-1996 (first entry)

XX Synthetic peptide contg. Factor VIIIa cross-linking sequence.

KW Pendant group; repeating unit; enzyme recognition site; sealant; elastin;
 KW enzymatic cross-linking; biocompatible material; structural integrity;
 KW medical adhesive; wound closure; tissue repair.

XX Synthetic.

```

PN WO9523611-A1.
XX
PD 08-SEP-1995.
XX
PF 03-MAR-1995; 95WO-US02728.
XX
PR 03-MAR-1994; 94US-0205518.
XX
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX
PI Cappello J;
XX
DR WPI; 1995-320413/41.
XX
XX Protein polymers comprising repeating units and sequences - capable
PT of enzyme-catalysed covalent bond formation useful as a
PT biocompatible material for wound closure and tissue repair
XX
PS Example 2; Page 33; 138pp; English.
XX
XX The sequence of a synthetic peptide corresponding to the bovine B-casein
CC residues 162-175. The sequence is known to be a Factor VIIIa
CC cross-linking substrate. The motif can be used in a novel polymer
CC comprising two spaced enzyme-recognition site and may contain repetitive
CC units of 3-8 amino acids with at least two pendent groups. The polymers
CC contg. the multimeric repeat sequence can be used as substrates for
CC enzymatic cross-linking. The polymers can be used in biological systems
CC where in situ formation of a biocompatible material with structural
CC integrity is required e.g. as medical adhesives and sealants or for wound
CC closure or tissue repair.
XX
SQ Sequence 14 AA;

Query Match 27.3%; Score 6; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVPV 10
DB |||||
8 KVLVPV 13

RESULT 55
AAW49705
ID AAW49705 standard; Peptide; 14 AA.
XX
AC AAW49705;
XX
DT 25-MAR-2003 (updated)
DT 12-OCT-1998 (first entry)
XX
XX Casein consensus for enzyme-catalysed isopeptide formation.
DE Protein polymer; cross-linking; casein; adhesive; sealant;
KW wound healing.
XX
XX Bos taurus.
OS
XX US5773577-A.
XX
PD 30-JUN-1998.
XX
PF 02-MAR-1995; 95US-0397633.
XX
PR 02-MAR-1995; 95US-0397633.
PR 03-MAR-1994; 94US-0205518.
XX
XX (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
PA
XX Cappello J;
PI
XX
DR WPI; 1998-387091/33.
XX

New recombinant protein polymers - containing naturally occurring
repetitive units for crosslinking by enzymes, useful as medical
adhesives and sealants, depots and matrices

Disclosure; Column 9; 70pp; English.

This peptide comprises a bovine casein consensus sequence (amino
acid residues 162-175) for enzyme-catalysed isopeptide formation.
A claimed recombinant protein polymer of 15-250 kDa comprises a
repetitive amino acid backbone of repetitive units having a
collagen, fibroin, elastin or keratin motif and at least 2 enzyme
recognition sequences comprising a glutamine capable of
enzyme-catalysed isopeptide formation. Such polymers are capable of
sequence of at least 25 amino acids. Such polymers are capable of
covalent crosslinking by enzymatic reaction to form products which
set quickly and have good adhesive properties and high strength.
The compositions can be used as medical adhesives and sealants, in
the closure of wounds and repair of damaged tissues, prostheses,
coatings, drug depots, and matrices for the transplantation of
cells. They can also be used in assays for analytes.
(CC Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 14 AA;

Query Match 27.3%; Score 6; DB 19; Length 14;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVPV 10
DB |||||
8 KVLVPV 13

RESULT 56
AAR80352
ID AAR80352 standard; peptide; 15 AA.
XX
AC AAR80352;
XX
DT 19-APR-1996 (first entry)
XX
XX Protein polymeric adhesion substrate glutamine donor peptide #2.
DE
XX Pendent group; repeating unit; enzyme recognition site; sealant; fibrin;
KW enzymatic cross-linking; biocompatible material; structural integrity;
KW medical adhesive; wound closure; tissue repair; transglutaminase;
KW protein polymer adhesive substrate.
XX
XX Synthetic.
OS
XX WO9523611-A1.
XX
PD 08-SEP-1995.
XX
PF 03-MAR-1995; 95WO-US02728.
XX
PR 03-MAR-1994; 94US-0205518.
XX
XX (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
PA
XX Cappello J;
PI
XX WPI; 1995-320413/41.
XX
XX Protein polymers comprising repeating units and sequences - capable
PT of enzyme-catalysed covalent bond formation useful as a
PT biocompatible material for wound closure and tissue repair
XX
XX Example 9; Page 75; 138pp; English.
XX
XX The peptides AAR80351-70 are examples of glutamine donor peptides which
CC can be used to generate protein polymeric adhesion substrate (PPAS)
CC contg. repeats of non-fibrin cross-linking donor peptide sequences (see

```

CC AAR80345-50 for examples of PPAS proteins). The PPAS proteins can be used as substrates in enzymatic cross-linking reactions catalysed by a transglutaminase enzyme e.g. Factor VIII or XIII. The polymers can be used in biological systems where in situ formation of a biocompatible material with structural integrity is required e.g. as medical adhesives and sealants or for wound closure or tissue repair.

XX
SQ Sequence 15 AA;

Query Match 27.3%; Score 6; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVPV 10
|||||

Db 9 KVLVPV 14
|||||

RESULT 57

AAR80355
ID AAR80355 standard; peptide; 15 AA.

XX
AC AAR80355;

XX
DT 19-APR-1996 (first entry)

XX
DE Protein polymeric adhesion substrate glutamine donor peptide #5.

XX
KW Pendant group; repeating unit; enzyme recognition site; sealant; fibrin;
KW enzymatic cross-linking; biocompatible material; structural integrity;
KW medical adhesive; wound closure; tissue repair; transglutaminase;
KW protein polymer adhesive substrate.

XX
OS Synthetic.

XX
PN WO9523611-A1.

XX
PD 08-SEP-1995.

XX
PF 03-MAR-1995; 95WO-US02728.

XX
PR 03-MAR-1994; 94US-0205518.

XX
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

XX
PI Cappello J;

XX
WPI; 1995-320413/41.

XX
PT Protein polymers comprising repeating units and sequences - capable
PT of enzyme-catalysed covalent bond formation useful as a
PT biocompatible material for wound closure and tissue repair

XX
PS Example 9; Page 75; 138pp; English.

XX
CC The peptides AAR80351-70 are examples of glutamine donor peptides which can be used to generate protein polymeric adhesion substrate (PPAS) contg. repeats of non-fibrin cross-linking donor peptide sequences (see AAR80345-50 for examples of PPAS proteins). The PPAS proteins can be used as substrates in enzymatic cross-linking reactions catalysed by a transglutaminase enzyme e.g. Factor VIII or XIII. The polymers can be used in biological systems where in situ formation of a biocompatible material with structural integrity is required e.g. as medical adhesives and sealants or for wound closure or tissue repair.

XX
SQ Sequence 15 AA;

Query Match 27.3%; Score 6; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVPV 10
|||||

Db 9 KVLVPV 14
|||||

RESULT 58

AAW49740
ID AAW49740 standard; Peptide; 15 AA.

XX
AC AAW49740;

XX
DT 25-MAR-2003 (updated)

XX
DT 12-OCT-1998 (first entry)

XX
DE Glutamine donor peptide.

XX
KW Protein polymer; adhesive sealant; wound healing; cross-linking.

XX
OS Synthetic.

XX
PN US5773577-A.

XX
PD 30-JUN-1998.

XX
PF 02-MAR-1995; 95US-0397633.

XX
PR 02-MAR-1995; 95US-0397633.

XX
PR 03-MAR-1994; 94US-0205518.

XX
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

XX
PI Cappello J;

XX
WPI; 1998-387091/33.

XX
PT New recombinant protein polymers - containing naturally occurring repetitive units for crosslinking by enzymes, useful as medical adhesives and sealants, depots and matrices

XX
PS Example 9; Column 48; 70pp; English.

XX
CC This is an example of a glutamine donor peptide that can be utilised in novel recombinant protein polymers of the invention. Such polymers (see AAW49710-28) typically comprise a repetitive amino acid backbone of repetitive units having a collagen, fibroin, elastin or keratin motif and at least 2 enzyme recognition sequences comprising a glutamine and/or lysine capable of enzyme catalysed isopeptide formation. The polymers are capable of covalent crosslinking by enzymatic reaction to form products which set quickly and have good adhesive properties and high strength. They can be used as medical adhesives and sealants, in the closure of wounds and repair of damaged tissues, prosthesis coatings, drug depots, and matrices for the transplantation of cells.

XX
SQ Sequence 15 AA;

Query Match 27.3%; Score 6; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVPV 10
|||||

Db 9 KVLVPV 14
|||||

RESULT 59

AAU83319
ID AAU83319 standard; Peptide; 15 AA.

XX
AC AAU83319;

XX
DT 23-APR-2002 (first entry)

XX
DE Antiviral composition peptide-A, fragment #37.

Query Match 27.3%; Score 6; DB 15; Length 18;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVPV 10
 DB 12 KVLVPV 17

RESULT 62
 AAU83285
 ID AAU83285 standard; Peptide; 8 AA.
 XX
 AC AAU83285;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #3.
 XX
 KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX
 OS Synthetic.
 XX
 PN US2002004579-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX
 PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX
 XX WPI; 2002-163727/21.
 XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 XX Disclosure; Page 7; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 SQ Sequence 8 AA;
 XX

Query Match 22.7%; Score 5; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 DMPIQ 22
 DB 1 DMPIQ 5

RESULT 63
 ABG67718
 ID ABG67718 standard; Peptide; 9 AA.
 XX
 AC ABG67718;
 XX
 DT 07-OCT-2002 (first entry)

Query Match 22.7%; Score 5; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVPQR 17
 DB 5 AVPQR 9

RESULT 64
 AAW25911
 ID AAW25911 standard; peptide; 10 AA.
 XX
 AC AAW25911;
 XX
 DT 04-NOV-1997 (first entry)
 XX
 DE Beta-2-microglobulin cryptic epitope 10 as anti-HIV peptide.
 XX

Query Match 22.7%; Score 5; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVPQR 17
 DB 5 AVPQR 9

RESULT 64
 AAW25911
 ID AAW25911 standard; peptide; 10 AA.
 XX
 AC AAW25911;
 XX
 DT 04-NOV-1997 (first entry)
 XX
 DE Beta-2-microglobulin cryptic epitope 10 as anti-HIV peptide.
 XX

Human ADPI tryptic digest peptide #427.
 Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;
 Alzheimer's disease-associated feature; neuroprotective;
 Alzheimer's disease-associated protein isoform; nootropic;
 ADPI tryptic digest peptide.
 Homo sapiens.
 WO200246767-A2.
 13-JUN-2002.
 29-NOV-2001; 2001WO-GB05289.
 08-DEC-2000; 2000US-254431P.
 (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 Herath HMAC, Parekh RB, Rohlf C;
 WPI; 2002-508575/54.
 Screening, diagnosis or prognosis of Alzheimer's disease in subject,
 comprises detecting Alzheimer's disease-associated features or
 Alzheimer's disease-associated protein isoforms in brain tissue
 from the subject -
 Claim 7; Page 70; 427pp; English.
 The present invention relates to methods and compositions for the
 screening, diagnosis or prognosis of Alzheimer's disease (AD) in
 a subject. The method comprises analysing a sample of brain tissue
 from a subject by 2D electrophoresis to generate a 2D array of
 Alzheimer's disease-associated features (ADFs), whose relative
 abundance correlates with the presence, absence, stage or severity of
 AD and comparing the abundance of each feature with the abundance of
 that chosen feature in brain tissue from persons free from AD. The
 invention also describes Alzheimer's disease-associated protein
 isoforms (ADPIs) detectable in brain tissue. The methods and
 compositions of the invention are useful for the screening, diagnosis
 or prognosis of AD in a subject, for determining the stage or severity
 of AD in a subject, for identifying a subject at risk of developing AD,
 or for monitoring the effect of therapy administered to a subject
 having AD. Antibodies capable of binding to ADPIs are useful for
 treating or preventing AD, and for determining the efficacy of a given
 treatment regime. An agent that modulates the activity of ADPI is
 useful in the manufacture of a medicament for the treatment or
 prevention of AD in a subject. ABG67292-ABG68038 represent human ADPI
 tryptic digest peptides.

KW Beta-2-microglobulin; cryptic; epitope; human immunodeficiency virus;
 KW HIV; multiplication; release; determinant; antigenic; extracellular; CMV;
 KW infectious agent; intracellular stage; host; reproductive cycle; vaccine;
 KW intracellular; parasite; enveloped virus; mutation; cytomegalovirus; HPV.
 XX
 XX
 OS Synthetic.
 PN WO9702344-A2.
 XX
 XX 23-JAN-1997.
 PD
 XX 28-JUN-1996; 96WO-FR01006.
 XX
 XX 30-JUN-1995; 95FR-0007914.
 PR
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA
 XX Chermann J, Galea P, Le Contel C;
 PI
 XX WPI; 1997-108957/10.
 DR
 XX Vaccine against diseases where the pathogen has an intracellular
 PT stage - contains cryptic epitope of component carried with the
 PT pathogen when it migrates out of the cell, esp. for treatment or
 PT prevention of HIV infection
 XX
 XX Claim 4; Page 35; 60pp; French.

XX Peptides AAW25902-23 represent peptides derived from the
 CC beta-2-microglobulin protein which act as cryptic epitopes and are
 CC revealed esp. when HIV multiplies and is released from an infected cell.
 CC The cryptic epitope is preferably on a host cell determinant but only
 CC become antigenic when they are carried extracellularly by the released
 CC infectious agent. The cryptic epitopes are used in a method for the
 CC treatment and/or prevention of infectious diseases caused by an
 CC infectious agent which has at least one intracellular stage in the host
 CC during its reproductive cycle. The method is used to protect against
 CC intracellular parasites or enveloped viruses, particularly where these
 CC are subject to rapid mutation, esp. CMV, HPV or esp. HIV.
 XX
 SQ Sequence 10 AA;

Query Match 22.7%; Score 5; DB 18; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQPK 5
 |||||
 Db 2 LSQPK 6

RESULT 65
 ABB56257
 ID ABB56257 standard; Peptide; 10 AA.

AC ABB56257;

DT 15-FEB-2002 (first entry)

XX Vascular dementia-associated protein isoform (VPI) 457.

DE Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
 KW diagnosis; prognosis; gene therapy.

XX Homo sapiens.

XX WO200169261-A2.

XX 20-SEP-2001.

PF 14-MAR-2001; 2001WO-GB01106.

XX 15-MAR-2000; 2000GB-0006285.

PR 24-NOV-2000; 2000GB-0028734.
 PR 28-NOV-2000; 2000US-0724391.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX
 XX Herath HMAc, Parekh RB, Rohlf C;
 PI
 XX WPI; 2001-557937/62.

XX Screening, diagnosis or prognosis of vascular dementia (VD), useful for
 PT determining stage of VD and monitoring the effect of VD therapy,
 PT comprises analysing body fluid by 2-dimensional electrophoresis for
 PT features correlated with VD -

PS Claim 6; Page 39; 151pp; English.

XX The invention relates to screening, diagnosis or prognosis of Vascular
 CC Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance
 CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
 CC protein isoforms (VPIs) (ABB5801-ABB56295) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for
 CC monitoring the effect of therapy administered to a subject having VD.
 CC Nucleic acids encoding a VPI or inhibiting the function of a VPI are
 CC useful for the treatment of VD and for gene therapy.

SQ Sequence 10 AA;

Query Match 22.7%; Score 5; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQPK 5
 |||||
 Db 6 LSQPK 10

RESULT 66

AAU68209

ID AAU68209 standard; Peptide; 10 AA.

XX AAU68209;

XX 16-JAN-2002 (first entry)

XX Human Breast cancer-associated protein isoform, BPI-39 peptide.

XX Human; Breast cancer-associated protein isoform; breast cancer;
 KW immunogen; cytostatic; BPI; tryptic digest peptide.

XX Homo sapiens.

XX WO200171357-A2.

XX 27-SEP-2001.

XX 20-MAR-2001; 2001WO-GB01219.

XX 20-MAR-2000; 2000GB-0006695.

PR 24-MAR-2000; 2000GB-0007265.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMAc, O'Hare MJ, Page MJ, Parekh RB, Waterfield MD;

XX WPI; 2001-611532/70.

XX Identifying proteins for clinical screening, diagnosis and prognosis of

PT breast cancer, comprises detecting Breast Cancer-Associated Protein
PT Isoforms (BPIs) using two-dimensional electrophoresis -
XX
XX Claim 9; Page 47; 197pp; English.
XX
XX The invention relates to diagnosing, determining the stage or severity,
CC or identifying the risk of a subject developing cancer (especially
CC breast cancer), or monitoring the effect of therapy on a subject with
CC cancer, comprising analysing a test sample using two-dimensional
CC electrophoresis and detecting Breast Cancer-Associated Protein
CC Isoforms (BPIs). The methods disclosed are used for the diagnosis and
CC prognosis of breast cancer, for determining the severity of breast
CC cancer, and for identifying a subject at risk of developing breast
CC cancer, and for identifying the effect of therapy administered to a subject.
CC Antibodies raised against the binding domain of a BPI, the binding domain
CC of a BPI, a nucleic acid encoding a BPI, or a nucleic acid that inhibits
CC the function of a BPI can be incorporated into a pharmaceutical
CC composition for treating or preventing breast cancer. The methods use
CC sensitive and specific biomarkers provide early diagnosis of breast
CC cancer, and the compositions are more potent, specific, and has a more
CC rapid effect with fewer side effects than other prior art methods.
CC The present sequence is a tryptic digest peptide from a BPI of the
CC invention.
XX
XX Sequence 10 AA;
SQ
Query Match 22.7%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LSQPK 5
DB 6 LSQPK 10

RESULT 67
AAU68513
ID AAU68513 standard; Peptide; 10 AA.
XX
XX AAU68513;
AC
XX
DT 16-JAN-2002 (first entry)
XX
XX Human Expression reference protein isoform, ERPI-5 peptide.
XX
XX Human; Breast cancer-associated protein isoform; breast cancer;
KW immunogen; cytostatic; BPI; tryptic digest peptide; ERPI;
KW expression reference protein isoform.
XX
XX Homo sapiens.
OS
XX WO200171357-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 20-MAR-2001; 2001WO-GB01219.
PF
XX
XX 20-MAR-2000; 2000GB-0006695.
PR
XX 24-MAR-2000; 2000GB-0007265.
PR
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA
XX
XX Herath HMAAC, O'Hare MJ, Page MJ, Parekh RB, Waterfield MD;
PI
XX WPI; 2001-611532/70.
DR
XX
XX Identifying proteins for clinical screening, diagnosis and prognosis of
PT breast cancer, comprises detecting Breast Cancer-Associated Protein
PT Isoforms (BPIs) using two-dimensional electrophoresis -
PT
XX Disclosure; Page 59; 197pp; English.
XX
XX The invention relates to diagnosing, determining the stage or severity,
CC

CC or identifying the risk of a subject developing cancer (especially
CC breast cancer), or monitoring the effect of therapy on a subject with
CC cancer, comprising analysing a test sample using two-dimensional
CC electrophoresis and detecting Breast Cancer-Associated Protein
CC Isoforms (BPIs). The methods disclosed are used for the diagnosis and
CC prognosis of breast cancer, for determining the severity of breast
CC cancer, and for identifying a subject at risk of developing breast
CC cancer, and for identifying the effect of therapy administered to a subject.
CC Antibodies raised against the binding domain of a BPI, the binding domain
CC of a BPI, a nucleic acid encoding a BPI, or a nucleic acid that inhibits
CC the function of a BPI can be incorporated into a pharmaceutical
CC composition for treating or preventing breast cancer. The methods use
CC sensitive and specific biomarkers provide early diagnosis of breast
CC cancer, and the compositions are more potent, specific, and has a more
CC rapid effect with fewer side effects than other prior art methods.
CC The present sequence is a tryptic digest peptide from an ERPI (expression
CC reference protein isoform) against which the BPIs of the invention are
CC normalised.
XX
XX Sequence 10 AA;
SQ
Query Match 22.7%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LSQPK 5
DB 6 LSQPK 10

RESULT 68
ABG32209
ID ABG32209 standard; peptide; 10 AA.
XX
XX ABG32209;
AC
XX
DT 05-NOV-2002 (first entry)
XX
XX Sheep colostrin derived peptide #3.
XX
XX Sheep; colostrin; colostrum; cytokine inducer; antigen; dementia;
KW central nervous system disorder; neurological disorder; neurosis;
KW mental disorder; psychosis; neurodegenerative disorder;
KW Alzheimer's disease; motor neuron disease; immune system disorder;
KW acquired immunological deficiency; bacterial infection; viral infection;
KW amyloid plaque; dietary supplement; cachexia; weight loss;
KW senile dementia; Parkinson's disease; emotional disturbance; depression;
KW drug addiction; drug withdrawal.
XX
XX Ovis aries.
OS
XX WO200246211-A2.
PN
XX
XX 13-JUN-2002.
PD
XX
XX 05-DEC-2001; 2001WO-GB05376.
PF
XX
XX 06-DEC-2000; 2000GB-0029777.
PR
XX
XX (REGG-) REGEN THERAPEUTICS PLC.
PA
XX
XX Georgiades JA;
PI
XX
XX WPI; 2002-619016/66.
DR
XX
XX Novel peptides isolated from colostrin polypeptide, useful for
PT treating viral and bacterial infections, disorders of immune system and
PT central nervous system e.g., Alzheimer's disease, dementia, and as food
PT additive -
XX
XX Claim 1; Page 8; 16pp; English.
XX
XX The invention relates to a peptide derived from colostrin (a colostrum

CC protein known to be a cytokine inducer) substantially entirely consists
 CC of the peptide sequences appearing as ABG32207-ABG32223. Also included
 CC are a composition comprising two or more of the peptides in combination
 CC with a carrier, a dietary supplement comprising an orally ingestible
 CC combination of the peptide in combination with a carrier and an antibody
 CC which binds to the peptide, and which is obtainable by using peptide as
 CC an antigen. The peptide is useful as a medicament for treating chronic
 CC disorders of central nervous system e.g., neurological disorders and/or
 CC mental disorders such as psychosis and/or neurosis, dementia,
 CC neurodegenerative disorders such as Alzheimer's disease, motor
 CC neuron disease, chronic disorders of immune system, diseases
 CC with bacterial and viral etiologies, acquired immunological deficiencies,
 CC chronic bacterial, viral infections. The peptide is also useful for
 CC creating diseases characterised by presence of amyloid plaque. The
 CC peptide is also useful as a dietary supplement for babies, small
 CC children, adults who have been subjected to chemotherapy and/or
 CC adults who have suffered from cachexia or weight loss due to chronic
 CC disease. The peptide is also useful for treating senile dementia,
 CC Parkinson's disease, emotional disturbances and depression. The peptides
 CC may also be used as an auxiliary withdrawal treatment for drug addicts,
 CC after a period of detoxification, and in persons dependent on stimulants.
 CC The present sequence is a colostrin derived peptide of the invention.
 XX
 SQ Sequence 10 AA;

Query Match 22.7%; Score 5; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

QY 5 KVLVP 9
 |||||
 Db 6 KVLVP 10

RESULT 69
 ABB84035
 ID ABB84035 standard; peptide; 10 AA.
 XX
 AC ABB84035;
 XX
 DT 21-AUG-2002 (first entry)
 XX
 DE Transglutaminase inhibitory peptide or type #5.
 XX
 KW Transglutaminase inhibitor; Factor XIII inhibitor; XIIIa inhibitor;
 KW ophthalmological; antiinflammatory; antirheumatic; antiarthritic;
 KW thrombolytic; neuroprotective; nootropic; antiseborrheic; dermatological;
 KW cytostatic; anti-HIV; antipsoriatic; cataract; inflammatory disease;
 KW arthritis; thrombosis; Alzheimer's disease; Huntington's chorea;
 KW acne; cancer; HIV infection; psoriasis.
 XX
 OS Unidentified.
 XX
 PN WO200236798-A2.
 XX
 PD 10-MAY-2002.
 XX
 PF 02-NOV-2001; 2001WO-BF12727.
 XX
 PR 03-NOV-2000; 2000DE-1054687.
 XX
 PA (NZYM-) N ZYME BIOTEC GMBH.
 XX
 PI Fuchsbauser H, Pasternack R, Zotzel J;
 XX
 DR WPI; 2002-444364/47.
 XX
 PT New amino acid or peptide derivatives or analogs, are selective
 PT transglutaminase inhibitors useful e.g. for treating cataract,
 PT inflammatory diseases, rheumatoid arthritis, thrombosis, Alzheimer's
 PT disease and cancer -
 XX
 PS Disclosure; Page 13; 44pp; German.

XX This invention describes novel amino acid or peptide derivatives or
 CC analogues (I), containing a modified side-chain (e.g. containing a formyl
 CC group) which are transglutaminase inhibitors and Factor XIII/XIIa
 CC inhibitors. The products of the invention have ophthalmological,
 CC antiinflammatory, antirheumatic, antiarthritic, thrombolytic,
 CC neuroprotective, nootropic, antiseborrheic, dermatological, cytostatic,
 CC anti-HIV and antipsoriatic activity. (I) are transglutaminase inhibitors,
 CC especially inhibitors of crosslinking of proteins or peptides
 CC (specifically fibrin and/or alpha 2-plasmin inhibitor), incorporation of
 CC primary amines in proteins and peptides, hydrolysis of the
 CC gamma-carboxamide group of glutamine residues bound in proteins or
 CC peptides, blood factor XIII/XIIa and mammalian, human, tissue, liver,
 CC brain, eye lens, keratinocyte, epidermal, prostate, plant, parasitic,
 CC and/or bacterial transglutaminases. The products of the invention can be
 CC used for treating cataract, inflammatory diseases, rheumatoid arthritis,
 CC chronic arthritis, thrombosis, Alzheimer's disease, Huntington's chorea,
 CC acne, cancer (by induction of apoptosis), HIV infections and psoriasis.
 CC (I) Are targeted and specific transglutaminase inhibitors, which can
 CC inhibit a specific type of transglutaminase in the human or animal body
 CC without affecting other transglutaminases. ABB84001-ABB84049 represent
 CC transglutaminase inhibitors described in the method of the invention.
 XX
 SQ Sequence 10 AA;

Query Match 22.7%; Score 5; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

QY 5 KVLVP 9
 |||||
 Db 2 KVLVP 6

RESULT 70
 AAU83300
 ID AAU83300 standard; Peptide; 12 AA.
 XX
 AC AAU83300;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #18.
 XX
 KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX
 OS Synthetic.
 XX
 PN US2002004579-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX
 PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX
 DR WPI; 2002-163727/21.
 XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 PS Disclosure; Page 7; 37pp; English.
 XX The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of

CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.

XX Sequence 12 AA;
 SQ

Query Match 22.7%; Score 5; DB 23; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 DMPDQ 22
 |||||
 DB 1 DMPDQ 5

RESULT 71
 AAM98483
 ID AAM98483 standard; Peptide; 13 AA.

AC AAM98483;

DT 24-JAN-2002 (first entry)

DE Human peptide #1758 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -

PS Disclosure; Page 4053; 4143pp; English.

XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus

CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms.

XX Sequence 13 AA;

Query Match 22.7%; Score 5; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 KAVPQ 16
 |||||

DB 6 KAVPQ 10

RESULT 72
 AAM98484
 ID AAM98484 standard; Peptide; 13 AA.

AC AAM98484;

DT 24-JAN-2002 (first entry)

DE Human peptide #1759 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -

PS Disclosure; Page 4053; 4143pp; English.

XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms.

```

XX SQ Sequence 13 AA;
Query Match 22.7%; Score 5; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAVPQ 16
   |||||
DB 6 KAVPQ 10

RESULT 73
AAU83309
ID AAU83309 standard; Peptide; 13 AA.
XX AC AAU83309;
XX DT 23-APR-2002 (first entry)
XX DE Antiviral composition peptide-A, fragment #27.
XX KW Virucide; Immunostimulant; interleukin-8; viral infection;
XX KW monocyte chemotactic protein 1; immune system.
XX OS Synthetic.
XX FN US2002004579-A1.
XX PD 10-JAN-2002.
XX PF 17-JAN-2001; 2001US-0764017.
XX PR 22-OCT-1996; 96US-0735236.
XX PR 25-JUN-1999; 99US-0344095.
XX PA (ADVI-) ADVANCED VIRAL RES CORP.
XX PI Friedland B, Hirschman SZ, Taraporewala IB;
XX WPI; 2002-163727/21.
XX DT New peptides compositions, useful for treating viral infections and
PT stimulating the immune system -
XX Disclosure; Page 7; 37pp; English.
XX CC The invention relates to a new peptide composition comprising a specified
CC peptide sequence. The composition comprises nucleotide-peptide comprising
CC a peptide linked through a serine residue and diphenylphosphine to a
CC nucleotide; or peptides with about 31 amino acid residues capable of
CC stimulating production of interleukin-8 in cultured cells; or peptides
CC with about 31 amino acid residues capable of stimulating production of
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC for treating viral infections and stimulating the immune system.
CC AAU83282-AAU83401 represent peptides used in the composition of the
CC invention.
XX SQ Sequence 13 AA;
Query Match 22.7%; Score 5; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 DMPIQ 22
   |||||
DB 1 DMPIQ 5

RESULT 74
AAW49741
ID AAW49741 standard; Peptide; 14 AA.
XX

```

```

AC AAW49741;
XX DT 25-MAR-2003 (updated)
XX DT 12-OCT-1998 (first entry)
XX DE Glutamine donor peptide.
XX KW Protein polymer; adhesive sealant; wound healing; cross-linking.
XX OS Synthetic.
XX PN US5773577-A.
XX PD 30-JUN-1998.
XX PF 02-MAR-1995; 95US-0397633.
XX PR 02-MAR-1995; 95US-0397633.
XX PR 03-MAR-1994; 94US-0205518.
XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX PI Cappello J;
XX WPI; 1998-387091/33.
XX PT New recombinant protein polymers - containing naturally occurring
PT repetitive units for crosslinking by enzymes, useful as medical
PT adhesives and sealants, depots and matrices
XX PS Example 9; Column 49; 70pp; English.
XX CC This is an example of a glutamine donor peptide that can be
CC utilised in novel recombinant protein polymers of the invention.
CC Such polymers (see AAW49710-28) typically comprise a repetitive
CC amino acid backbone of repetitive units having a collagen, fibroin,
CC elastin or keratin motif and at least 2 enzyme recognition
CC sequences comprising a glutamine and/or lysine capable of enzyme
CC catalysed isopeptide formation. The polymers are capable of
CC covalent crosslinking by enzymatic reaction to form products which
CC set quickly and have good adhesive properties and high strength.
CC They can be used as medical adhesives and sealants, in the closure
CC of wounds and repair of damaged tissues, prosthesis coatings, drug
CC depots, and matrices for the transplantation of cells.
XX CC (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 14 AA;
Query Match 22.7%; Score 5; DB 19; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPVP 10
   |||||
DB 9 VLPVP 13

RESULT 75
AAU83316
ID AAU83316 standard; Peptide; 14 AA.
XX AC AAU83316;
XX DT 23-APR-2002 (first entry)
XX DE Antiviral composition peptide-A, fragment #34.
XX KW Virucide; Immunostimulant; interleukin-8; viral infection;
XX KW monocyte chemotactic protein 1; immune system.
XX OS Synthetic.
XX PN US2002004579-A1.

```

```

XX 10-JAN-2002.
PD
XX
XX PF 17-JAN-2001; 2001US-0764017.
XX
XX PR 22-OCT-1996; 96US-0735236.
PR 25-JUN-1999; 99US-0344095.
XX
XX (ADVI-) ADVANCED VIRAL RES CORP.
XX
XX Friedland B, Hirschman SZ, Taraporewala IB;
PI WPI; 2002-163727/21.
XX
XX New peptides compositions, useful for treating viral infections and
PT stimulating the immune system -
XX
XX Disclosure; Page 8; 37pp; English.
XX
XX The invention relates to a new peptide composition comprising a specified
CC peptide sequence. The composition comprises nucleotide-peptide comprising
CC a peptide linked through a serine residue and diphosphodiester to a
CC nucleotide; or peptides with about 31 amino acid residues capable of
CC stimulating production of interleukin-8 in cultured cells; or peptides
CC with about 31 amino acid residues capable of stimulating production of
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC for treating viral infections and stimulating the immune system.
CC AAU83282-AAU83401 represent peptides used in the composition of the
CC invention.
XX
XX Sequence 14 AA;
SQ
Query Match 22.7%; Score 5; DB 23; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 DMEIQ 22
Db 1 DMEIQ 5

```

Search completed: November 25, 2003, 19:27:15
 Job time : 57.1512 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 35.3023 Seconds
(without alignments)
114.943 Million cell updates/sec

Title: US-09-641-801-27

Perfect score: 22

Sequence: 1 LSQPKVLPVQKAVPQDRDMPQ 22

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/ECTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	31.8	7	16	US-10-305-346-8
2	5	22.7	10	11	US-09-827-345-10
3	5	22.7	15	8	US-08-927-939-64
4	5	22.7	15	11	US-09-827-345-3
5	5	22.7	16	12	US-10-161-791-195
6	5	22.7	19	12	US-10-280-833-7
7	4	18.2	5	11	US-09-788-006-138
8	4	18.2	5	11	US-09-788-006-140
9	4	18.2	6	10	US-09-865-018-23
10	4	18.2	6	10	US-09-071-838-278
11	4	18.2	6	15	US-10-029-115-15
12	4	18.2	6	15	US-10-213-512-278
13	4	18.2	7	9	US-09-832-723-16
14	4	18.2	7	11	US-09-827-345-5
15	4	18.2	7	11	US-09-827-345-21

4	18.2	7	12	US-10-303-331-16	Sequence 16, Appl
4	18.2	7	12	US-10-386-457-252	Sequence 252, Appl
4	18.2	7	15	US-10-024-123-4	Sequence 4, Appl
4	18.2	7	15	US-10-028-075B-142	Sequence 142, Appl
4	18.2	7	15	US-10-029-206A-142	Sequence 142, Appl
4	18.2	8	15	US-10-028-075B-144	Sequence 144, Appl
4	18.2	8	15	US-10-029-206A-144	Sequence 144, Appl
4	18.2	9	12	US-10-137-867-210	Sequence 210, Appl
4	18.2	9	14	US-10-042-202-49	Sequence 49, Appl
4	18.2	10	9	US-09-220-920-111	Sequence 111, Appl
4	18.2	10	11	US-09-572-404B-1169	Sequence 1169, Appl
4	18.2	10	11	US-09-915-914B-39	Sequence 39, Appl
4	18.2	10	12	US-10-200-708-372	Sequence 372, Appl
4	18.2	10	12	US-09-573-822C-600	Sequence 600, Appl
4	18.2	12	9	US-09-347-084-16	Sequence 16, Appl
4	18.2	12	9	US-09-789-561-163	Sequence 163, Appl
4	18.2	12	10	US-09-911-838-203	Sequence 203, Appl
4	18.2	12	11	US-09-845-612B-3	Sequence 3, Appl
4	18.2	12	11	US-09-954-385-124	Sequence 124, Appl
4	18.2	12	11	US-09-954-385-332	Sequence 332, Appl
4	18.2	12	12	US-10-247-946-3	Sequence 2, Appl
4	18.2	12	12	US-10-251-526-2	Sequence 2, Appl
4	18.2	12	12	US-10-251-526-3	Sequence 3, Appl
4	18.2	12	12	US-10-354-955-5	Sequence 5, Appl
4	18.2	13	12	US-10-224-999A-794	Sequence 794, Appl
4	18.2	13	15	US-10-062-710-34	Sequence 34, Appl
4	18.2	14	12	US-10-125-187-19	Sequence 19, Appl
4	18.2	14	12	US-10-125-187-20	Sequence 20, Appl
4	18.2	14	12	US-10-125-187-21	Sequence 21, Appl
4	18.2	14	12	US-10-125-187-53	Sequence 53, Appl
4	18.2	14	12	US-10-125-187-54	Sequence 54, Appl
4	18.2	14	12	US-10-125-187-55	Sequence 55, Appl
4	18.2	14	12	US-10-224-999A-804	Sequence 804, Appl
4	18.2	14	12	US-10-224-999A-805	Sequence 805, Appl
4	18.2	15	7	US-08-996-140-9	Sequence 9, Appl
4	18.2	15	10	US-09-908-322-59	Sequence 59, Appl
4	18.2	15	10	US-09-764-176-13	Sequence 13, Appl
4	18.2	15	11	US-09-783-931-59	Sequence 59, Appl
4	18.2	15	12	US-10-212-198-15	Sequence 15, Appl
4	18.2	15	12	US-10-349-023-18	Sequence 18, Appl
4	18.2	15	12	US-10-294-891-17	Sequence 17, Appl
4	18.2	15	12	US-10-224-999A-815	Sequence 815, Appl
4	18.2	15	12	US-10-224-999A-816	Sequence 816, Appl
4	18.2	15	12	US-10-224-999A-817	Sequence 817, Appl
4	18.2	15	12	US-10-161-791-306	Sequence 306, Appl
4	18.2	15	15	US-10-126-474A-3	Sequence 3, Appl
4	18.2	15	15	US-10-174-105A-149	Sequence 149, Appl
4	18.2	15	15	US-10-174-105A-175	Sequence 175, Appl
4	18.2	15	15	US-10-281-652-5	Sequence 5, Appl
4	18.2	16	11	US-09-880-748-2228	Sequence 2228, Appl
4	18.2	16	11	US-09-880-748-2334	Sequence 2334, Appl
4	18.2	16	12	US-10-224-999A-827	Sequence 827, Appl
4	18.2	16	12	US-10-224-999A-828	Sequence 828, Appl
4	18.2	16	12	US-10-224-999A-829	Sequence 829, Appl
4	18.2	16	12	US-10-224-999A-830	Sequence 830, Appl
4	18.2	16	12	US-10-006-760-61	Sequence 61, Appl
4	18.2	16	15	US-10-043-487-442	Sequence 442, Appl
4	18.2	17	11	US-09-996-069-30	Sequence 30, Appl
4	18.2	17	11	US-09-996-069-31	Sequence 31, Appl
4	18.2	17	12	US-10-195-730-375	Sequence 375, Appl
4	18.2	17	12	US-10-224-999A-840	Sequence 840, Appl
4	18.2	17	12	US-10-224-999A-842	Sequence 842, Appl
4	18.2	17	12	US-10-224-999A-843	Sequence 843, Appl
4	18.2	17	12	US-10-224-999A-844	Sequence 844, Appl
4	18.2	17	12	US-10-224-999A-845	Sequence 845, Appl
4	18.2	17	12	US-10-029-386-29377	Sequence 29377, A
4	18.2	17	12	US-10-029-386-33100	Sequence 33100, A
4	18.2	17	15	US-10-028-075B-139	Sequence 139, Appl
4	18.2	17	15	US-10-029-206A-139	Sequence 139, Appl
4	18.2	18	9	US-09-864-761-48166	Sequence 48166, A
4	18.2	18	10	US-09-554-000-56	Sequence 56, Appl

Sequence 54, Appl
Sequence 131, App
Sequence 19, Appl
Sequence 20, Appl
Sequence 71, Appl
Sequence 854, App
Sequence 855, App
Sequence 856, App
Sequence 857, App
Sequence 858, App
Sequence 859, App
Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-305-346-8
; Sequence 8, Application US/10305346
; Publication No. US20030130195A1
; GENERAL INFORMATION:
; APPLICANT: AMIOT, Jean
; TITLE OF INVENTION: ENZYMATIC HYDROLYSATE OF MILK PROTEINS
; FILE REFERENCE: 6013-57"US"-1
; CURRENT APPLICATION NUMBER: US/10/305,346
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk proteins
US-10-305-346-8

Query Match 31.8%; Score 7; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPVPQK 12
Db 1 VLPVPQK 7

RESULT 2
US-09-827-345-10
; Sequence 10, Application US/09827345
; Publication No. US20030021800A1
; GENERAL INFORMATION:
; APPLICANT: CHERMANN, JEAN-CLAUDE
; APPLICANT: LE CONTEL, CAROLE
; APPLICANT: GALEA, PASCALE
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING AN
; TITLE OF INVENTION: INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
; TITLE OF INVENTION: DIAGNOSIS
; FILE REFERENCE: 065691-0216
; CURRENT APPLICATION NUMBER: US/09/827,345
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/599,549
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: PCT/FR96/01006
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 08/973,551
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: FR 95/07914
; PRIOR FILING DATE: 1995-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-827-345-10

Query Match 22.7%; Score 5; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQPK 5
Db 2 LSQPK 6

RESULT 3
US-08-927-939-64
; Sequence 64, Application US/08927939
; Publication No. US20010006640A1
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauen Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; TITLE OF INVENTION: augment an inflammatory response.
; FILE REFERENCE: 295-022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-927-939-64

Query Match 22.7%; Score 5; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 POKAV 14
Db 11 POKAV 15

RESULT 4
US-09-827-345-3
; Sequence 3, Application US/09827345
; Publication No. US20030021800A1
; GENERAL INFORMATION:
; APPLICANT: CHERMANN, JEAN-CLAUDE
; APPLICANT: LE CONTEL, CAROLE
; APPLICANT: GALEA, PASCALE
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING AN
; TITLE OF INVENTION: INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
; TITLE OF INVENTION: DIAGNOSIS
; FILE REFERENCE: 065691-0216
; CURRENT APPLICATION NUMBER: US/09/827,345
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/599,549
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: PCT/FR96/01006
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 08/973,551
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: FR 95/07914
; PRIOR FILING DATE: 1995-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3

; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-827-345-3

Query Match 22.7%; Score 5; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQPK 5
|||||
Db 9 LSQPK 13

RESULT 5
US-10-161-791-195
; Sequence 195, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 195:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-195

Query Match 22.7%; Score 5; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVPQR 17
|||||

Db 8 AVPQR 12

RESULT 6

US-10-280-833-7
; Sequence 7, Application US/10280833
; Publication No. US20030195150A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Charles Eric
; APPLICANT: Dasher, Stuart Geoffrey
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Talbo, Gert Hoy
; APPLICANT: Malkoski, Marina
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: BWP-001CON
; CURRENT APPLICATION NUMBER: US/10/280,833
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/554,997
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: PP 0514
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 19
; TYPE: PRT
; ORGANISM: bovine
US-10-280-833-7

Query Match 22.7%; Score 5; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 DMPIQ 22
|||||
Db 1 DMPIQ 5

RESULT 7

US-09-788-006-138
; Sequence 138, Application US/09788006
; Publication No. US20030036093A1
; GENERAL INFORMATION:
; APPLICANT: Floudas, Christopher A.
; APPLICANT: Klepeis, John L.
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets,
; TITLE OF INVENTION: Polypeptide Tertiary Structures
; FILE REFERENCE: PU-0007
; CURRENT APPLICATION NUMBER: US/09/788,006
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 138
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-788-006-138

Query Match 18.2%; Score 4; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
|||||
Db 2 VLPV 5

RESULT 8

US-09-788-006-140
; Sequence 140, Application US/09788006
; Publication No. US20030036093A1
; GENERAL INFORMATION:
; APPLICANT: Floudas, Christopher A.

APPLICANT: Klepeis, John L.
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
; FILE REFERENCE: PU-0007
; CURRENT APPLICATION NUMBER: US/09/788,006
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 140
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-788-006-140

Query Match 18.2%; Score 4; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
Db 1 VLPV 4

RESULT 9
US-09-865-018-23
; Sequence 23, Application US/09865018
; Patent No. US20020110886A1
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; Roberts, James M.
; Koff, Andrew
; Polyak, Kornelia
; TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS
; PRODUCTION AND USE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: POLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,018
; FILING DATE: 24-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,039
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-865-018-23

Query Match 18.2%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4
Db 1 LSQP 4

us-09-641-801-27.oligo.rapb

US-09-071-838-278
; Sequence 278, Application US/09071838
; Patent No. US20020152501A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; NUMBER OF SEQUENCES: 324
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,838
; FILING DATE: 01-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-086100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 278:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-071-838-278

Query Match 18.2%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKVL 7
Db 3 PKVL 6

RESULT 11
US-10-029-115-15
; Sequence 15, Application US/10029115
; Publication No. US20030077597A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Fu, Alan C
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: Methods of Use
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: A-70229/RMS/DHR
; CURRENT APPLICATION NUMBER: US/10/029,115

```
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-115-15

Query Match      18.2%; Score 4; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 VPQR 17
        ||||
Db       3 VPQR 6

RESULT 12
US-10-213-512-278
; Sequence 278, Application US/10213512
; Publication No. US20030110536A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Chad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; FILE REFERENCE: 023070-0861100S
; CURRENT APPLICATION NUMBER: US/10/213,512
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US/09/177,206
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: US 09/071,838
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 278
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-10-213-512-278

Query Match      18.2%; Score 4; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PKVL 7
        ||||
Db       3 PKVL 6

RESULT 13
US-09-832-723-16
; Sequence 16, Application US/09832723
; Patent No. US20020098524A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 117

; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-09-832-723-16

Query Match      18.2%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LSQP 4
        ||||
Db       1 LSQP 4

RESULT 14
US-09-827-345-5
; Sequence 5, Application US/09827345
; Publication No. US20030021800A1
; GENERAL INFORMATION:
; APPLICANT: CHERMANN, JEAN-CLAUDE
; APPLICANT: LE CONTEL, CAROLE
; APPLICANT: GALEA, PASCALE
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING AN
; TITLE OF INVENTION: INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
; TITLE OF INVENTION: DIAGNOSIS
; FILE REFERENCE: 065691-0216
; CURRENT APPLICATION NUMBER: US/09/827,345
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/599,549
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: PCT/FR96/01006
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 08/973,551
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: FR 95/07914
; PRIOR FILING DATE: 1995-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-827-345-5

Query Match      18.2%; Score 4; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 SQPK 5
        ||||
Db       1 SQPK 4

RESULT 15
US-09-827-345-21
; Sequence 21, Application US/09827345
; Publication No. US20030021800A1
; GENERAL INFORMATION:
; APPLICANT: CHERMANN, JEAN-CLAUDE
; APPLICANT: LE CONTEL, CAROLE
; APPLICANT: GALEA, PASCALE
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING AN
; TITLE OF INVENTION: INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
```


; TITLE OF INVENTION: DIAGNOSIS
; FILE REFERENCE: 065691-0216
; CURRENT APPLICATION NUMBER: US/09/827,345
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/599,549
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: PCT/FR96/01006
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 08/973,551
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: FR 95/07914
; PRIOR FILING DATE: 1995-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-827-345-21

Query Match 18.2%; Score 4; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQPK 5
Db 1 SQPK 4

RESULT 16
US-10-303-331-16
; Sequence 16, Application US/10303331
; Publication No. US20030152976A1
; GENERAL INFORMATION:
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Winetasky, Deborah S.
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: G0617-3
; CURRENT APPLICATION NUMBER: US/10/303,331
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 09/832,723
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-10-303-331-16

Query Match 18.2%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSQP 4
Db 1 LSQP 4

RESULT 17
US-10-286-457-252
; Sequence 252, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.

; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 252
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, b.
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-252

Query Match 18.2%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PQKA 13
Db 2 PQKA 5

RESULT 18
US-10-024-123-4
; Sequence 4, Application US/10024123
; Publication No. US2003002263A1
; GENERAL INFORMATION:
; APPLICANT: Kastan, Michael
; APPLICANT: Canman, Christine
; APPLICANT: Kim, Seong-Tae
; APPLICANT: Lim, Dae-Sik
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and
; FILE REFERENCE: 2427/1F142
; CURRENT APPLICATION NUMBER: US/10/024,123
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 09/400,653
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: 09/248,061
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PHOSPHORYLATION
; LOCATION: 4
; OTHER INFORMATION: Xaa at position seven is any amino acid.
US-10-024-123-4

Query Match 18.2%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSQP 4
Db 3 LSQP 6

RESULT 19
US-10-028-075B-142
; Sequence 142, Application US/10028075B
; Publication No. US2003011373A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.

; APPLICANT: Benner, Robert
 ; TITLE OF INVENTION: Gene regulator
 ; FILE REFERENCE: 2183-5223US
 ; CURRENT APPLICATION NUMBER: US/10/028,075B
 ; CURRENT FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: EP 01203748.7
 ; PRIOR FILING DATE: 2001-10-04
 ; NUMBER OF SEQ ID NOS: 175
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 142
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:
 ; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN
 US-10-028-075B-142

Query Match 18.2%; Score 4; DB 15; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;

QY 8 PVPQ 11
 ||||
 Db 4 PVPQ 7

RESULT 20
 US-10-029-206A-142
 ; Sequence 142, Application US/10029206A
 ; Publication No. US20030119720A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Khan, Nisar A.
 ; TITLE OF INVENTION: Oligopeptide treatment of anthrax
 ; FILE REFERENCE: 2183-5222US
 ; CURRENT APPLICATION NUMBER: US/10/029,206A
 ; CURRENT FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: 09/821,380
 ; PRIOR FILING DATE: 2001-03-29
 ; NUMBER OF SEQ ID NOS: 175
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 142
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:
 ; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN
 US-10-029-206A-142

Query Match 18.2%; Score 4; DB 15; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;

QY 8 PVPQ 11
 ||||
 Db 4 PVPQ 7

RESULT 21
 US-10-028-075B-144
 ; Sequence 144, Application US/10028075B
 ; Publication No. US20030113733A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Khan, Nisar A.
 ; TITLE OF INVENTION: Gene regulator
 ; FILE REFERENCE: 2183-5223US
 ; CURRENT APPLICATION NUMBER: US/10/028,075B
 ; CURRENT FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: EP 01203748.7
 ; PRIOR FILING DATE: 2001-10-04

; NUMBER OF SEQ ID NOS: 175
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 144
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:
 ; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN
 US-10-028-075B-144

Query Match 18.2%; Score 4; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;

QY 8 PVPQ 11
 ||||
 Db 5 PVPQ 8

RESULT 22
 US-10-029-206A-144
 ; Sequence 144, Application US/10029206A
 ; Publication No. US20030119720A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Khan, Nisar A.
 ; TITLE OF INVENTION: Oligopeptide treatment of anthrax
 ; FILE REFERENCE: 2183-5222US
 ; CURRENT APPLICATION NUMBER: US/10/029,206A
 ; CURRENT FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: 09/821,380
 ; PRIOR FILING DATE: 2001-03-29
 ; NUMBER OF SEQ ID NOS: 175
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 144
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:
 ; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN
 US-10-029-206A-144

Query Match 18.2%; Score 4; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;

QY 8 PVPQ 11
 ||||
 Db 5 PVPQ 8

RESULT 23
 US-10-137-867-210
 ; Sequence 210, Application US/10137867
 ; Publication No. US20030207349A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K

```
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 210
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-137-867-210

Query Match      18.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 KVLV 8
        ||||
Db      3 KVLV 6

RESULT 24
US-10-042-202-49
; Sequence 49, Application US/10042202
; Publication No. US20020136733A1
; GENERAL INFORMATION:
; APPLICANT: Adrian Vivian Sinton Hill, Michael AIDOO,
; Catherine Elizabeth Margaret ALLSOPP, Ajit LALVANI, Magdalena
; PLESANSKI, Hilton Carter WHITTLE,
; TITLE OF INVENTION: MALARIA PEPTIDES
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDROTH, LIND & PONACK, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800,
; CITY: Washington
; STATE: D.C.,
; COUNTRY: U.S.A.
; ZIP: 20006-1021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordpad for Windows 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/042,202
; FILING DATE: 11-Jan-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/714,175
; FILING DATE: 28-JAN-1997
; APPLICATION NUMBER: WO PCT/GB95/26982
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: GB 9406492.0
; FILING DATE: 31-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER: 2002_0026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)-721-8200
; TELEFAX: (202)-721-8250
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:

US-10-042-202-49
```

```
Query Match      18.2%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PKVL 7
        ||||
Db      6 PKVL 9

RESULT 25
US-09-220-920-111
; Sequence 111, Application US/09220920
; Patent No. US2002002269A1
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Baloh, Robert H.
; TITLE OF INVENTION: Artemin, A No. US2002002269A1el Neurotrophic Factor
; FILE REFERENCE: 6029-7996
; CURRENT APPLICATION NUMBER: US/09/220,920
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-220-920-111

Query Match      18.2%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 VLPV 9
        ||||
Db      2 VLPV 5

RESULT 26
US-09-572-404B-1169
; Sequence 1169, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1169
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in C3AR1 OR C3R1 OR AZ3B OR HNFAG09 at 10-19
; OTHER INFORMATION: interact with Sequence 1170 in this patent.
; US-09-572-404B-1169

Query Match      18.2%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LSQP 4
        ||||
Db      5 LSQP 8
```

RESULT 27
US-09-915-914B-39
; Sequence 39, Application US/09915914B
; Publication No. US20030119725A1
; GENERAL INFORMATION:
; APPLICANT: Divita, Gilles
; APPLICANT: Fernandez, Joseph
; APPLICANT: Heitz, Frederic
; APPLICANT: Morris, May
; APPLICANT: Mery, Jean
; APPLICANT: Archdeacon, John
; APPLICANT: Hornsdor, Kyle
; TITLE OF INVENTION: PEPTIDE-MEDIATED DELIVERY OF MOLECULES INTO CELLS
; FILE REFERENCE: AM-00105.P.1.1
; CURRENT APPLICATION NUMBER: US/09/915,914B
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 60/221,932
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic sequence
US-09-915-914B-39

Query Match 18.2%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPK 5
Db 2 SQPK 5

RESULT 28
US-10-200-708-372
; Sequence 372, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 372
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-372

Query Match 18.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPK 5
Db 5 SQPK 8

RESULT 29
US-09-573-822C-600
; Sequence 600, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: Patent version 1.0
; SEQ ID NO 600
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG458 at 12-21 and may interact with Sequ
US-09-573-822C-600

Query Match 18.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QKAV 14
Db 7 QKAV 10

RESULT 30
US-09-347-064-16
; Sequence 16, Application US/09347064A
; Patent No. US20020045208A1
; GENERAL INFORMATION:
; APPLICANT: Eck, Jurgan
; APPLICANT: Schmidt, Arno
; APPLICANT: Zinke, Holger
; TITLE OF INVENTION: Recombinant Fusion Proteins Based on
; TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
; FILE REFERENCE: 09282-5
; CURRENT APPLICATION NUMBER: US/09/347,064A
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: PCT/EP98/00009
; EARLIER FILING DATE: 1998-01-02
; EARLIER APPLICATION NUMBER: EP 97 10 0012.0
; EARLIER FILING DATE: 1997-01-02
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Fig. 20: amino
; OTHER INFORMATION: acid sequence encoded by portion of SEQ ID NO: 15
US-09-347-064-16

Query Match 18.2%; Score 4; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10
Db 9 LPVP 12

RESULT 31
US-09-789-561-163
; Sequence 163, Application US/09789561
; Patent No. US20020064818A1
; GENERAL INFORMATION:

```
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 52 Human secreted proteins
; FILE REFERENCE: P2043P1
; CURRENT APPLICATION NUMBER: US/09/789,561
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,317
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 163
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-561-163

Query Match      18.2%; Score 4; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PKVL 7
Db      3 PKVL 6

RESULT 32
US-09-911-838-203
; Sequence 203, Application US/09911838
; Patent No. US20020151678A1
; GENERAL INFORMATION:
; APPLICANT: ARLINGHAUS, RALPH
; TITLE OF INVENTION: PROPHYLAXIS AND THERAPY OF ACQUIRED IMMUNODEFICIENCY
; FILE REFERENCE: UTSC-267USCH
; CURRENT APPLICATION NUMBER: US/09/911,838
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 07/834,923
; PRIOR FILING DATE: 1992-02-13
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 203
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-911-838-203

Query Match      18.2%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 PVPQ 11
Db      6 PVPQ 9

RESULT 33
US-09-845-612B-3
; Sequence 3, Application US/09845612B
; Publication No. US20030083261A1
; GENERAL INFORMATION:
; APPLICANT: YU, HONGTAO
; APPLICANT: TANG, ZHANYUN
; APPLICANT: LUO, XUELIAN
; APPLICANT: RIZO-REY, JOSE
; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF THE MITOCHONDRIAL PROTEIN MAD2
; TITLE OF INVENTION: POINT PROTEIN MAD2
; FILE REFERENCE: UTSD:795

; APPLICANT: Ni et al.
; TITLE OF INVENTION: 52 Human secreted proteins
; FILE REFERENCE: P2043P1
; CURRENT APPLICATION NUMBER: US/09/789,561
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,317
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 163
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-561-163

Query Match      18.2%; Score 4; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PKVL 7
Db      3 PKVL 6

RESULT 32
US-09-911-838-203
; Sequence 203, Application US/09911838
; Patent No. US20020151678A1
; GENERAL INFORMATION:
; APPLICANT: ARLINGHAUS, RALPH
; TITLE OF INVENTION: PROPHYLAXIS AND THERAPY OF ACQUIRED IMMUNODEFICIENCY
; FILE REFERENCE: UTSC-267USCH
; CURRENT APPLICATION NUMBER: US/09/911,838
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 07/834,923
; PRIOR FILING DATE: 1992-02-13
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 203
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-911-838-203

Query Match      18.2%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 PVPQ 11
Db      6 PVPQ 9

RESULT 33
US-09-845-612B-3
; Sequence 3, Application US/09845612B
; Publication No. US20030083261A1
; GENERAL INFORMATION:
; APPLICANT: YU, HONGTAO
; APPLICANT: TANG, ZHANYUN
; APPLICANT: LUO, XUELIAN
; APPLICANT: RIZO-REY, JOSE
; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF THE MITOCHONDRIAL PROTEIN MAD2
; TITLE OF INVENTION: POINT PROTEIN MAD2
; FILE REFERENCE: UTSD:795

; CURRENT APPLICATION NUMBER: US/09/845,612B
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(12)
; OTHER INFORMATION: synthetic peptide
US-09-845-612B-3

Query Match      18.2%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 LPVP 10
Db      7 LPVP 10

RESULT 34
US-09-954-385-124
; Sequence 124, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Ruaming
; APPLICANT: Winetzk, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; TITLE OF INVENTION: Complexes
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-124

Query Match      18.2%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 QKAV 14
Db      7 QKAV 10

RESULT 35
US-09-954-385-332
; Sequence 332, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Ruaming
; APPLICANT: Winetzk, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; TITLE OF INVENTION: Complexes
```

```

; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 332
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-332

Query Match      18.2%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 LPVP 10
      ||||
Db      9 LPVP 12

RESULT 36
US-10-247-946-2
; Sequence 2, Application US/10247946
; Publication No. US20030144485A1
; GENERAL INFORMATION:
; APPLICANT: Rodman, Toby C.
; TITLE OF INVENTION: Monoclonal Human Natural Antibodies
; FILE REFERENCE: 4436/1C074-US1
; CURRENT APPLICATION NUMBER: US/10/247,946
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/462,118
; PRIOR FILING DATE: 1999-12-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human
US-10-247-946-2

Query Match      18.2%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SQPK 5
      ||||
Db      9 SQPK 12

RESULT 37
US-10-247-946-3
; Sequence 3, Application US/10247946
; Publication No. US20030144485A1
; GENERAL INFORMATION:
; APPLICANT: Rodman, Toby C.
; TITLE OF INVENTION: Monoclonal Human Natural Antibodies
; FILE REFERENCE: 4436/1C074-US1
; CURRENT APPLICATION NUMBER: US/10/247,946
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/462,118
; PRIOR FILING DATE: 1999-12-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human
US-10-247-946-3

Query Match      18.2%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SQPK 5
      ||||
Db      9 SQPK 12

RESULT 38
US-10-251-526-2
; Sequence 2, Application US/10251526
; Publication No. US20030144486A1
; GENERAL INFORMATION:
; APPLICANT: Rodman, Toby C.
; TITLE OF INVENTION: Monoclonal Human Natural Antibodies
; FILE REFERENCE: 4436/1C074-US1
; CURRENT APPLICATION NUMBER: US/10/251,526
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/462,118
; PRIOR FILING DATE: 1999-12-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human
US-10-251-526-2

Query Match      18.2%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SQPK 5
      ||||
Db      9 SQPK 12

RESULT 39
US-10-251-526-3
; Sequence 3, Application US/10251526
; Publication No. US20030144486A1
; GENERAL INFORMATION:
; APPLICANT: Rodman, Toby C.
; TITLE OF INVENTION: Monoclonal Human Natural Antibodies
; FILE REFERENCE: 4436/1C074-US1
; CURRENT APPLICATION NUMBER: US/10/251,526
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/462,118
; PRIOR FILING DATE: 1999-12-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human
US-10-251-526-3

Query Match      18.2%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SQPK 5
      ||||
Db      2 SQPK 5

RESULT 40
US-10-354-955-5
; Sequence 5, Application US/10354955
; Publication No. US20030171291A1
; GENERAL INFORMATION:
; APPLICANT: Gary Christie
; APPLICANT: Ishrut Hussain
; APPLICANT: David J. Powell

```

; TITLE OF INVENTION: No. US20030171291A1el Treatment
; FILE REFERENCE: P32448
; CURRENT APPLICATION NUMBER: US/10/354,955
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: 09/693,744
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 9925136.5
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bovine
US-10-354-955-5

Query Match 18.2%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVP 8
Db 7 KVLVP 10

RESULT 41
US-10-224-999A-794
; Sequence 794, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: S004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 794
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-224-999A-794

Query Match 18.2%; Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4
Db 10 LSQP 13

RESULT 42
US-10-062-710-34
; Sequence 34, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08

; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV Helper-T Cell Epitopes
US-10-062-710-34

Query Match 18.2%; Score 4; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVPQ 11
Db 7 PVPQ 10

RESULT 43
US-10-125-187-19
; Sequence 19, Application US/10125187
; Publication No. US20030162229A1
; GENERAL INFORMATION:
; APPLICANT: MILNE-ROBERTSON, David M.
; APPLICANT: STANTON, Peter G.
; APPLICANT: CAHIR, Nicholas F.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR DEVELOPMENT OF DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: METHODS OF USING SAME
; FILE REFERENCE: 10338-9
; CURRENT APPLICATION NUMBER: US/10/125,187
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: PCT/AU00/01248
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: AU PQ 9162
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: AU PQ 3485
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: inhibit alpha C amino acid sequence corresponding to peptide
; OTHER INFORMATION: f TABLE 1
US-10-125-187-19

Query Match 18.2%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10
Db 9 LPVP 12

RESULT 44
US-10-125-187-20
; Sequence 20, Application US/10125187
; Publication No. US20030162229A1
; GENERAL INFORMATION:
; APPLICANT: MILNE-ROBERTSON, David M.
; APPLICANT: STANTON, Peter G.
; APPLICANT: CAHIR, Nicholas F.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR DEVELOPMENT OF DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: METHODS OF USING SAME
; FILE REFERENCE: 10338-9
; CURRENT APPLICATION NUMBER: US/10/125,187
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: PCT/AU00/01248
; PRIOR FILING DATE: 2000-10-18

```

; PRIOR APPLICATION NUMBER: AU PQ 9162
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: AU PQ 3485
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: inhibit alpha C amino acid sequence corresponding to peptide 20
; OTHER INFORMATION: f TABLE 1
US-10-125-187-20

```

```

Query Match      18.2%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 LPVP 10
        ||||
Db      5 LPVP 8

```

```

RESULT 45
US-10-125-187-21
; Sequence 21, Application US/10125187
; Publication No. US20030162229A1
; GENERAL INFORMATION:
; APPLICANT: MILNE-ROBERTSON, David M.
; APPLICANT: STANTON, Peter G.
; APPLICANT: CAHIR, Nicholas F.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR DEVELOPMENT OF DIAGNOSTIC AND THERAPEUTIC AGENTS
; TITLE OF INVENTION: METHODS OF USING SAME
; FILE REFERENCE: 10338-9
; CURRENT APPLICATION NUMBER: US/10/125.187
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: PCT/AU00/01248
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: AU PQ 9162
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: AU PQ 3485
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: inhibit alpha C amino acid sequence corresponding to peptide 21
; OTHER INFORMATION: f TABLE 1
US-10-125-187-21

```

```

Query Match      18.2%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 LPVP 10
        ||||
Db      1 LPVP 4

```

```

RESULT 46
US-10-125-187-53
; Sequence 53, Application US/10125187
; Publication No. US20030162229A1
; GENERAL INFORMATION:
; APPLICANT: MILNE-ROBERTSON, David M.
; APPLICANT: STANTON, Peter G.
; APPLICANT: CAHIR, Nicholas F.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR DEVELOPMENT OF DIAGNOSTIC AND THERAPEUTIC AGENTS
; TITLE OF INVENTION: METHODS OF USING SAME

```

```

; FILE REFERENCE: 10338-9
; CURRENT APPLICATION NUMBER: US/10/125.187
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: PCT/AU00/01248
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: AU PQ 9162
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: AU PQ 3485
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: inhibit alpha C amino acid sequence corresponding to peptide 2
; OTHER INFORMATION: f TABLE 7
US-10-125-187-53

```

```

Query Match      18.2%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 LPVP 10
        ||||
Db      9 LPVP 12

```

```

RESULT 47
US-10-125-187-54
; Sequence 54, Application US/10125187
; Publication No. US20030162229A1
; GENERAL INFORMATION:
; APPLICANT: MILNE-ROBERTSON, David M.
; APPLICANT: STANTON, Peter G.
; APPLICANT: CAHIR, Nicholas F.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR DEVELOPMENT OF DIAGNOSTIC AND THERAPEUTIC AGENTS
; TITLE OF INVENTION: METHODS OF USING SAME
; FILE REFERENCE: 10338-9
; CURRENT APPLICATION NUMBER: US/10/125.187
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: PCT/AU00/01248
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: AU PQ 9162
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: AU PQ 3485
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: inhibit alpha C amino acid sequence corresponding to peptide 2
; OTHER INFORMATION: f TABLE 7
US-10-125-187-54

```

```

Query Match      18.2%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 LPVP 10
        ||||
Db      5 LPVP 8

```

```

RESULT 48
US-10-125-187-55
; Sequence 55, Application US/10125187
; Publication No. US20030162229A1
; GENERAL INFORMATION:

```


; APPLICANT: MILNE-ROBERTSON, David M.
; APPLICANT: STANTON, Peter G.
; APPLICANT: CAHILL, Nicholas F.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR DEVELOPMENT OF DIAGNOSTIC AND THERAPEUTIC AGENTS
; FILE REFERENCE: 10338-9
; CURRENT APPLICATION NUMBER: US/10/125,187
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: PCT/AU00/01248
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: AU PQ 9162
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: AU PQ 3485
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: inhibin alpha C amino acid sequence corresponding to peptide 22 of
; OTHER INFORMATION: f TABLE 7
US-10-125-187-55

Query Match 18.2%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVP 10
Db 1 LPVP 4

RESULT 49
US-10-224-999A-804
; Sequence 804, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 804
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-224-999A-804

Query Match 18.2%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSQP 4
Db 11 LSQP 14

RESULT 50
US-10-224-999A-805
; Sequence 805, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 805
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-224-999A-805

Query Match 18.2%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSQP 4
Db 10 LSQP 13

RESULT 51
US-08-996-140-9
; Sequence 9, Application US/08996140
; Publication No. US20030190318A1
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: USHIO, Shimpei
; APPLICANT: KUNIKATA, Toshio
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,140
; FILING DATE: 22-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 356,426/1996
; FILING DATE: 26-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 52,526/1997
; FILING DATE: 21-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 163,490/1997
; FILING DATE: 6-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 215,490/1997
; FILING DATE: 28-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal fragment
US-08-996-140-9

Query Match 18.2%; Score 4; DB 7; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
Db 11 VLPV 14

RESULT 52

US-09-908-322-59
; Sequence 59, Application US/09908322
; Patent No. US20020107194A1

GENERAL INFORMATION:

; APPLICANT: NOTBORN, Mathieu Hubertus Maria
; APPLICANT: DANEN-VAN COERSCHOT, Astrid Adriana Anna Maria
; APPLICANT: ROHN, Jennifer Leigh
; APPLICANT: WEISS, Bertram
; TITLE OF INVENTION: APOPTIN-ASSOCIATING PROTEIN
; FILE REFERENCE: 4725US
; CURRENT APPLICATION NUMBER: US/09/764,176
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: peptide based on sequence
; OTHER INFORMATION: AAP-2 protei

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF

COMPUTER READABLE FORM:

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7326-123

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 59:

US-09-908-322-59

Query Match 18.2%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10
Db 2 LPVP 5

RESULT 53

US-09-764-176-13
; Sequence 13, Application US/09764176
; Patent No. US20020127553A1

GENERAL INFORMATION:

; APPLICANT: NOTBORN, Mathieu Hubertus Maria
; APPLICANT: DANEN-VAN COERSCHOT, Astrid Adriana Anna Maria
; APPLICANT: ROHN, Jennifer Leigh
; APPLICANT: WEISS, Bertram

; TITLE OF INVENTION: APOPTIN-ASSOCIATING PROTEIN

; FILE REFERENCE: 4725US

; CURRENT APPLICATION NUMBER: US/09/764,176

; CURRENT FILING DATE: 2001-01-17

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 13

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Description of Artificial Sequence: peptide based on sequence

; OTHER INFORMATION: AAP-2 protei

US-09-764-176-13

Query Match

Best Local Similarity 100.0%; Score 4; DB 10; Length 15;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKVL 7

Db 12 PKVL 15

RESULT 54

US-09-783-931-59

; Sequence 59, Application US/09783931

; Publication No. US20030073620A1

; GENERAL INFORMATION:

; APPLICANT: Ish-Horowicz, David

; Henrique, Domingos Manuel Pinto

; Lewis, Julian Hart

; Artavanis-Tsakonas, Spyridon

; Gray, Grace

; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS

AND FRAGMENTS

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/783,931

FILING DATE: 15-Feb-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/981,392

FILING DATE: 22-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Artler, Adriane M.

REGISTRATION NUMBER: 32,605

REFERENCE/DOCKET NUMBER: 7326-122

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-783-931-59

Query Match 18.2%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10
|
|
|
|
Db 2 LPVP 5

RESULT 55

US-10-212-198-15
Sequence 15, Application US/10212198
Publication No. US20030138804A1
GENERAL INFORMATION:
APPLICANT: Boyle, Bryan J
APPLICANT: Ford, John E.
APPLICANT: Mize, Nancy K.
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dmanac, Radoje T.
APPLICANT: Dickson, Mark C.
APPLICANT: Arterburn, Matthew C.
APPLICANT: Binnerts, Minke
TITLE OF INVENTION: Methods and Materials Relating to No. US20030138804A1el C-type Le
TITLE OF INVENTION: Polypeptides and Polynucleotides
FILE REFERENCE: HVS-5CIP
CURRENT APPLICATION NUMBER: US/10/212,198
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: 09/545,283
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-10-212-198-15

Query Match 18.2%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VPQK 12
|
|
|
|
Db 8 VPQK 11

RESULT 56

US-10-349-023-18
Sequence 18, Application US/10349023
Publication No. US2003013919A1
GENERAL INFORMATION:
APPLICANT: TORIGOE, Kakuji
OKURA, Takanori
KURIMOTO, Musashi
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/349,023
FILING DATE: 23-Jan-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/556,972
FILING DATE: 24-Apr-2000
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE=3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-349-023-18

Query Match 18.2%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
|
|
|
|
Db 11 VLPV 14

RESULT 57

US-10-294-891-17
Sequence 17, Application US/10294891
Publication No. US20030166569A1
GENERAL INFORMATION:
APPLICANT: AVERBACK, PAUL
APPLICANT: GEMMEL, JACK
TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
FILE REFERENCE: 59003.000010
CURRENT APPLICATION NUMBER: US/10/294,891
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 60/331,447
PRIOR FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.2
SEQ ID NO 17
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-10-294-891-17

Query Match 18.2%; Score 4; DB 12; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 LSQP 4
|||
Db 4 LSQP 7

RESULT 58

US-10-224-999A-815
; Sequence 815, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 815
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-224-999A-815

Query Match 18.2%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4
|||
Db 12 LSQP 15

RESULT 59

US-10-224-999A-816
; Sequence 816, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 816
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-224-999A-816

Query Match 18.2%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4
|||
Db 11 LSQP 14

RESULT 60

US-10-224-999A-817

US-10-224-999A-817
; Sequence 817, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 817
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-224-999A-817

Query Match 18.2%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4
|||
Db 10 LSQP 13

RESULT 61

US-10-161-791-306
; Sequence 306, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAN, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 306:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-306

Query Match 18.2%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10
|
|
|
|
Db 7 LPVP 10

RESULT 62
US-10-126-474A-3
; Sequence 3, Application US/10126474A
; Publication No. US20030054994A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030054994A1aleborn, Mathieu H.M.
; APPLICANT: Weiss, Bertram
; TITLE OF INVENTION: APOPTOSIS INDUCING PROTEINACEOUS SUBSTANCE
; FILE REFERENCE: 5334US (P51373US00)
; CURRENT APPLICATION NUMBER: US/10/126,474A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: PCT/NL00/00767
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: EP 99203467.8
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunogenic peptide for production of polyclonal antibodies against
; OTHER INFORMATION: st TAP proteins
US-10-126-474A-3

Query Match 18.2%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10
|
|
|
|
Db 4 LPVP 7

RESULT 63
US-10-174-105A-149
; Sequence 149, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,
; FILE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 149

; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: MOD_RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 9 is phosphorylated
US-10-174-105A-149

Query Match 18.2%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10
|
|
|
|
Db 10 LPVP 13

RESULT 64
US-10-174-105A-175
; Sequence 175, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,
; FILE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 175
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: MOD_RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 9 is phosphorylated
US-10-174-105A-175

Query Match 18.2%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10
|
|
|
|
Db 10 LPVP 13

RESULT 65
US-10-281-652-5
; Sequence 5, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652

; CURRENT FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: US/09/641,803
 ; PRIOR FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: 60/149,310
 ; PRIOR FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
 ; OTHER INFORMATION: peptide
 US-10-281-652-5

Query Match 18.2%; Score 4; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
 ||||
 Db 6 VLPV 9

RESULT 66
 US-09-880-748-2228
 ; Sequence 2228, Application US/09880748
 ; Publication No. US2003005937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; FILE REFERENCE: PF523
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2228
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-2228

Query Match 18.2%; Score 4; DB 11; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
 ||||
 Db 10 VLPV 13

RESULT 67
 US-09-880-748-2334
 ; Sequence 2334, Application US/09880748
 ; Publication No. US2003005937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2334
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-2334

Query Match 18.2%; Score 4; DB 11; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
 ||||
 Db 10 VLPV 13

RESULT 68
 US-10-224-999A-827
 ; Sequence 827, Application US/10224999A
 ; Publication No. US20030171318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
 ; FILE REFERENCE: 5004.01
 ; CURRENT APPLICATION NUMBER: US/10/224,999A
 ; CURRENT FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/313,695
 ; PRIOR FILING DATE: 2001-08-20
 ; NUMBER OF SEQ ID NOS: 3484
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 827
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Human herpesvirus 4
 US-10-224-999A-827

Query Match 18.2%; Score 4; DB 12; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4
 ||||
 Db 13 LSQP 16

RESULT 69
 US-10-224-999A-828
 ; Sequence 828, Application US/10224999A
 ; Publication No. US20030171318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
 ; FILE REFERENCE: 5004.01
 ; CURRENT APPLICATION NUMBER: US/10/224,999A
 ; CURRENT FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/313,695
 ; PRIOR FILING DATE: 2001-08-20

; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 828
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-224-999A-828

Query Match 18.2%; Score 4; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4
|||
DB 12 LSQP 15

RESULT 70
US-10-224-999A-829
; Sequence 829, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Mornham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 829
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-224-999A-829

Query Match 18.2%; Score 4; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4
|||
DB 11 LSQP 14

RESULT 71
US-10-224-999A-830
; Sequence 830, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Mornham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 830
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-224-999A-830

Query Match 18.2%; Score 4; DB 12; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4
|||
DB 10 LSQP 13

RESULT 72
US-10-006-760-61
; Sequence 61, Application US/10006760
; Publication No. US20030186385A1
; GENERAL INFORMATION:
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND
; TITLE OF INVENTION: TO TARGET PROTEINS AND USE THEREOF
; FILE REFERENCE: 176/60901
; CURRENT APPLICATION NUMBER: US/10/006,760
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/249,756
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FG loop
; OTHER INFORMATION: sequence for polypeptide monobody in PY747F16
; OTHER INFORMATION: library
US-10-006-760-61

Query Match 18.2%; Score 4; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4
|||
DB 6 LSQP 9

RESULT 73
US-10-043-487-442
; Sequence 442, Application US/10043487
; Publication No. US20030055220A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, LEGRAIN
; TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polype
; FILE REFERENCE: B4778A
; CURRENT APPLICATION NUMBER: US/10/043,487
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/261,130
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 561
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 442
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Shigella Flexneri
US-10-043-487-442

Query Match 18.2%; Score 4; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
|||
DB 9 VLPV 12

RESULT 74

US-09-996-069-30
; Sequence 30, Application US/09996069
; Publication No. US20030036199A1
; GENERAL INFORMATION:
; APPLICANT: Bamdad, R. Shoshana
; TITLE OF INVENTION: DIAGNOSTIC TUMOR MARKERS, DRUG SCREENING FOR TUMORIGENESIS INHIBITORS
; FILE REFERENCE: M01015/70071
; CURRENT APPLICATION NUMBER: US/09/996,069
; CURRENT FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-069-30

Query Match 18.2%; Score 4; DB 11; Length 17;
Best Local Similarity 100.0%; Pred.No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPV 9
|
|
|
|
Db 6 VLPV 9

RESULT 75

US-09-996-069-31
; Sequence 31, Application US/09996069
; Publication No. US20030036199A1
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia
; TITLE OF INVENTION: DIAGNOSTIC TUMOR MARKERS, DRUG SCREENING FOR TUMORIGENESIS INHIBITORS
; FILE REFERENCE: M01015/70071
; CURRENT APPLICATION NUMBER: US/09/996,069
; CURRENT FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-069-31

Query Match 18.2%; Score 4; DB 11; Length 17;
Best Local Similarity 100.0%; Pred.No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPV 9
|
|
|
|
Db 6 VLPV 9

Search completed: November 25, 2003, 20:37:04
Job time : 36.3023 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 17.7791 Seconds
(without alignments)
52.356 Million cell updates/sec

Title: US-09-641-801-27

Perfect score: 22

Sequence: 1 LSQPKVLVPQKAVPQDRMPIQ 22

Scoring table: OIIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: listing first 100 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

				SUMMARIES	
Result No.	Score	Query Match	Length DB ID	Description	
1	7	31.8	7	4	US-09-492-766-8
2	6	27.3	14	1	US-08-642-255-103
3	6	27.3	14	1	US-08-397-633A-5
4	6	27.3	14	1	US-08-397-633A-10
5	6	27.3	15	1	US-08-397-633A-80
6	6	27.3	15	1	US-08-397-633A-83
7	6	27.3	20	3	US-08-505-250-12
8	6	27.3	20	4	US-08-505-250-12
9	5	22.7	20	3	US-08-973-551-10
10	5	22.7	15	1	US-08-397-633A-81
11	5	22.7	15	3	US-08-973-551-3
12	5	22.7	16	3	US-08-602-999A-195
13	5	22.7	16	4	US-09-500-124-195
14	5	22.7	18	6	5175113-7
15	4	18.2	6	3	US-09-177-249-278
16	4	18.2	6	3	US-08-776-059-56
17	4	18.2	6	4	US-08-854-039B-23
18	4	18.2	6	4	US-09-645-456A-33
19	4	18.2	6	4	US-09-425-324A-33
20	4	18.2	6	4	US-09-645-791-33
21	4	18.2	7	1	US-08-230-047-37
22	4	18.2	7	3	US-08-973-551-5
23	4	18.2	7	3	US-08-973-551-21
24	4	18.2	7	4	US-09-400-653A-4
25	4	18.2	7	4	US-09-248-061B-4
26	4	18.2	8	1	US-08-571-985-21
27	4	18.2	8	2	US-09-116-766-21

28	4	18.2	8	4	US-08-635-886C-138
29	4	18.2	9	2	US-08-350-260A-385
30	4	18.2	9	2	US-08-318-856A-54
31	4	18.2	9	4	US-09-343-011B-7
32	4	18.2	9	4	US-09-104-337A-385
33	4	18.2	10	1	US-07-869-933-19
34	4	18.2	10	2	US-08-361-517-13
35	4	18.2	10	2	US-08-361-517-14
36	4	18.2	10	2	US-08-361-517-15
37	4	18.2	10	2	US-08-361-517-16
38	4	18.2	10	2	US-08-361-517-17
39	4	18.2	10	2	US-08-361-517-19
40	4	18.2	10	2	US-08-361-517-20
41	4	18.2	10	2	US-08-318-856A-58
42	4	18.2	10	3	US-09-103-663-19
43	4	18.2	10	3	US-09-220-528-111
44	4	18.2	10	5	PCT-US93-07964-13
45	4	18.2	10	5	PCT-US93-07964-14
46	4	18.2	10	5	PCT-US93-07964-15
47	4	18.2	10	5	PCT-US93-07964-16
48	4	18.2	10	5	PCT-US93-07964-17
49	4	18.2	10	5	PCT-US93-07964-19
50	4	18.2	10	5	PCT-US93-07964-20
51	4	18.2	11	2	US-08-361-517-5
52	4	18.2	11	2	US-08-361-517-31
53	4	18.2	11	3	US-08-802-981-136
54	4	18.2	11	5	PCT-US93-07964-5
55	4	18.2	12	1	US-08-230-047-36
56	4	18.2	12	1	US-08-053-079A-2
57	4	18.2	12	1	US-08-053-079A-3
58	4	18.2	12	1	US-08-397-633A-101
59	4	18.2	12	2	US-08-361-517-4
60	4	18.2	12	2	US-08-361-517-30
61	4	18.2	12	4	US-09-147-208-55
62	4	18.2	12	4	US-09-347-926-16
63	4	18.2	12	4	US-09-550-117A-55
64	4	18.2	12	5	PCT-US93-07964-4
65	4	18.2	13	2	US-08-361-517-3
66	4	18.2	13	2	US-08-361-517-27
67	4	18.2	13	2	US-08-361-517-28
68	4	18.2	13	2	US-08-361-517-29
69	4	18.2	13	3	US-09-043-937A-16
70	4	18.2	13	5	PCT-US93-07964-3
71	4	18.2	13	5	PCT-US94-10257A-13
72	4	18.2	13	5	PCT-US94-10257A-57
73	4	18.2	13	6	5223254-6
74	4	18.2	14	2	US-08-361-517-2
75	4	18.2	14	2	US-08-361-517-6
76	4	18.2	14	2	US-08-361-517-25
77	4	18.2	14	2	US-08-361-517-26
78	4	18.2	14	5	PCT-US93-07964-2
79	4	18.2	14	5	PCT-US93-07964-6
80	4	18.2	14	6	5164482-18
81	4	18.2	15	1	US-08-230-047-28
82	4	18.2	15	1	US-08-449-207-4
83	4	18.2	15	2	US-08-480-190-73
84	4	18.2	15	2	US-08-488-379-73
85	4	18.2	15	2	US-08-361-517-1
86	4	18.2	15	2	US-08-361-517-24
87	4	18.2	15	2	US-08-735-253-18
88	4	18.2	15	3	US-08-159-339A-1120
89	4	18.2	15	3	US-08-996-338-18
90	4	18.2	15	3	US-08-602-999A-306
91	4	18.2	15	3	US-08-981-392-59
92	4	18.2	15	4	US-09-500-124-306
93	4	18.2	15	4	US-09-641-803-5
94	4	18.2	15	4	US-08-475-399A-73
95	4	18.2	15	4	US-09-556-872-18
96	4	18.2	15	5	PCT-US93-07545-73
97	4	18.2	15	5	PCT-US93-07964-1
98	4	18.2	16	1	5378464-31
99	4	18.2	16	1	US-08-133-011-141
100	4	18.2	16	2	US-08-649-619B-5

Sequence 138, App
Sequence 385, App
Sequence 54, Appl
Sequence 7, Appl
Sequence 385, App
Sequence 19, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 58, Appl
Sequence 19, Appl
Sequence 111, App
Sequence 13, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 5, Appl
Sequence 31, Appl
Sequence 136, App
Sequence 5, Appl
Sequence 36, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 101, App
Sequence 4, Appl
Sequence 30, Appl
Sequence 55, Appl
Sequence 16, Appl
Sequence 55, Appl
Sequence 4, Appl
Sequence 3, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 16, Appl
Sequence 3, Appl
Sequence 13, Appl
Sequence 57, Appl
Patent No. 5223254
Sequence 2, Appl
Sequence 6, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 2, Appl
Sequence 6, Appl
Patent No. 5164482
Sequence 28, Appl
Sequence 4, Appl
Sequence 73, Appl
Sequence 73, Appl
Sequence 1, Appl
Sequence 24, Appl
Sequence 18, Appl
Sequence 1120, Ap
Sequence 18, Appl
Sequence 306, App
Sequence 59, Appl
Sequence 306, App
Sequence 5, Appl
Sequence 73, Appl
Sequence 18, Appl
Sequence 1, Appl
Patent No. 5378464
Sequence 141, App
Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-492-766-8
; Sequence 8, Application US/09492766
; Patent No. 6508732
; GENERAL INFORMATION:
; APPLICANT: AMIOT, Jean
; TITLE OF INVENTION: ENZYMATIC HYDROLYSATE OF MILK PROTEINS
; FILE REFERENCE: 6013-57"US"
; CURRENT APPLICATION NUMBER: US/09/492,766
; CURRENT FILING DATE: 2000-01-27
; EARLIER APPLICATION NUMBER: 60/117,661
; EARLIER FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk
; OTHER INFORMATION: proteins
US-09-492-766-8

Query Match 31.8%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPVPOK 12
Db 1 VLPVPOK 7

RESULT 2
US-08-642-255-103
; Sequence 103, Application US/08642255
; Patent No. 5773249
; GENERAL INFORMATION:
; APPLICANT: CAPPELLO, Joseph
; APPLICANT: FERRARI, Franco A.
; TITLE OF INVENTION: High Molecular Weight Collagen-Like
; TITLE OF INVENTION: Protein Polymers
; NUMBER OF SEQUENCES: 135
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,255
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ROWLAND, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A55556-3/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-642-255-103
Query Match 27.3%; Score 6; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 KVLVPV 10
Db 8 KVLVPV 13

RESULT 3
US-08-397-633A-5
; Sequence 5, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-633A-5

Query Match 27.3%; Score 6; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVPV 10
Db 8 KVLVPV 13

RESULT 4
US-08-397-633A-10
; Sequence 10, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph

;; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
;; OF ENZYMATIC CROSS-LINKING
;; NUMBER OF SEQUENCES: 105
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
;; STREET: 4 Embarcadero Center, Suite 3400
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-4187
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/397,633A
;; FILING DATE:
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rowland, Bertram I
;; REGISTRATION NUMBER: 20,015
;; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 781-1989
;; TELEFAX: (415) 398-3249
;; TELEX: 910 277299
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-397-633A-10

Query Match 27.3%; Score 6; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLVPP 10
Db 8 KVLVPP 13

RESULT 5
US-08-397-633A-80
; Sequence 80, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; OF ENZYMATIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-633A-83

Query Match 27.3%; Score 6; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLVPP 10
Db 9 KVLVPP 14

;; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 781-1989
;; TELEFAX: (415) 398-3249
;; TELEX: 910 277299
;; INFORMATION FOR SEQ ID NO: 80:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-397-633A-80

Query Match 27.3%; Score 6; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLVPP 10
Db 9 KVLVPP 14

RESULT 6
US-08-397-633A-83
; Sequence 83, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; OF ENZYMATIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-633A-83

Query Match 27.3%; Score 6; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLVPP 10
Db 9 KVLVPP 14

```
RESULT 7
US-08-505-250-12
; Sequence 12, Application US/08505250
; Patent No. 6183983
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kokichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Sakagami, Masahiro
; APPLICANT: Taniguchi, Makoto
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
; FILE REFERENCE: 110-511
; CURRENT APPLICATION NUMBER: US/08/505,250
; CURRENT FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: PCT/JP95/00298
; EARLIER FILING DATE: 1995-02-27
; EARLIER APPLICATION NUMBER: JP 198187/94
; EARLIER FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-08-505-250-12
Query Match          27.3%; Score 6; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KVLVPP 10
        |||||
DB      12 KVLVPP 17

RESULT 8
US-08-505-250-12
; Sequence 12, Application US/08505250
; Patent No. 6322996
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kokichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Sakagami, Masahiro
; APPLICANT: Taniguchi, Makoto
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
; FILE REFERENCE: 110-511
; CURRENT APPLICATION NUMBER: US/08/505,250
; CURRENT FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: PCT/JP95/00298
; EARLIER FILING DATE: 1995-02-27
; EARLIER APPLICATION NUMBER: JP 198187/94
; PRIOR FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-08-505-250-12
Query Match          27.3%; Score 6; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KVLVPP 10
        |||||
DB      12 KVLVPP 17

RESULT 9
US-08-973-551-10
; Sequence 10, Application US/08973551
; Patent No. 6113902
; GENERAL INFORMATION:
; APPLICANT: Chermann, Jean-Claude
; APPLICANT: Le Contel, Carole
; APPLICANT: Galea, Pascale
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING
; TITLE OF INVENTION: AN INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
; TITLE OF INVENTION: DIAGNOSIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,551
; FILING DATE: 30-DEC-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/01006
; FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9507914
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 65691/130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-973-551-10
Query Match          22.7%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LSQPK 5
        |||||
DB      2 LSQPK 6

RESULT 10
US-08-397-633A-81
; Sequence 81, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
```

```

; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-633A-81

Query Match 22.7%; Score 5; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPVP 10
Db 10 VLPVP 14

RESULT 11
US-08-973-551-3
; Sequence 3, Application US/08973551
; Patent No. 6113902
; GENERAL INFORMATION:
; APPLICANT: Chermann, Jean-Claude
; APPLICANT: Le Contel, Carole
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING
; TITLE OF INVENTION: AN INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
; TITLE OF INVENTION: DIAGNOSIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,551
; FILING DATE: 30-DEC-1997

```

```

; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/01006
; FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9507914
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 65691/130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-973-551-3

Query Match 22.7%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSQPK 5
Db 9 LSQPK 13

RESULT 12
US-08-602-999A-195
; Sequence 195, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 195:

```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-195

Query Match      22.7%; Score 5; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 AVPQR 17
      |||||
Db      8 AVPQR 12

RESULT 13
US-09-500-124-195
; Sequence 195, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 195:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-195

Query Match      22.7%; Score 5; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 AVPQR 17
      |||||
Db      8 AVPQR 12

; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-195

Query Match      22.7%; Score 5; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LSQPK 5
      |||||
Db      7 LSQPK 11

RESULT 14
5175113-7
; Patent No. 5175113
; APPLICANT: NISSEN, MOGENS H.; ZEUTHEN, JESPER, LARSEN,
; FLEMMING S.; THIM, LARS; CHRISTENSEN, MOGENS
; TITLE OF INVENTION: MODIFIED B-2 MICROGLOBULIN
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/550,919
; FILING DATE: 29-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 3436
; FILING DATE: 15-JAN-1987
; SEQ ID NO: 7:
; LENGTH: 18
5175113-7

Query Match      22.7%; Score 5; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LSQPK 5
      |||||
Db      7 LSQPK 11

RESULT 15
US-09-177-249-278
; Sequence 278, Application US/09177249
; Patent No. 6229084
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Chad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Vadehari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; TITLE OF INVENTION: Development in Plants
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 278
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-278

Query Match      18.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PKVL 7
      |||||
Db      3 PKVL 6

RESULT 16
US-08-776-059-56
; Sequence 56, Application US/08776059B
; Patent No. 6271368
; GENERAL INFORMATION:
; APPLICANT: LENTZEN, Hans
; APPLICANT: ECK, Jurgen
; APPLICANT: BAUR, Axel
```

APPLICANT: ZINKE, Holger
; TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
; FILE REFERENCE: 674503-2003
; CURRENT APPLICATION NUMBER: US/08/776,059B
; CURRENT FILING DATE: 1999-06-19
; EARLIER APPLICATION NUMBER: PCT/EP96/02273
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 95109949.8
; EARLIER FILING DATE: 1995-06-26
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Spodoptera frugiperda
US-08-776-059-56

Query Match 18.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVP 10
Db 3 LPVP 6

RESULT 17
US-08-854-039B-23
; Sequence 23, Application US/08854039B
; Patent No. 6355774
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Roberts, James M.
; APPLICANT: Koiff, Andrew
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS
; TITLE OF INVENTION: PRODUCTION AND USE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HONG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,039B
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-854-039B-23

Query Match 18.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSQP 4
Db 1 LSQP 4

RESULT 18
US-09-645-456A-33
; Sequence 33, Application US/09645456A
; Patent No. 6562580
; GENERAL INFORMATION:
; APPLICANT: Fu, C. Alan
; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS
; FILE REFERENCE: A-68344/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/645,456A
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US/09/425,324
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-645-456A-33

Query Match 18.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 VPQR 17
Db 3 VPQR 6

RESULT 19
US-09-425-324A-33
; Sequence 33, Application US/09425324A
; Patent No. 6562591
; GENERAL INFORMATION:
; APPLICANT: Fu, C. Alan
; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS
; FILE REFERENCE: A-68344/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/425,324A
; CURRENT FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-425-324A-33

Query Match 18.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 VPQR 17
Db 3 VPQR 6

RESULT 20
US-09-645-791-33
; Sequence 33, Application US/09645791
; Patent No. 6569658
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying

APPLICANT: Fu, Alan C
APPLICANT: Shen, Mary
TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS; COMPOSITIONS AN
FILE REFERENCE: A-68344-1/RMS/DHR
CURRENT APPLICATION NUMBER: US/09/645,791
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 09/425,324
PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 33
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-09-645-791-33

Query Match 18.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VPQR 17
Db 3 VPQR 6

RESULT 21
US-08-230-047-37
Sequence 37, Application US/08230047
Patent No. 5541109
GENERAL INFORMATION:
APPLICANT: Searfoss III, George H.
APPLICANT: Ivashchenko, Yuri D.
APPLICANT: Jaye, Michael C.
TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.0 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/230,047
FILING DATE: 19-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Rosanne
REGISTRATION NUMBER: 32,534
REFERENCE/DOCKET NUMBER: A1465-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3817
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-230-047-37

Query Match 18.2%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICANT: Fu, Alan C
APPLICANT: Shen, Mary
TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS; COMPOSITIONS AN
FILE REFERENCE: A-68344-1/RMS/DHR
CURRENT APPLICATION NUMBER: US/09/645,791
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 09/425,324
PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 33
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-09-645-791-33

Query Match 18.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VPQR 17
Db 3 VPQR 6

RESULT 21
US-08-230-047-37
Sequence 37, Application US/08230047
Patent No. 5541109
GENERAL INFORMATION:
APPLICANT: Searfoss III, George H.
APPLICANT: Ivashchenko, Yuri D.
APPLICANT: Jaye, Michael C.
TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.0 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/230,047
FILING DATE: 19-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Rosanne
REGISTRATION NUMBER: 32,534
REFERENCE/DOCKET NUMBER: A1465-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3817
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-230-047-37

Query Match 18.2%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10
Db 3 LPVP 6

RESULT 22
US-08-973-551-5
Sequence 5, Application US/08973551
Patent No. 6113902
GENERAL INFORMATION:
APPLICANT: Chermann, Jean-Claude
APPLICANT: Le Contel, Carole
APPLICANT: Galea, Pascale
TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING
TITLE OF INVENTION: AN INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND
TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
TITLE OF INVENTION: DIAGNOSIS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,551
FILING DATE: 30-DEC-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/01006
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9507914
FILING DATE: 30-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 65691/130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-973-551-5

Query Match 18.2%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPK 5
Db 1 SQPK 4

RESULT 23
US-08-973-551-21
Sequence 21, Application US/08973551
Patent No. 6113902
GENERAL INFORMATION:
APPLICANT: Chermann, Jean-Claude


```
; APPLICANT: Le Contel, Carole
; APPLICANT: Galea, Pascale
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING
; TITLE OF INVENTION: AN INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
; TITLE OF INVENTION: DIAGNOSIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,551
; FILING DATE: 30-DEC-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/01006
; FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9507914
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 65691/130
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-973-551-21

Query Match      18.2%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SQPK 5
Db      1 SQPK 4

RESULT 24
US-09-400-653A-4
; Sequence 4, Application US/09400653A
; Patent No. 6348311
; GENERAL INFORMATION:
; APPLICANT: Kastan, Michael
; APPLICANT: Canman, Christine
; APPLICANT: Kim, Seong-Tae
; APPLICANT: Lim, Dae-Sik
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
; FILE REFERENCE: 2427/0F142
; CURRENT APPLICATION NUMBER: US/09/400,653A
; CURRENT FILING DATE: 1999-02-21
; PRIOR APPLICATION NUMBER: 09/248,061
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: PHOSPHORYLATION
; LOCATION: 4
; OTHER INFORMATION: Artificial sequence is a synthetic sequence.
; OTHER INFORMATION: Xaa at position seven is any amino acid.
US-09-400-653A-4

Query Match      18.2%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LSQP 4
Db      3 LSQP 6

RESULT 25
US-09-248-061B-4
; Sequence 4, Application US/09248061B
; Patent No. 6387640
; GENERAL INFORMATION:
; APPLICANT: Kastan, M.
; APPLICANT: Canman, C.
; APPLICANT: Kim, S-T.
; APPLICANT: Lim, D-S.
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
; FILE REFERENCE: 2427/0F142
; CURRENT APPLICATION NUMBER: US/09/248,061B
; CURRENT FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: PHOSPHORYLATION
; LOCATION: 4
; OTHER INFORMATION: Artificial sequence is a synthetic sequence.
; OTHER INFORMATION: Xaa at position seven is any amino acid.
US-09-248-061B-4

Query Match      18.2%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LSQP 4
Db      3 LSQP 6

RESULT 26
US-08-571-985-21
; Sequence 21, Application US/08571985
; Patent No. 5783557
; GENERAL INFORMATION:
; APPLICANT: Burstein, Yigal
; APPLICANT: Trainin, Nathan
; APPLICANT: Rycus, Avigail
; TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical
; TITLE OF INVENTION: Compositions Comprising Them
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5783557thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: USA
```

ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/571,985
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106214
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 2163.00048
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-571-985-21

Query Match 18.2%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKVL 7
DB 5 PKVL 8

RESULT 27
US-09-116-766-21
Sequence 21, Application US/09116766
Patent No. 5968898
GENERAL INFORMATION:
APPLICANT: Burstein, Yigal
APPLICANT: Trainin, Nathan
APPLICANT: Rykus, Avigail
TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical
TITLE OF INVENTION: Compositions Comprising Them
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5968898thwestern Hwy., Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: USA
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,766
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106214
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2163.00050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050

TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-116-766-21

Query Match 18.2%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKVL 7
DB 5 PKVL 8

RESULT 28
US-08-635-886C-138
Sequence 138, Application US/08635886C
Patent No. 6555114
GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELREYS, Robert
APPLICANT: MAERTENS, Geert
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
FILE REFERENCE: 2752-18
CURRENT APPLICATION NUMBER: US/08/635,886C
CURRENT FILING DATE: 1996-04-25
PRIOR APPLICATION NUMBER: PCT/EP94/03555
PRIOR FILING DATE: 1994-10-28
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PatentIn version 3.1
SEQ ID NO 138
LENGTH: 8
TYPE: PRT
ORGANISM: hepatitis C virus
US-08-635-886C-138

Query Match 18.2%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVPQ 16
DB 1 AVPQ 4

RESULT 29
US-08-350-260A-385
Sequence 385, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois

```

; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-350-260A-385

```

```

Query Match      18.2%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 LSQP 4
Db      4 LSQP 7

```

```

RESULT 30
US-08-318-856A-54
; Sequence 54, Application US/08318856A
; Patent No. 5972351
; GENERAL INFORMATION:
; APPLICANT: Adrian V.S. Hill, et al.
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
; TITLE OF INVENTION: RESTRICTED CYT B EPTOTYPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
; TITLE OF INVENTION: ANTIGENS (AS AMENDED)
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1+
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,856A
; FILING DATE: October 3, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92 08 068.8
; FILING DATE: April 3, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92 17 704.7
; FILING DATE: August 20, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB93/00711
; FILING DATE: April 5, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee Cheng
; REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 263-PPIR1577US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 721-8200
; TELEFAX: (202) 721-8250
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-318-856A-54

```

```

Query Match      18.2%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      4 PKVL 7
Db      2 PKVL 5

```

```

RESULT 31
US-09-343-011B-7
; Sequence 7, Application US/09343011B
; Patent No. 6300473
; GENERAL INFORMATION:
; APPLICANT: Stephane Richard
; TITLE OF INVENTION: SIM-1 AND SIM-2; NOVEL
; TITLE OF INVENTION: SAM68-LIKE MAMMALIAN PROTEINS
; FILE REFERENCE: A32561
; CURRENT APPLICATION NUMBER: US/09/343.011B
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: CA 2265271
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-343-011B-7

```

```

Query Match      18.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 LPVP 10
Db      4 LPVP 7

```

```

RESULT 32
US-09-104-337A-385

```

; Sequence 385, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 385:
US-09-104-337A-385

Query Match 18.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSQP 4
| | | |
Db 4 LSQP 7

RESULT 33
US-07-869-933-19
; Sequence 19, Application US/07869933
; Patent No. 5770396
; GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,933
; FILING DATE: 19920416
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-869-933-19

Query Match 18.2%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VFQK 12
| | | |
Db 2 VFQK 5

RESULT 34
US-08-361-517-13
; Sequence 13, Application US/08361517
; Patent No. 5916876
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; ADHESION
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; and No. 5916876ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/941,652
FILING DATE: September 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0209
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acid residues
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE:
DESCRIPTION: Amide terminated
US-08-361-517-13

Query Match 18.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 KVLp 8
| | | |
Db 1 KVLp 4

RESULT 35
US-08-361-517-14
Sequence 14, Application US/08361517
Patent No. 5916876
GENERAL INFORMATION:
APPLICANT: George A. Heavner and Leon A. Epps
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
TITLE OF INVENTION: Adhesion
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: and No. 5916876ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,517
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/941,652
FILING DATE: September 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0209
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acid residues
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE:
DESCRIPTION: Amide terminated
US-08-361-517-14

Query Match 18.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 KVLp 8
| | | |
Db 1 KVLp 4

RESULT 36
US-08-361-517-15
Sequence 15, Application US/08361517
Patent No. 5916876
GENERAL INFORMATION:
APPLICANT: George A. Heavner and Leon A. Epps
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
TITLE OF INVENTION: Adhesion
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: and No. 5916876ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,517
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/941,652
FILING DATE: September 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0209
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acid residues
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE:
DESCRIPTION: Amide terminated
US-08-361-517-15
Query Match 18.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 KVLp 8
| | | |
Db 1 KVLp 4

RESULT 37
US-08-361-517-16
Sequence 16, Application US/08361517
Patent No. 5916876
GENERAL INFORMATION:
APPLICANT: George A. Heavner and Leon A. Epps
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
TITLE OF INVENTION: Adhesion
US-08-361-517-16

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: and No. 5916876ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,517
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/941,652
FILING DATE: September 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0209
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acid residues
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE:
DESCRIPTION: Amide terminated
US-08-361-517-16

Query Match 18.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLP 8
Db 1 KVLP 4

RESULT 38
US-08-361-517-17
Sequence 17, Application US/08361517
Patent No. 5916876
GENERAL INFORMATION:
APPLICANT: George A. Heavner and Leon A. Epps
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: and No. 5916876ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,517
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/941,652
FILING DATE: September 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0209
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acid residues
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE:
DESCRIPTION: Amide terminated

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/941,652
FILING DATE: September 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0209
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acid residues
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE:
DESCRIPTION: Amide terminated
US-08-361-517-17

Query Match 18.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLP 8
Db 1 KVLP 4

RESULT 39
US-08-361-517-19
Sequence 19, Application US/08361517
Patent No. 5916876
GENERAL INFORMATION:
APPLICANT: George A. Heavner and Leon A. Epps
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: and No. 5916876ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,517
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/941,652
FILING DATE: September 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0209
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acid residues
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE:
DESCRIPTION: Amide terminated

US-08-361-517-19

Query Match 18.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 KVL P 8
|||
Db 1 KVL P 4

RESULT 40

US-08-361-517-20
; Sequence 20, Application US/08361517
; Patent No. 5916876
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; Adhesion
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; and No. 5916876ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/941,652
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Eldarkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated

US-08-361-517-20

Query Match 18.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 KVL P 8
|||
Db 1 KVL P 4

RESULT 41

US-08-318-856A-58
; Sequence 58, Application US/08318856A
; Patent No. 5972351
; GENERAL INFORMATION:
; APPLICANT: Adrian V.S. Hill, et al.
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-

; TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
; ANTIGENS (AS AMENDED)
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1+
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,856A
; FILING DATE: October 3, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92 08 068.8
; FILING DATE: April 3, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92 17 704.7
; FILING DATE: August 20, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB93/00711
; FILING DATE: April 5, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee Cheng

REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 263-PP1R1577US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 721-8200
; TELEFAX: (202) 721-8250
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-318-856A-58

Query Match 18.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PKVL 7
|||
Db 3 PKVL 6

RESULT 42

US-09-103-663-19
; Sequence 19, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinnet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; subunit of the high affinity receptor for
; immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 10
; TYPE: PPT
; ORGANISM: Homo sapiens
US-09-103-663-19

```
Query Match      18.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 VPOK 12
        |||||
Db       2 VPOK 5

RESULT 43
US-09-220-528-111
; Sequence 111, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor
; FILE REFERENCE: 6029-7998
; CURRENT APPLICATION NUMBER: US/09/220,528A
; EARLIER FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-220-528-111

Query Match      18.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 VLPV 9
        |||||
Db       2 VLPV 5

RESULT 44
PCT-US93-07964-13
; Sequence 13, Application 93/07964
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 93/07964
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: COOR-0025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated.
PCT-US93-07964-14

Query Match      18.2%; Score 4; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KVLV 8
        |||||
Db       1 KVLV 4

RESULT 45
PCT-US93-07964-14
; Sequence 14, Application 93/07964
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 93/07964
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: COOR-0025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated.
PCT-US93-07964-14

Query Match      18.2%; Score 4; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PCT-US93-07964-13
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: COOR-0025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated.
PCT-US93-07964-13

Query Match      18.2%; Score 4; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PCT-US93-07964-14
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: COOR-0025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated.
PCT-US93-07964-14
```


Qy 5 KVLp 8
 ||||
 Db 1 KVLp 4

RESULT 46

PCT-US93-07964-15
 ; Sequence 15, Application 93/07964
 ; GENERAL INFORMATION:
 ; APPLICANT: George A. Heavner and Leon A. Epps
 ; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
 ; TITLE OF INVENTION: Adhesion
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
 ; ADDRESSEE: Norris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WORDPERFECT 5.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: 93/07964
 ; FILING DATE: Herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dianne B. Elderkin
 ; REGISTRATION NUMBER: 28,598
 ; REFERENCE/DOCKET NUMBER: CCOR-0025
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 568-3100
 ; TELEFAX: (215) 568-3439
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE:
 ; DESCRIPTION: Amide terminated.
 ; PCT-US93-07964-15

Query Match 18.2%; Score 4; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred.No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 KVLp 8
 ||||
 Db 1 KVLp 4

RESULT 47

PCT-US93-07964-16
 ; Sequence 16, Application 93/07964
 ; GENERAL INFORMATION:
 ; APPLICANT: George A. Heavner and Leon A. Epps
 ; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
 ; TITLE OF INVENTION: Adhesion
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
 ; ADDRESSEE: Norris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia

; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WORDPERFECT 5.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: 93/07964
 ; FILING DATE: Herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dianne B. Elderkin
 ; REGISTRATION NUMBER: 28,598
 ; REFERENCE/DOCKET NUMBER: CCOR-0025
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 568-3100
 ; TELEFAX: (215) 568-3439
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE:
 ; DESCRIPTION: Amide terminated.
 ; PCT-US93-07964-16

Query Match 18.2%; Score 4; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred.No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 KVLp 8
 ||||
 Db 1 KVLp 4

RESULT 48

PCT-US93-07964-17
 ; Sequence 17, Application 93/07964
 ; GENERAL INFORMATION:
 ; APPLICANT: George A. Heavner and Leon A. Epps
 ; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
 ; TITLE OF INVENTION: Adhesion
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
 ; ADDRESSEE: Norris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WORDPERFECT 5.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: 93/07964
 ; FILING DATE: Herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dianne B. Elderkin
 ; REGISTRATION NUMBER: 28,598
 ; REFERENCE/DOCKET NUMBER: CCOR-0025

ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,517
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/941,652
FILING DATE: September 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0209
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acid residues
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE:
DESCRIPTION: Amide terminated
US-08-361-517-5

Query Match 18.2%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVP 8
DB 1 KVLVP 4

RESULT 52

US-08-361-517-31
Sequence 31, Application US/08361517
Patent No. 5916876
GENERAL INFORMATION:
APPLICANT: George A. Heavner and Leon A. Epps
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
ADHESION
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: and No. 5916876ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,517
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/941,652
FILING DATE: September 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0209
TELECOMMUNICATION INFORMATION:

Query Match 18.2%; Score 4; DB 3; Length 11;

TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acid residues
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE:
DESCRIPTION: Amide terminated
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: cysteine forms disulfide bond
with cysteine at position 11
US-08-361-517-31

Query Match 18.2%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVP 8
DB 3 KVLVP 6

RESULT 53

US-08-802-981-136
Sequence 136, Application US/08802981
Patent No. 6037137
GENERAL INFORMATION:
APPLICANT: Komoriya, Akira
TITLE OF INVENTION: Compositions for the Detection of Enzyme
ACTIVITY
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-0003000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /product= "Aib"
US-08-802-981-136

Query Match 18.2%; Score 4; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPK 5
Db 8 SQPK 11

RESULT 54
PCT-US93-07964-5
; Sequence 5, Application 93/07964
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESS: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 93/07964
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated.
PCT-US93-07964-5

Query Match 18.2%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLP 8
Db 1 KVLP 4

RESULT 55
US-08-230-047-36
; Sequence 36, Application US/08230047
; Patent No. 5541109
; GENERAL INFORMATION:
; APPLICANT: Searfoss III, George H.
; APPLICANT: Ivashchenko, Yuri D.
; APPLICANT: Jaye, Michael C.
; TITLE OF INVENTION: EXPRESSION CLOWING OF C-SRC SH3 BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230,047
; FILING DATE: 19-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A1465-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-230-047-36

Query Match 18.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10
Db 5 LPVP 8

RESULT 56
US-08-053-079A-2
; Sequence 2, Application US/08053079A
; Patent No. 5606026
; GENERAL INFORMATION:
; APPLICANT: Rodman
; TITLE OF INVENTION: Natural Human Igm Antibodies
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby
; STREET: 805 Third Ave.
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,079A
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Robinson, Joseph, R.
; REGISTRATION NUMBER: 33,448
; REFERENCE/DOCKET NUMBER: 4436/16060US4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Human immunodeficiency virus type 1
IMMEDIATE SOURCE:
CLONE: tat #2
US-08-053-079A-2

Query Match 18.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 SQPK 5
Db 9 SQPK 12

RESULT 57
US-08-053-079A-3
Sequence 3, Application US/08053079A
Patent No. 5606026
GENERAL INFORMATION:
APPLICANT: Rodman
TITLE OF INVENTION: Natural Human IgM Antibodies
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
STREET: 805 Third Ave.
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053.079A
FILING DATE: 26-APR-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph, R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 4436/16060U54
TELEPHONE: (212)527-7700
TELEFAX: (212)753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Human immunodeficiency virus type 1
IMMEDIATE SOURCE:
CLONE: tat #3
US-08-053-079A-3

Query Match 18.2%; Score 4; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 SQPK 5
Db 2 SQPK 5

RESULT 58
US-08-397-633A-101
Sequence 101, Application US/08397633A
Patent No. 5773577
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
OF ENZYMATIC CROSS-LINKING
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,633A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-633A-101

Query Match 18.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLP 8
Db 1 KVLP 4

RESULT 59
US-08-361-517-4
Sequence 4, Application US/08361517
Patent No. 5916876
GENERAL INFORMATION:
APPLICANT: George A. Heavner and Leon A. Epps
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
ADHESION
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia

```
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/941,652
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: Amide terminated
; DESCRIPTION:
; Query Match 18.2%; Score 4; DB 2; Length 12;
; Best Local Similarity 100.0%; Pred. No. 2.6e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 5 KVLVP 8
; Db 2 KVLVP 5
;
; RESULT 60
; US-08-361-517-30
; Sequence 30, Application US/08361517
; Patent No. 5916876
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; TITLE OF INVENTION: Adhesion
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5916876ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/941,652
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
```

```
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: Amide terminated
; DESCRIPTION:
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: cysteine forms disulfide bond
; OTHER INFORMATION: with cysteine at position 11
; US-08-361-517-30
;
; Query Match 18.2%; Score 4; DB 2; Length 12;
; Best Local Similarity 100.0%; Pred. No. 2.6e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 5 KVLVP 8
; Db 3 KVLVP 6
;
; RESULT 61
; US-09-147-208-55
; Sequence 55, Application US/09147208
; Patent No. 6333303
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antiviral Ricin-Like Proteins
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/147,208
; FILING DATE: 02-MAR-1999
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Rudolph, John R.
; REGISTRATION NUMBER: 38,003
; REFERENCE/DOCKET NUMBER: 7841-76
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-147-208-55
;
; Query Match 18.2%; Score 4; DB 4; Length 12;
; Best Local Similarity 100.0%; Pred. No. 2.6e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 6 VLPV 9
```

STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 93/07964
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE:
DESCRIPTION: Amide terminated.
PCT-US93-07964-4

Query Match 18.2%; Score 4; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 5 KLPV 8
DB 2 KLPV 5

RESULT 65
US-08-361-517-3
Sequence 3, Application US/08361517
Patent No. 5916876
GENERAL INFORMATION:
APPLICANT: George A. Heavner and Leon A. Epps
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
ADHESION
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: and No. 5916876is
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,517
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/941,652
FILING DATE: September 8, 1992
ATTORNEY/AGENT INFORMATION:

STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 93/07964
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE:
DESCRIPTION: Amide terminated.
PCT-US93-07964-4

Query Match 18.2%; Score 4; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 5 KLPV 8
DB 2 KLPV 5

RESULT 65
US-08-361-517-3
Sequence 3, Application US/08361517
Patent No. 5916876
GENERAL INFORMATION:
APPLICANT: George A. Heavner and Leon A. Epps
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
ADHESION
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: and No. 5916876is
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,517
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/941,652
FILING DATE: September 8, 1992
ATTORNEY/AGENT INFORMATION:

```
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated
; US-08-361-517-3

Query Match      18.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY      5 KVLVP 8
Db      3 KVLVP 6

RESULT 66
US-08-361-517-27
; Sequence 27, Application US/08361517
; Patent No. 5916876
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; TITLE OF INVENTION: Adhesion
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5916876ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; APPLICATION NUMBER: US/08/361,517
; FILING DATE: herewith
; CLASSIFICATION: 514
; APPLICATION NUMBER: 07/941,652
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: cysteine forms disulfide bond
; US-08-361-517-28
```

```
; OTHER INFORMATION: with cysteine at position 13
; US-08-361-517-27

Query Match      18.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY      5 KVLVP 8
Db      5 KVLVP 8

RESULT 67
US-08-361-517-28
; Sequence 28, Application US/08361517
; Patent No. 5916876
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; TITLE OF INVENTION: Adhesion
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5916876ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: cysteine forms disulfide bond
; OTHER INFORMATION: with cysteine at position 12
; US-08-361-517-28

Query Match      18.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY      5 KVLVP 8
Db      4 KVLVP 7

RESULT 68
```


US-08-361-517-29
 ; Sequence 29, Application US/08361517
 ; Patent No. 5916876
 ; GENERAL INFORMATION:
 ; APPLICANT: George A. Heavner and Leon A. Eppe
 ; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
 ; TITLE OF INVENTION: Adhesion
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
 ; ADDRESSEE: and No. 5916876ris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: U.S.A.
 ; ZIP: 19103

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/361.517
 FILING DATE: herewith
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/941.652
 FILING DATE: September 8, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Dianne B. Elderkin
 REGISTRATION NUMBER: 28,598
 REFERENCE/DOCKET NUMBER: COOR-0209
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-568-3100
 TELEFAX: 215-568-3439
 INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acid residues
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE:
 DESCRIPTION: Amide terminated
 FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: cysteine forms disulfide bond

OTHER INFORMATION: with cysteine at position 11

US-08-361-517-29

Query Match 18.2%; Score 4; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLV 8

Db 3 KVLV 6

RESULT 69

US-09-043-937A-16
 ; Sequence 16, Application US/09043937A
 ; Patent No. 6211432

GENERAL INFORMATION:

APPLICANT: BOUDET, ALAIN-MICHEL
 PICHON, MAGALIE
 GRIMA-PETTENATI, JACQUELINE
 BECKERT, MICHEL
 GAMAS, PASCAL
 BRIAT, JEAN-FRANCOIS

TITLE OF INVENTION: DNA SEQUENCES CODING FOR CINNAMOYL-CoA
 REDUCTASE, AND APPLICATIONS THEREOF IN THE CONTROL OF
 LIGNIN CONTENTS IN PLANTS

NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHUYE, P.C.
 STREET: 110 NORTH GLEBE ROAD, 8TH FLOOR
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/043.937A
 FILING DATE: 24-Jul-1998
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/FR96/01544

FILING DATE: 03-OCT-1996

APPLICATION NUMBER: FR 95.11623

FILING DATE: 03-OCT-1995

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36.663

REFERENCE/DOCKET NUMBER: 1487-20

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-816-4000

TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 6

OTHER INFORMATION: /label= xaa

/note= "any amino acid"

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-043-937A-16
 Query Match 18.2%; Score 4; DB 3; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVP 10

Db 2 LPVP 5

RESULT 70

PCT-US93-07964-3

; Sequence 3, Application 93/07964

GENERAL INFORMATION:

APPLICANT: George A. Heavner and Leon A. Eppe

TITLE OF INVENTION: Peptide Inhibitors of Leukocyte

TITLE OF INVENTION: Adhesion

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

ADDRESSEE: Norris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

;; SOFTWARE: WORDPERFECT 5.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: 93/07964
;; FILING DATE: Herewith
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Dianne B. Elderkin
;; REGISTRATION NUMBER: 28,598
;; REFERENCE/DOCKET NUMBER: CCOR-0025
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 13 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
;; MOLECULE TYPE:
;; DESCRIPTION: Amide terminated.
PCT-US93-07964-3

Query Match 18.2%; Score 4; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVP 8
Db 3 KVLVP 6

RESULT 71
PCT-US94-10257A-13
; Sequence 13, Application PC/TUS9410257A
; GENERAL INFORMATION:
; APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION
; APPLICANT: BRIGITTE DEVAUX
; APPLICANT: JONATHAN B. ROTHBARD
; APPLICANT: DAWN SMILEK
; TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE
; TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS
; TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10257A
; FILING DATE: 1 SEPTEMBER 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/116,824
; FILING DATE: 03-SEP-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ANNE I CRAIG
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 071.1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US94-10257A-57

Query Match 18.2%; Score 4; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
Db 6 VLPV 9

;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 13 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
PCT-US94-10257A-13

Query Match 18.2%; Score 4; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
Db 9 VLPV 12

RESULT 72
PCT-US94-10257A-57
; Sequence 57, Application PC/TUS9410257A
; GENERAL INFORMATION:
; APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION
; APPLICANT: BRIGITTE DEVAUX
; APPLICANT: JONATHAN B. ROTHBARD
; APPLICANT: DAWN SMILEK
; TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE
; TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS
; TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10257A
; FILING DATE: 1 SEPTEMBER 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/116,824
; FILING DATE: 03-SEP-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ANNE I CRAIG
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 071.1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US94-10257A-57

Query Match 18.2%; Score 4; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
Db 6 VLPV 9

RESULT 73
5223254-6
; PATENT NO. 5223254
; APPLICANT: PARADISO, PETER R.; HILDRETH, STEPHEN W.; HU,
BRANDA T.; MARTIN-GALLARDO, ANTONIA; ARUMUGHAM, RASAPPA
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/247,017
; FILING DATE: 20-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 102,180
; FILING DATE: 29-SEP-1987
; SEQ ID NO: 6:
; LENGTH: 13
5223254-6

Query Match 18.2%; Score 4; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 18 DMPI 21
|||
Db 3 DMPI 6

RESULT 74
US-08-361-517-2
; Sequence 2, Application US/08361517
; Patent No. 5916876
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; TITLE OF INVENTION: Adhesion
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSER: and No. 5916876ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/941,652
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated
US-08-361-517-2

Query Match 18.2%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 KVLP 8
|||
Db 4 KVLP 7

RESULT 75
US-08-361-517-6
; Sequence 6, Application US/08361517
; Patent No. 5916876
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; TITLE OF INVENTION: Adhesion
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSER: and No. 5916876ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/941,652
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated
US-08-361-517-6

Query Match 18.2%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 KVLP 8
|||
Db 5 KVLP 8

Search completed: November 25, 2003, 20:30:03
Job time : 18.7791 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 4.80233 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-28

Perfect score: 7

Sequence: 1 AFLLYQE 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	57.1	17	2 S05917	chorion class A pr
2	4	57.1	17	2 S05919	chorion class A pr
3	4	57.1	17	2 S05921	chorion class A pr
4	3	42.9	9	2 JN0027	[Phe-6]-mosact - s
5	3	42.9	10	2 PX0030	triacylglycerol li
6	3	42.9	11	2 C53652	rhLR protein - pse
7	3	42.9	11	2 B41935	translation elonga
8	3	42.9	12	2 S01122	photosystem II 3.7
9	3	42.9	12	2 A35585	cytokinin-binding
10	3	42.9	13	2 S01119	photosystem II pro
11	3	42.9	13	2 B47415	mannose-1-phosphat
12	3	42.9	13	4 I70075	glycophorin B [mis
13	3	42.9	14	2 S22236	lipoxxygenase (EC 1
14	3	42.9	14	2 B38222	excinnuclease ABC c
15	3	42.9	14	2 B61597	cytochrome P450 AL
16	3	42.9	15	2 C37765	hypothetical prote
17	3	42.9	15	2 S03955	acidic fibroblast
18	3	42.9	16	2 S65520	phospholipase A2 (
19	3	42.9	16	2 S24667	protein-tyrosine k
20	3	42.9	16	2 F54226	light-harvesting p
21	3	42.9	16	2 T14224	NADH2 dehydrogenas
22	3	42.9	17	2 S05913	chorion class A pr
23	3	42.9	17	2 S71327	hypothetical prote
24	3	42.9	17	2 A61557	major merozoite su
25	3	42.9	18	2 D56049	kidney stone prote
26	3	42.9	18	2 I50389	myosin heavy chain
27	3	42.9	18	2 A42016	mammary-derived gr
28	3	42.9	19	2 I40063	shikimate 5-dehydr
29	3	42.9	19	2 A61144	probable flagellar

30	3	42.9	19	2 A38386	Ca2+-transporting
31	3	42.9	20	2 A60822	cytochrome P450 PB
32	3	42.9	20	2 A26380	cytochrome P450 4A
33	3	42.9	20	2 A38566	GTP-binding protei
34	3	42.9	20	2 PL0161	hemagglutinin - in
35	3	42.9	20	2 A56045	urinary tract ston
36	3	42.9	20	2 S61278	nikkomycin synthe
37	3	42.9	20	2 A61150	2-oxoglutarate dec
38	3	42.9	20	2 PC2248	lambda 112 protein
39	3	42.9	3	3 A33802	thyrotropin-releas
40	3	42.9	3	3 S68328	blood cell protein
41	2	28.6	4	2 A35779	neuropeptide Antho
42	2	28.6	5	2 A26830	mitosis inhibiting
43	2	28.6	5	2 I40469	dnazX-like protein
44	2	28.6	5	2 PQ0009	angiotensin-conver
45	2	28.6	5	2 B61445	leu-enkephalin - b
46	2	28.6	5	2 S69237	surface protein te
47	2	28.6	6	2 A60986	N-formyl oligopept
48	2	28.6	6	2 JH0784	neuropeptide TE-6
49	2	28.6	6	2 A61068	locustakinin - mlg
50	2	28.6	6	2 I37263	Y protein - human
51	2	28.6	6	2 H48394	glycoprotein compo
52	2	28.6	6	2 I49424	cytotoxic T-lympho
53	2	28.6	7	1 A61324	dermorphin - Rohde
54	2	28.6	7	2 S36662	dermorphin (Lys-7)
55	2	28.6	7	2 S21230	dermorphin (Trp-4,
56	2	28.6	7	2 S08606	hypothetical prote
57	2	28.6	7	2 A34818	vicilin 72K chain
58	2	28.6	7	2 S78024	ribosomal protein
59	2	28.6	7	2 A34026	acetylcholinestera
60	2	28.6	7	2 S68004	hucolin, 75K chain
61	2	28.6	7	2 A11483	aspartate transami
62	2	28.6	7	2 PX0008	glucuronosyltransf
63	2	28.6	7	2 PN0649	pullulanase (EC 3.
64	2	28.6	8	2 S20162	leghemoglobin III
65	2	28.6	8	2 B24749	neuropeptide B - b
66	2	28.6	8	2 S37141	rpsA protein - Erw
67	2	28.6	8	2 S68802	nitrate reductase
68	2	28.6	8	2 S16324	hypothetical prote
69	2	28.6	8	2 A46306	spasmogenic toxin
70	2	28.6	8	2 JS0317	leucokinin VII - M
71	2	28.6	8	2 S66646	cardioacceleratory
72	2	28.6	8	2 A28719	thymic humoral fac
73	2	28.6	8	2 A42057	fibroblast growth
74	2	28.6	8	2 PN0043	phosphatidylethano
75	2	28.6	8	2 A35180	neutral proteinase
76	2	28.6	9	2 B45796	dihydrolipoamide S
77	2	28.6	9	2 A61102	parathyroid hormon
78	2	28.6	9	2 S07205	litorin 2-Glu - Au
79	2	28.6	9	2 A61357	phyllocaeerulein -
80	2	28.6	9	2 D28854	fibrinopeptide B -
81	2	28.6	9	2 F28854	fibrinopeptide B -
82	2	28.6	9	2 E28854	fibrinopeptide B -
83	2	28.6	9	2 S66607	quinoline 2-oxidor
84	2	28.6	9	2 S63491	dissimilatory sulf
85	2	28.6	9	2 S36898	ribosomal protein
86	2	28.6	9	2 S70334	endosperm protein,
87	2	28.6	9	2 S13333	alpha/beta-gliadin
88	2	28.6	9	2 A12872	transaldolase (EC
89	2	28.6	9	2 A11497	transaldolase (EC
90	2	28.6	9	2 A26363	cardioactive pepti
91	2	28.6	9	2 S39766	cardioactive pepti
92	2	28.6	9	2 S27233	cardioactive pepti
93	2	28.6	9	2 S10920	venom protein HR-3
94	2	28.6	9	2 PT0315	Ig heavy chain CRD
95	2	28.6	9	2 A28924	fructose-bisphosph
96	2	28.6	9	2 I52974	seminal vesicle pr
97	2	28.6	9	2 PH0942	T-cell receptor be
98	2	28.6	9	2 S39767	cardioactive pepti
99	2	28.6	9	2 PD0027	pev-tachykinin - p
100	2	28.6	10	2 C26997	unspecific monooxy

ALIGNMENTS

RESULT 1

S05917
 chorion class A protein L4 precursor - silkworm (fragment)
 C:Species: Bombyx mori (silkworm)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Aug-1999
 C:Accession: S05917
 R:Spoerel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.
 J. Mol. Biol. 209, 1-19, 1989
 A>Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybridization
 A:Reference number: S05913; MUID:90040707; PMID:2810362
 A:Accession: S05917
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-17 <SPO>
 A:Cross-references: EMBL:X15560; NID:G5781; PIDN:CAA33571.1; PID:G5782
 A:Note: this sequence was submitted to the EMBL Data Library, Jun-1989
 C:Genetics:
 A:Map position: 2
 C:Superfamily: chorion class A protein pc292

Query Match 57.1%; Score 4; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
 ||||
 Db 5 AFLL 8

RESULT 2

S05919
 chorion class A protein L5 precursor - silkworm (fragment)
 C:Species: Bombyx mori (silkworm)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Aug-1999
 C:Accession: S05919
 R:Spoerel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.
 J. Mol. Biol. 209, 1-19, 1989
 A>Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybridization
 A:Reference number: S05913; MUID:90040707; PMID:2810362
 A:Accession: S05919
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-17 <SPO>
 A:Cross-references: EMBL:X15561; NID:G5786; PIDN:CAA33573.1; PID:G5787
 A:Note: this sequence was submitted to the EMBL Data Library, Jun-1989
 C:Genetics:
 A:Map position: 2
 C:Superfamily: chorion class A protein pc292

Query Match 57.1%; Score 4; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
 ||||
 Db 5 AFLL 8

RESULT 3

S05921
 chorion class A protein L6 precursor - silkworm (fragment)
 C:Species: Bombyx mori (silkworm)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Aug-1999
 C:Accession: S05921
 R:Spoerel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.
 J. Mol. Biol. 209, 1-19, 1989
 A>Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybridization
 A:Reference number: S05913; MUID:90040707; PMID:2810362
 A:Accession: S05921
 A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-17 <SPO>

A:Cross-references: EMBL:X15562; NID:G5791; PIDN:CAA33575.1; PID:G5792

A:Note: this sequence was submitted to the EMBL Data Library, Jun-1989

C:Genetics:

A:Map position: 2

C:Superfamily: chorion class A protein pc292

Query Match 57.1%; Score 4; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
 ||||
 Db 5 AFLL 8

RESULT 4

JN0027
 [Phe-6]-mosact - sea urchin (Clypeaster japonicus)
 C:Species: Clypeaster japonicus
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Dec-1992
 C:Accession: JN0027
 R:Suzuki, N.; Kurita, M.; Yoshino, K.I.; Kajiuira, H.; Nomura, K.; Yamaguchi, M.
 Zool. Sci. 4, 649-656, 1987
 A>Title: Purification and structure of mosact and its derivatives from the egg jelly
 A:Reference number: JN0025
 A:Accession: JN0027
 A:Molecule type: protein
 A:Residues: 1-9 <SUZ>
 C:Comment: Mosact, one of several sperm activating peptides located in egg jelly, and

Query Match 42.9%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3
 ||||
 Db 5 AFL 7

RESULT 5

PX0030
 triacylglycerol lipase (EC 3.1.1.3) II - Yeast (Geotrichum candidum) (fragments)
 C:Species: Geotrichum candidum
 C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 30-Sep-1993
 C:Accession: PX0030
 R:Sugihara, A.; Shimada, Y.; Tomimaga, Y.
 J. Biochem. 107, 426-430, 1990
 A>Title: Separation and characterization of two molecular forms of Geotrichum candidum
 A:Reference number: PX0030; MUID:90256718; PMID:2341377
 A:Accession: PX0030

A:Molecule type: protein

A:Residues: 1-10 <SUG>

C:Comment: Lipase catalyzes the hydrolysis of triacylglycerols. This fungus contains

C:Keywords: carboxylic ester hydrolase

Query Match 42.9%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLY 5
 ||||
 Db 7 LLY 9

RESULT 6

CS3652
 rhlR protein - Pseudomonas aeruginosa (fragment)
 C:Species: Pseudomonas aeruginosa
 C>Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Aug-1998
 C:Accession: CS3652
 R:Ochsner, U.A.; Fiechter, A.; Reiser, J.

J. Biol. Chem. 269, 19787-19795, 1994
 A;Title: Isolation, characterization, and expression in *Escherichia coli* of the Pseudomonas
 A;Reference number: A53652; MUID:94327521; PMID:8051059
 A;Accession: C53652
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-11 <OCH>
 A;Cross-references: GB:L28170
 C;Superfamily: sdia regulatory protein

Query Match 42.9%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4
 |||
 Db 7 FLL 9

RESULT 7
 B41835
 translation elongation factor EF-G homolog - *Bacillus subtilis* (fragment)
 C;Species: *Bacillus subtilis*
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Dec-1997
 C;Accession: B41835
 R;Mitchell, C.; Morris, P.W.; Vary, J.C.
 J. Bacteriol. 174, 2474-2477, 1992
 A;Title: Identification of proteins phosphorylated by ATP during sporulation of *Bacillus*
 A;Reference number: A41835; MUID:92210489; PMID:1556067
 A;Accession: B41835
 A;Molecule type: protein
 A;Residues: 1-11 <MUT>
 A;Note: this protein is phosphorylated during stationary phase but not during exponential
 C;Keywords: phosphoprotein

Query Match 42.9%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4
 |||
 Db 1 FLL 3

RESULT 8
 S01122
 photosystem II 3.7K protein - spinach (fragment)
 C;Species: *Spinacia oleracea* (spinach)
 C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
 C;Accession: S01122
 R;Schroeder, W.P.; Henrysson, T.; Akerlund, H.E.
 FEBS Lett. 235, 289-292, 1988
 A;Title: Characterization of low molecular mass proteins of photosystem II by N-terminal
 A;Reference number: S01120
 A;Accession: S01122
 A;Molecule type: protein
 A;Residues: 1-12 <SCH>
 C;Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

Query Match 42.9%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3
 |||
 Db 7 AFL 9

RESULT 9
 A35585
 cytokinin-binding factor 1 - durum wheat
 C;Species: *Triticum durum* (durum wheat)
 C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 30-Sep-1993

C;Accession: A35585
 R;Brinegar, A.C.; Cooper, G.; Stevens, A.; Hauer, C.R.; Shabanowitz, J.; Hunt, D.F.;
 Proc. Natl. Acad. Sci. U.S.A. 85, 5927-5931, 1988
 A;Title: Characterization of a benzyladenine binding-site peptide isolated from a whe
 by mass spectrometry.
 A;Reference number: A35585; MUID:88320357; PMID:3413067
 A;Accession: A35585
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-12 <BRI>

Query Match 42.9%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3
 |||
 Db 1 AFL 3

RESULT 10
 S01119
 photosystem II protein psbK - spinach chloroplast (fragment)
 C;Species: chloroplast *Spinacia oleracea* (spinach)
 C;Date: 30-Jun-1989 #sequence_revision 31-Dec-1990 #text_change 19-Jan-1996
 C;Accession: S01119
 R;Murata, N.; Miyao, M.; Hayaashida, N.; Hidaka, T.; Sugiura, M.
 FEBS Lett. 235, 283-288, 1988
 A;Title: Identification of a new gene in the chloroplast genome encoding a low-molecu
 A;Reference number: S01119
 A;Accession: S01119
 A;Molecule type: protein
 A;Residues: 1-13 <MUR>
 C;Genetics:
 A;Gene: psbK
 A;Genome: chloroplast
 C;Superfamily: photosystem II protein psbK
 C;Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem II;

Query Match 42.9%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3
 |||
 Db 7 AFL 9

RESULT 11
 B47415
 mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) 43K alpha chain - pig (fragment
 N;Alternate names: GDP-mannose pyrophosphorylase 43K alpha chain
 C;Species: *Sus scrofa domestica* (domestic pig)
 C;Date: 25-Feb-1994 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
 C;Accession: B47415
 R;Szumilo, T.; Drake, R.R.; York, J.L.; Elbein, A.D.
 J. Biol. Chem. 268, 17943-17950, 1993
 A;Title: GDP-mannose pyrophosphorylase. Purification to homogeneity, properties, and
 A;Reference number: A47415; MUID:93352609; PMID:7688733
 A;Accession: B47415
 A;Molecule type: protein
 A;Residues: 1-13 <SZU>
 A;Experimental source: liver
 C;Complex: The enzyme appears to be a heterodimer of alpha and beta chains.
 C;Function:
 A;Description: generates GDP-mannose and pyrophosphate from mannose-1-phosphate and G
 A;Note: also catalyzes synthesis of GDP-glucose from glucose-1-phosphate (EC 2.7.7.34
 C;Keywords: blocked amino end; nucleotidyltransferase

Query Match 42.9%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4
|||
Db 11 FLL 13

RESULT 12

I70075
glycophorin B (mistranslated) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 21-Feb-1997 #sequence_revision 14-Aug-1997 #text_change 20-Apr-2000
C:Accession: I70075
R:Rearden, A.; Phan, H.; Dubnicoff, T.; Kudo, S.; Fukuda, M.
J. Biol. Chem. 265, 9259-9263, 1990
A:Title: Identification of the crossing-over point of a hybrid gene encoding human glycoprotein B (gp130) from a human-mouse hybrid cell line.
A:Reference number: I55334; MUID:90264417; PMID:1971625
A:Accession: I70075
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-13 <REA>
A:Cross-references: GB:M33505; GB:J05465; NID:G183726; PID:AA53152.1; PID:G442425
A:Note: this sequence was not determined in this report; the translation is from an incorrect reading frame.
C:Genetics:
A:Gene: GDB:GYBP
A:Cross-references: GDB:118891
A:Map position: 4q28-q31

Query Match 42.9%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6
|||
Db 11 LYQ 13

RESULT 13

S22236
lipoxigenase (EC 1.13.11.12) 1 - barley (fragment)
C:Species: Hordeum vulgare (barley)
C>Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C:Accession: S22236
R:Doderer, A.; Kokkelink, I.; van der Veen, S.; Valk, B.E.; Schram, A.W.; Douma, A.C.
Biochim. Biophys. Acta 1120, 97-104, 1992
A:Title: Purification and characterization of two lipoxigenase isoenzymes from germinating barley grains.
A:Reference number: S21772; MUID:92207997; PMID:1554746
A:Accession: S22236
A:Molecule type: protein
A:Residues: 1-14 <DOD>
A:Experimental source: var. Triumph, seed
C:Function:
A:Description: catalyzes the peroxidation of polyunsaturated fatty acids to their corresponding hydroperoxides
C:Superfamily: lipoxigenase
C:Keywords: monomer; oxidoreductase; seed

Query Match 42.9%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLY 5
|||
Db 5 LLY 7

RESULT 14

B38222
excinuclease ABC chain C (uvrC) [imported] - Pseudomonas fluorescens (fragment)
C:Species: Pseudomonas fluorescens
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: B38222
R:Laville, J.; Voisard, C.; Keel, C.; Maurhofer, M.; Defago, G.; Haas, D.
Proc. Natl. Acad. Sci. U.S.A. 89, 1562-1566, 1992
A:Title: Global control in Pseudomonas fluorescens mediating antibiotic synthesis and sporulation.
A:Reference number: A38222; MUID:92179223; PMID:1311842

A:Contents: CHAO
A:Accession: B38222
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-14 <LAV>
A:Note: sequence extracted from NCBI backbone (NCBIN:85369, NCBI:94242)

Query Match 42.9%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3
|||
Db 9 AFL 11

RESULT 15

B61597
cytochrome P450 AL-2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: B61597
R:Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.
Drug Metab. Dispos. 19, 291-297, 1991
A:Title: Purification and aminopyrine monooxygenase activity of liver microsomal cytochrome P450 AL-2 from rat liver.
A:Reference number: A61597; MUID:91292910; PMID:1676625
A:Accession: B61597
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <SHI>

Query Match 42.9%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4
|||
Db 9 FLL 11

RESULT 16

C37765
hypothetical protein (csma 3' region) - Chloroflexus aurantiacus (fragment)
C:Species: Chloroflexus aurantiacus
C>Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 30-Sep-1993
C:Accession: C37765
R:Theroux, S.J.; Redlinger, T.E.; Fuller, R.C.; Robinson, S.J.
J. Bacteriol. 172, 4497-4504, 1990
A:Title: Gene encoding the 5.7-kilodalton chlorosome protein of Chloroflexus aurantiacus.
A:Reference number: A37765; MUID:90330558; PMID:2376566
A:Accession: C37765
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-15 <THE>
A:Cross-references: GB:M33964

Query Match 42.9%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLY 5
|||
Db 4 LLY 6

RESULT 17

S03955
acidic fibroblast growth factor - dog (fragment)
N:Alternate names: alpha-endothelial cell growth factor
C:Species: Canis lupus familiaris (dog)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
C:Accession: S03955
R:Quinkler, W.; Maasberg, M.; Bernotat-Danielowski, S.; Luethe, N.; Sharma, H.S.; Sci

```

Eur. J. Biochem. 181, 67-73, 1989
A:Title: Isolation of heparin-binding growth factors from bovine, porcine and canine hea
A:Reference number: S03953; MUID:89231704; PMID:27114282
A:Accession: S03955
A:Molecule type: protein
A:Residues: 1-15 <QUI>
C:Keywords: growth factor

Query Match      42.9%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 LLY 5
Db      7 LLY 9

RESULT 18
S65520
Phospholipase A2 (EC 3.1.1.4) - Malayan spitting cobra (fragment)
N:Contains: muscarinic acetylcholine receptor inhibitor
C:Species: Naja naja sputatrix (Malayan spitting cobra)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 17-Mar-2000
C:Accession: S65520
R:Miyoshi, S.; Tu, A.T.
Arch. Biochem. Biophys. 328, 17-25, 1996
A:Title: Phospholipase A(2) from Naja naja sputatrix venom is a muscarinic acetylcholine
A:Reference number: S65520; MUID:96195757; PMID:8638927
A:Accession: S65520
A:Molecule type: protein
A:Residues: 1-16 <MIV>
C:Superfamily: phospholipase A2
C:Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; pres

Query Match      42.9%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 LYQ 6
Db      2 LYQ 4

RESULT 19
S24667
protein-tyrosine kinase (EC 2.7.1.112) kit - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1994 #sequence_revision 13-Mar-1997 #text_change 04-Feb-2000
C:Accession: S24667
R:Sorrentino, V.
submitted to the EMBL Data Library, May 1992
A:Reference number: S24666
A:Accession: S24667
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <SOR>
A:Cross-references: EMBL:X65998; NID:G50433; PIDN:CAA46799.1; PID:G50434
C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Query Match      42.9%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AFL 3
Db      10 AFL 12

RESULT 20
F54226
light-harvesting protein B-830 beta-2 chain - Chromatium purpuratum (fragment)
C:Species: Chromatium purpuratum
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996

```

```

C:Accession: P54226
R:Kerfeld, C.A.; Yeates, T.O.; Thornber, J.P.
Biochemistry 33, 2178-2184, 1994
A:Title: Purification and characterization of the peripheral antenna of the purple-su
A:Reference number: A54226; MUID:94162224; PMID:8117674
A:Accession: P54226
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <KER>
C:Keywords: antenna complex; light-harvesting polypeptide

Query Match      42.9%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AFL 3
Db      1 AFL 3

RESULT 21
T14224
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 6 - Euhadra herklotsi mitochondri
C:Species: mitochondrion Euhadra herklotsi
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C:Accession: T14224
R:Yamazaki, N.; Ueshima, R.; Terrett, J.A.; Yokobori, S.; Kaifu, M.; Segawa, R.; Koba
submitted to the EMBL Data Library, May 1996
A:Description: Evolution of pulmonate gastropod mitochondrial genomes: Comparisons of
A:Reference number: Z17932
A:Accession: T14224
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <YAM>
A:Cross-references: EMBL:Z71694; NID:e912660; PID:e244560; PIDN:CAA96364.1
A:Experimental source: adult; hepatopancreas
C:Genetics:
A:Genome: mitochondrion
C:Keywords: mitochondrion; NAD; oxidoreductase

Query Match      42.9%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FLL 4
Db      10 FLL 12

RESULT 22
S05913
chorion class A protein L2 precursor - silkworm (fragment)
C:Species: Bombyx mori (silkworm)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Aug-1999
C:Accession: S05913
R:Spoerel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.
J. Mol. Biol. 209, 1-19, 1989
A:Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybridi
A:Reference number: S05913; MUID:90040707; PMID:2810362
A:Accession: S05913
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-17 <SPO>
A:Cross-references: EMBL:X15558; NID:G5771; PIDN:CAA33567.1; PID:G5772
A>Note: this sequence was submitted to the EMBL Data Library, Jun-1989
C:Genetics:
A:Map position: 2
C:Superfamily: chorion class A protein pc292

Query Match      42.9%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


QY 2 FLL 4
 |||
 Db 7 FLL 9

RESULT 23
 S71327
 hypothetical protein - yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C>Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 29-Oct-1999
 C:Accession: S71327
 R:Sasaki, K.; Abid, M.R.; Miyazaki, M.
 FEBS Lett. 384, 151-154, 1996
 A>Title: Deoxyhypusine synthase gene is essential for cell viability in the yeast *Saccharomyces cerevisiae*
 A:Reference number: S71326; MUID:96201956; PMID:8612813
 A:Accession: S71327
 A>Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-17 <SAS>
 A:Cross-references: EMBL:D78185; NID:gl375086; PIDN:BAA11252.1; PID:d1011914; PID:gl3750

Query Match 42.9%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
 |||
 Db 12 LYQ 14

RESULT 24
 A61557
 major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (strain FCB-1)
 C:Species: Plasmodium falciparum
 C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
 C:Accession: A61557
 R:Heidrich, H.G.
 Biol. Cell 64, 205-214, 1988
 A>Title: Isolation and functional characterization of Plasmodium falciparum merozoite antigen
 A:Reference number: A61557; MUID:89150734; PMID:3067799
 A:Accession: A61557
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-17 <HEI>
 C:Keywords: surface antigen

Query Match 42.9%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YQE 7
 |||
 Db 6 YQE 8

RESULT 25
 D56049
 kidney stone protein, 34.5K - unidentified organism (fragment)
 C:Species: unidentified organism
 C>Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 20-Apr-2000
 C:Accession: D56049
 R:Binette, J.P.; Binette, M.B.
 Scanning Microsc. 8, 233-239, 1994
 A>Title: Sequencing of proteins extracted from stones.
 A:Reference number: A56049; MUID:95215817; PMID:7701298
 A:Accession: D56049
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-18 <BIN>
 A:Experimental source: urate-calcium oxalate kidney stone
 A>Note: the source is designated as Homo sapiens, however the true source probably originates from a different source
 C:Superfamily: sulfate-binding protein

Query Match 42.9%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
 |||
 Db 16 LYQ 18

RESULT 26
 I50389
 myosin heavy chain - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C:Accession: I50389
 R:Preyer, G.A.; Robbins, J.
 J. Biol. Chem. 258, 7149-7154, 1983
 A>Title: the analysis of a chicken myosin heavy chain cDNA clone.
 A:Reference number: I50388; MUID:83213464; PMID:6304080
 A:Accession: I50389
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-18 <PRE>
 A:Cross-references: GB:K00815; NID:g212369; PIDN:AAA48969.1; PID:g212370

Query Match 42.9%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
 |||
 Db 7 FLL 9

RESULT 27
 A42016
 mammary-derived growth factor 1 - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 30-Sep-1993
 C:Accession: A42016
 R:Bano, M.; Lupu, R.; Kidwell, W.R.; Lippman, M.E.; Dickson, R.B.
 Biochemistry 31, 610-616, 1992
 A>Title: Production and characterization of mammary-derived growth factor 1 in mammary gland
 A:Reference number: A42016; MUID:92118863; PMID:1731916
 A:Accession: A42016
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-18 <BAN>

Query Match 42.9%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
 |||
 Db 11 FLL 13

RESULT 28
 I40063
 strikinate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)
 C:Species: Buchnera aphidicola
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Oct-1999
 C:Accession: I40063
 R:Roubakhsh, D.; Baumann, P.
 Gene 155, 107-112, 1995
 A>Title: Characterization of a putative 23S-5S rRNA operon of *Buchnera aphidicola* (eubacterial strain) from the aphid *Acyrthosiphon pisum*
 A:Reference number: I40061; MUID:95212914; PMID:7535281
 A:Accession: I40063
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-19 <RES>

A;Cross-references: EMBL:U10497; NID:9854713; PIDN:AAA79126.1; PID:9854714
 C;Genetics:
 A;Gene: aroE
 C;Keywords: oxidoreductase

Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4
 |||
 Db 2 FLL 4

RESULT 29

A61144
 probable flagellar protein (clone FCH-F8-4) - Trypanosoma cruzi (fragment)
 C;Species: Trypanosoma cruzi
 C;Date: 10-Mar-1994 #sequence_revision 07-Apr-1994 #text_change 24-Feb-1995
 C;Accession: A61144
 R;Bua, J.; Bontempi, E.J.; Levin, M.; Orn, A.; Velasco, D.; Moreno, M.; Levi-Yeyati, P.;
 Exp. Parasitol. 72, 54-62, 1991
 A;Title: Trypanosoma cruzi: cellular and antibody response against the parasite in mice
 A;Reference number: A61144; MUID:91130571; PMID:1993465
 A;Accession: A61144
 A;Molecule type: mRNA
 A;Residues: 1-19 <BUA>

Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3
 |||
 Db 2 AFL 4

RESULT 30

A38386
 Ca2+-transporting ATPase (EC 3.6.3.8) - rat (fragments)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 19-Apr-2002
 C;Accession: A38386
 R;Kessler, F.; Bernardini, F.; Bachs, O.; Serratosa, J.; James, P.; Caride, A.J.; Gazzot
 J. Biol. Chem. 265, 16012-16019, 1990
 A;Title: Partial purification and characterization of the Ca(2+)-pumping ATPase of the l
 A;Reference number: A38386; MUID:90368826; PMID:2144292
 A;Accession: A38386
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-19 <KES>
 C;Keywords: hydrolase

Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6
 |||
 Db 3 LYQ 5

RESULT 31

A60822
 cytochrome P450 PB-3a - rat (fragment)
 N;Contains: oxidoreductase (EC 1.-.-.-)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Jun-1999
 C;Accession: A60822; I55191
 R;Ameliazad, Z.; Narbonne, J.F.; Wolf, C.R.; Robertson, L.W.; Oesch, F.
 Biochem. Pharmacol. 37, 3245-3249, 1988
 A;Title: Effect of nutritional imbalances on cytochrome P-450 isozymes in rat liver.
 A;Reference number: A60822; MUID:88293549; PMID:3041969

A;Accession: A60822
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <AME>
 R;Hashimoto, T.; Matsumoto, T.; Nishizawa, M.; Kawabata, S.
 J. Biochem. 103, 487-492, 1988
 A;Title: A mutant rat strain deficient in induction of a phenobarbital-inducible for
 A;Reference number: I55191; MUID:88273074; PMID:2839467
 A;Accession: I55191
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: DNA
 A;Residues: 1-20 <RES>
 A;Cross-references: GB:D00250; NID:9220727; PIDN:BAA00181.1; PID:9220728
 C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
 C;Keywords: electron transfer; heme; monooxygenase; oxidoreductase; transmembrane prc

Query Match 42.9%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4
 |||
 Db 15 FLL 17

RESULT 32

A26380
 cytochrome P450 4A2 - rat (fragment)
 N;Alternate names: cytochrome P450K-5
 N;Contains: oxidoreductase (EC 1.-.-.-)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 05-Mar-1999
 C;Accession: A26380
 R;Imaoka, S.; Funae, Y.
 Biochem. Biophys. Res. Commun. 141, 711-717, 1986
 A;Title: Purification and NH2-terminal sequence of cytochrome P-450 from kidney micro
 A;Reference number: A26380; MUID:87100198; PMID:3801020
 A;Accession: A26380
 A;Molecule type: protein
 A;Residues: 1-20 <IMA>
 A;Experimental source: kidney, untreated rats
 R;Kimura, S.; Hardwick, J.P.; Kozak, C.A.; Gonzalez, F.J.
 DNA 8, 517-525, 1989
 A;Title: The rat clofibrate-inducible CYP4A subfamily II. cDNA sequence of IVA3, mapp
 A;Reference number: A32966; MUID:89356272; PMID:2766933
 A;Contents: annotation; identification of constitutive kidney form as CYP4A2
 C;Genetics:
 A;Gene: CYP4A2
 C;Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology
 C;Keywords: electron transfer; heme; monooxygenase; oxidoreductase; transmembrane pro

Query Match 42.9%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3
 |||
 Db 18 AFL 20

RESULT 33

A38566
 GTP-binding protein G25K - bovine (fragments)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 16-Jul-1999
 C;Accession: A38566
 R;Yamane, H.K.; Farnsworth, C.C.; Xie, H.; Evans, T.; Howald, W.N.; Gelb, M.H.; Gloms
 Proc. Natl. Acad. Sci. U.S.A. 88, 286-290, 1991
 A;Title: Membrane-binding domain of the small G protein G25K contains an S-(all-trans
 A;Reference number: A38566; MUID:91095446; PMID:1898776
 A;Accession: A38566
 A;Status: preliminary
 A;Molecule type: protein

A;Residues: 1-20 <YAM>

C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding
F;8-11/Region: GTP-binding NKXD motif

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
|||
Db 3 FLL 5

RESULT 34

PL0161

hemagglutinin - Influenza H2N2 (fragment)

C;Species: Influenza H2N2

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-May-1997

C;Accession: PL0161

R;Sweetser, M.T.; Braciale, V.L.; Braciale, T.J.

J. Exp. Med. 170, 1357-1368, 1989

A;Title: Class I major histocompatibility complex-restricted T lymphocyte recognition of PL0161; MUID:90010790; PMID:2477491

A;Accession: PL0161

A;Molecule type: mRNA

A;Residues: 1-20 <SWE>

A;Experimental source: strain A/JAP/305/57

C;Comment: This protein plays a major role in initiation of infection and in the pathogenesis of influenza virus hemagglutinin

C;Superfamily: influenza virus hemagglutinin

C;Keywords: hemagglutinin

F;1-20/Region: immunodominant site recognized by T-lymphocytes

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
|||
Db 3 LYQ 5

RESULT 35

A56045

urinary tract stone matrix protein 12, 43K - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 12-Apr-1995

C;Accession: A56045

R;Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.

submitted to the Protein Sequence Database, February 1995

A;Description: Isolation, characterization and sequence of stone proteins.

A;Reference number: A56046

A;Accession: A56045

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-20 <BIN>

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
|||
Db 9 FLL 11

RESULT 36

S61278

nikkomycin synthesis protein P4 - Streptomyces tendae (fragment)

C;Species: Streptomyces tendae

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999

C;Accession: S61278

R;Moehle, V.; Roos, U.; Bormann, C.

Mol. Microbiol. 15, 561-571, 1995

A;Title: Identification of cellular proteins involved in nikkomycin production in Streptomyces tendae
A;Reference number: S61278; MUID:95302967; PMID:7783626

A;Accession: S61278

A;Molecule type: protein

A;Residues: 1-20 <MOE>

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
|||
Db 8 FLL 10

RESULT 37

AG1150

2-oxoglutarate decarboxylase (EC 4.1.1.71) - Euglena gracilis (fragment)

C;Species: Euglena gracilis

C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-Apr-1994

C;Accession: AG1150

R;Shigeoka, S.; Nakano, Y.

Arch. Biochem. Biophys. 288, 22-28, 1991

A;Title: Characterization and molecular properties of 2-oxoglutarate decarboxylase from Euglena gracilis

A;Reference number: AG1150; MUID:91378443; PMID:1910306

A;Accession: AG1150

A;Molecule type: protein

A;Residues: 1-20 <SHI>

C;Keywords: carbon-carbon lyase; carboxy-lyase; homotetramer; mitochondrion

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
|||
Db 12 FLL 14

RESULT 38

PC2248

lambda 112 protein - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Sep-1997

C;Accession: PC2248

R;Sakai, N.; Inui, K.; Fujii, N.; Fukushima, H.; Nishimoto, J.; Yanagihara, I.; Iseig.

Biochem. Biophys. Res. Commun. 198, 485-491, 1994

A;Title: Krabbe disease: isolation and characterization of a full-length cDNA for human lambda 112 protein

A;Reference number: JC2397; MUID:94128088; PMID:8297359

A;Accession: PC2248

A;Molecule type: mRNA

A;Residues: 1-20 <SAK>

A;Cross-references: DDBJ:D25284

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLY 5
|||
Db 12 LLY 14

RESULT 39

A33802

thyrotropin-releasing hormone-like peptide - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: A33802

R;Cockle, S.M.; Aitken, A.; Beg, F.; Smyth, D.G.

J. Biol. Chem. 264, 7788-7791, 1989

A;Title: A novel peptide, pyroglutamylglutamylproline amide, in the rabbit prostate

A:Reference number: A33802; MUID:89255196; PMID:2498305

A:Accession: A33802

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-3 <GOC>

C:Superfamily: unassigned animal peptides

C:Keywords: amidated carboxyl end; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 28.6%; Score 2; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QE 7

Db 1 QE 2

RESULT 40

S68328 Blood cell protein A - *Molgula manhattensis* (fragment)

C:Species: *Molgula manhattensis*

C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C:Accession: S68328

R:Taylor, S.W.; Ross, M.M.; Waite, J.H.

Arch. Biochem. Biophys. 324, 228-240, 1995

A:Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from the

A:Reference number: S68325; MUID:96132650; PMID:8554314

A:Accession: S68328

A:Molecule type: protein

A:Residues: 1-3 <IAY>

Query Match 28.6%; Score 2; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AF 2

Db 1 AF 2

RESULT 41

A35779

neuropeptide Antho-RNAmide - sea anemone (*Anthopleura elegantissima*)

C:Species: *Anthopleura elegantissima*

C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 08-Dec-1995

C:Accession: A35779

R:Grimmelikhuizen, C.J.P.; Rinehart, K.L.; Jacob, E.; Graff, D.; Reinscheid, R.K.; North

Proc. Natl. Acad. Sci. U.S.A. 87, 5410-5414, 1990

A:Title: Isolation of L-3-phenylacetyl-Leu-Arg-Asn-NH₂ (Antho-RNAmide), a sea anemone ne-

A:Reference number: A35779; MUID:90319122; PMID:1973541

A:Accession: A35779

A:Molecule type: protein

A:Residues: 1-4 <GRI>

C:Comment: The L-3-phenylacetyl blocking group probably arises from an amino-terminal ph

C:Keywords: amidated carboxyl end; neuropeptide; phenylacetylation

F:1/Modified site: L-3-phenylacetic acid (Phe) #status experimental

F:4/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FL 3

Db 1 FL 2

RESULT 42

A26830

mitosis inhibiting peptide - mouse

C:Species: *Mus musculus* (house mouse)

C:Date: 19-Nov-1988 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000

C:Accession: A26830

R:Reichelt, K.; Elgjo, K.; Edminson, P.D.

Biochem. Biophys. Res. Commun. 146, 1493-1501, 1987

A:Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.

A:Reference number: A26830; MUID:87298602; PMID:3619940

A:Accession: A26830

A:Molecule type: protein

A:Residues: 1-5 <REI>

C:Superfamily: unassigned animal peptides

C:Keywords: blocked amino end; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QE 7

Db 1 QE 2

RESULT 43

I40469

dnazX-like protein - *Bacillus subtilis* (fragment)

C:Species: *Bacillus subtilis*

C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000

C:Accession: I40469

R:Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.

Mol. Gen. Genet. 215, 478-482, 1989

A:Title: Transcription and processing of *Bacillus subtilis* small cytoplasmic RNA.

A:Reference number: I40469; MUID:89218958; PMID:2468993

A:Accession: I40469

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-5 <RES>

A:Cross-references: EMBL:X14796; MID:g40130; PIDN:CAA32902.1; PID:g4376204

C:Genetics:

A:Start codon: GTG

Query Match 28.6%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YQ 6

Db 3 YQ 4

RESULT 44

PQ0009

angiotensin-converting enzyme inhibitor (FLP-2) - common fig

N:Alternate names: ficus latex peptide 2

C:Species: *Ficus carica* (common fig)

C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995

C:Accession: PQ0009

R:Maruyama, S.; Miyoshi, S.; Tanaka, H.

Agric. Biol. Chem. 53, 2763-2767, 1989

A:Title: Angiotensin I-converting enzyme inhibitors derived from *Ficus carica*.

A:Reference number: PQ0008

A:Accession: PQ0009

A:Molecule type: protein

A:Residues: 1-5 <MAR>

A:Experimental source: latex

C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 28.6%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LY 5

Db 1 LY 2

```

RESULT 45
B61445
Leu-enkephalin - blue mussel
C:Species: Mytilus edulis (blue mussel)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C:Accession: B61445
R:Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis
A:Reference number: A61445; MUID:84144823; PMID:6583690
A:Accession: B61445
A:Molecule type: protein
A:Residues: 1-5 <LEU>
A:Experimental source: pedal ganglia
C:Keywords: neuropeptide; opioid peptide

Query Match      28.6%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FL 3
      |||
Db      4 FL 5

RESULT 46
S69237
surface protein tetra-brachion heavy chain - Staphylothermus marinus (fragment)
C:Species: Staphylothermus marinus
C>Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
C:Accession: S69237
R:Peters, J.; Nitsch, M.; Kuehlmoorgen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; Engelh
J. Mol. Biol. 245, 385-401, 1995
A:Title: Tetra-brachion: a filamentous archaeobacterial surface protein assembly of unusua
A:Reference number: S69237; MUID:95139088; PMID:7837271
A:Accession: S69237
A:Molecule type: protein
A:Residues: 1-5 <PET>
A:Experimental source: strain F1, DSM 3639
C:Keywords: cell wall; glycoprotein; heat-stable protein

Query Match      28.6%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LL 4
      |||
Db      3 LL 4

RESULT 47
A60986
N-formyl oligopeptide - Escherichia coli (fragment)
C:Species: Escherichia coli
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
C:Accession: A60986
R:Broom, M.F.; Mellor, D.M.; Chadwick, V.S.
Experientia 45, 1097-1099, 1989
A:Title: Purification and amino acid sequencing of naturally occurring N-formyl-methionyl
A:Reference number: A60986; MUID:90092408; PMID:2689204
A:Accession: A60986
A:Molecule type: protein
A:Residues: 1-6 <BRO>
C:Comment: This hexapeptide was the longest of several N-formyl oligopeptides reported.
F:1/Modified site: N-formylmethionine #status experimental

Query Match      28.6%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LL 4

us-09-641-801-28.oligo.rpr

Db      5 LL 6

RESULT 48
JH0784
neuropeptide TE-6 - pig roundworm (fragment)
C:Species: Ascaris suum (pig roundworm)
C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 28-Apr-1995
C:Accession: JH0784
R:Smart, D.; Shaw, C.; Curry, W.J.; Johnston, C.F.; Thim, L.; Halton, D.W.; Buchanan
Biochem. Biophys. Res. Commun. 187, 1323-1329, 1992
A:Title: The primary structure of TE-6: a novel neuropeptide from the nematode Ascar
A:Reference number: JH0784; MUID:93038603; PMID:14117808
A:Accession: JH0784
A:Molecule type: protein
A:Residues: 1-6 <SMA>
A:Experimental source: gonoduct
C:Keywords: neuropeptide

Query Match      28.6%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 QE 7
      |||
Db      3 QE 4

RESULT 49
A61068
locustakinin - migratory locust
C:Species: Locusta migratoria (migratory locust)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
C:Accession: A61068
R:Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.
Regul. Pept. 37, 49-57, 1992
A:Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation,
A:Reference number: A61068; MUID:92262851; PMID:1585017
A:Accession: A61068
A:Molecule type: protein
A:Residues: 1-6 <SCH>
C:Keywords: amidated carboxyl end; cephalomylotropic peptide; neuropeptide
F:6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match      28.6%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AF 2
      |||
Db      1 AF 2

RESULT 50
I37263
Y protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
C:Accession: I37263
R:Waeber, G.; Habener, J.F.
Endocrinology 131, 2010-2015, 1992
A:Title: Novel testis germ cell-specific transcript of the CREB gene contains an alt.
A:Reference number: I37263; MUID:93010691; PMID:1396344
A:Accession: I37263
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816
C:Genetics:
A:Gene: CREB

Query Match      28.6%; Score 2; DB 2; Length 6;

```

```

Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4
  ||
Db 5 LL 6

RESULT 51
H48394
Glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C;Accession: H48394
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
II-like sequences.
A;Reference number: A48394; MUID:93250576; PMID:8485470
A;Accession: H48394
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <MAT>
A;Experimental source: milk
A;Note: sequence extracted from NCBI backbone (NCBIP:131518)
C;Keywords: glycoprotein

Query Match 28.6%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4
  ||
Db 3 LL 4

RESULT 52
I49424
Cytotoxic T-lymphocyte proteinase 3 (EC 3.4.21.-) - western wild mouse (fragment)
C;Species: Mus spretus (western wild mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I49424
R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maeraki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A;Reference number: I48934; MUID:94319082; PMID:8043949
A;Accession: I49424
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross-references: EMBL:U05745; NID:9497084; PIDN:AAB60481.1; PID:G642831
C;Keywords: hydrolase; serine proteinase

Query Match 28.6%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4
  ||
Db 5 LL 6

RESULT 53
A61324
dermorphin - Rohde's leaf frog
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
C;Date: 17-Jul-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C;Accession: A61324
R;Montecucchi, P.C.; De Castiglione, R.; Erspamer, V.
Int. J. Pept. Protein Res. 17, 316-321, 1981
A;Title: Identification of dermorphin and Hyp(6)-dermorphin in skin extracts of the Braz
A;Reference number: A61324; MUID:82029915; PMID:7287302
A;Accession: A61324

```

```

A;Molecule type: protein
A;Residues: 1-7 <MON>
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
C;Keywords: amidated carboxyl end; D-amino acid; hydroxyproline; neuropeptide; skin
F;2/Modified site: D-alanine (Ala) #status experimental
F;6/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
F;7/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 28.6%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AF 2
  ||
Db 2 AF 3

RESULT 54
S36662
dermorphin (Lys-7) [validated] - two-colored leaf frog
C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Date: 10-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 18-Aug-2000
C;Accession: S36662
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil,
FEBS Lett. 302, 151-154, 1992
A;Title: Identification and characterization of two dermorphins from skin extracts of
A;Reference number: S21152; MUID:92339502; PMID:1633846
A;Accession: S36662
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIG>
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AF 2
  ||
Db 2 AF 3

RESULT 55
S21230
dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)
C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000
C;Accession: S21230
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil,
FEBS Lett. 302, 151-154, 1992
A;Title: Identification and characterization of two dermorphins from skin extracts of
A;Reference number: S21152; MUID:92339502; PMID:1633846
A;Accession: S21230
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIG>
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AF 2
  ||
Db 2 AF 3

RESULT 56
S08606
hypothetical protein 2 estrogen receptor 5'-region - chicken
C;Species: Gallus gallus (chicken)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 18-Aug-2000
C;Accession: S08606

```

R;Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P.
EMBO J. 5, 891-897, 1986
A;Title: The chicken oestrogen receptor sequence: homology with v-erbA and the human oes
A;Reference number: S07192; MUID:86247578; PMID:3755102
A;Accession: S08806
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <XRU>
A;Cross-references: EMBL:X03805; NID:G63378; PIDN:CAA27432.1; PID:G584490
C;Superfamily: unassigned leader peptides

Query Match 28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
DB 2 FL 3

RESULT 57
A34818
vicilin 72K chain - pigeon pea (fragment)
C;Species: Cajanus cajan (pigeon pea)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 30-Sep-1993
C;Accession: A34818
R;Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.
Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990
A;Title: Unusual denaturation properties of vicilin from Cajanus cajan.
A;Reference number: A34818; MUID:90165956; PMID:2306256
A;Accession: A34818
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MAW>

Query Match 28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QE 7
DB 6 QE 7

RESULT 58
S78024
ribosomal protein YmL21, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)
C;Species: Saccharomyces cerevisiae
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997
C;Accession: S78024
R;Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittma
Eur. J. Biochem. 245, 449-456, 1997
A;Title: Identification and characterization of the genes for mitochondrial ribosomal pr
A;Reference number: S78018; MUID:97296414; PMID:9151978
A;Accession: S78024
A;Molecule type: protein
A;Residues: 1-7 <KIT>
C;Genetics:
A;Genome: nuclear
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LL 4
DB 5 LL 6

RESULT 59
A34026
acetylcholinesterase (EC 3.1.1.7) 5.6S form - Pacific electric ray (fragment)

C;Species: Torpedo californica (Pacific electric ray)
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 08-Nov-1996
C;Accession: A34026
R;Gibney, G.; MacPhee-Quigley, K.; Thompson, B.; Vedvick, T.; Low, M.G.; Taylor, S.S
J. Biol. Chem. 263, 1140-1145, 1988
A;Title: Divergence in primary structure between the molecular forms of acetylcholin
A;Reference number: A34026; MUID:88087239; PMID:3335534
A;Accession: A34026
A;Molecule type: protein
A;Residues: 1-7 <GIB>
C;Keywords: alternative splicing; carboxylic ester hydrolase

Query Match 28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LL 4
DB 1 LL 2

RESULT 60
S68004
huocolin, 75K chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S68004
R;Edgar, P.F.
FEBS Lett. 375, 159-161, 1995
A;Title: Huocolin, a new corticosteroid-binding protein from human plasma with struct
A;Reference number: S68004; MUID:96087107; PMID:7498469
A;Accession: S68004
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <EDG>

Query Match 28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2
DB 2 AF 3

RESULT 61
A11483
aspartate transaminase (EC 2.6.1.1), mitochondrial - sheep (fragment)
N;Alternate names: aspartate aminotransferase, mitochondrial
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 20-Aug-1999
C;Accession: A11483
R;Campos-Cavieres, M.; Milstein, C.P.
Biochem. J. 147, 275-281, 1975
A;Title: The sequences of the coenzyme-binding peptide in the cytoplasmic and the mi
A;Reference number: A11483; MUID:76039441; PMID:1180894
A;Accession: A11483
A;Molecule type: protein
A;Residues: 1-7 <CAM>
A;Experimental source: liver
C;Keywords: aminotransferase; mitochondrion; phosphoprotein; pyridoxal phosphate
F;2/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LY 5
DB 6 LY 7

RESULT 62

PX0008
glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)
N;Alternate names: UDP-glucuronosyltransferase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 07-Feb-1997
C;Accession: PX0008
R;Yokota, H.; Yuasa, A.; Sato, R.
J. Biochem. 104, 531-536, 1988
A;Title: Purification and properties of a form of UDP-glucuronosyltransferase from liver
A;Reference number: PX0008; MUID:89197852; PMID:3149280
A;Accession: PX0008
A;Molecule type: protein
A;Residues: 1-7 <YOK>
C;Keywords: glycosyltransferase; hexosyltransferase; liver

Query Match 28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4
Db 3 LL 4

RESULT 63
PX0649
pullulanase (EC 3.2.1.41) - Bacillus sp. (strain S-1) (fragment)
C;Species: Bacillus sp.
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 03-Jun-2002
C;Accession: PX0649
R;Kim, C.H.; Choi, H.I.; Lee, D.S.
Biosci. Biotechnol. Biochem. 57, 1632-1637, 1993
A;Title: Purification and biochemical properties of an alkaline pullulanase from alkalop
A;Reference number: PX0649; MUID:94080025; PMID:7764261
A;Accession: PX0649
A;Molecule type: protein
A;Residues: 1-7 <KIM>
C;Comment: This enzyme is used together with glucoamylase to improve the efficiency of st
ntent in high maltose syrups.
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FL 3
Db 1 FL 2

RESULT 64
S20162
leghemoglobin III - Sesbania rostrata (fragment)
C;Species: Sesbania rostrata
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 04-Mar-2000
C;Accession: S20162
R;Metz, B.A.; Welters, P.; Hoffmann, H.J.; Jensen, E.O.; Schell, J.; de Bruijn, F.J.
Mol. Gen. Genet. 214, 181-191, 1988
A;Title: Primary structure and promoter analysis of leghemoglobin genes of the stem-nodu
A;Reference number: S08322; MUID:89181515; PMID:3237206
A;Accession: S20162
A;Molecule type: DNA
A;Residues: 1-8 <MET>
A;Cross-references: EMBL:X13504; NID:G21383; PIDN:CAA31858.1; PID:G579482
C;Genetics:
A;Gene: glb3
C;Superfamily: globin; globin homology
C;Keywords: heme; oxygen carrier

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QE 7
Db 7 QE 8

RESULT 65
B24749
neuropeptide B - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2000
C;Accession: B24749
R;Yang, H.Y.T.; Pratta, W.; Majane, E.A.; Costa, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985
A;Title: Isolation, sequencing, synthesis, and pharmacological characterization of tw
A;Reference number: A94074; MUID:86067985; PMID:3865193
A;Accession: B24749
A;Molecule type: protein
A;Residues: 1-8 <YAN>
C;Superfamily: unassigned animal peptides
C;Keywords: neuropeptide

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FL 3
Db 1 FL 2

RESULT 66
S37141
rpsA protein - Erwinia chrysanthemi
C;Species: Erwinia chrysanthemi
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1999
C;Accession: S37141
R;Duillie, A.; Toussaint, A.; Faalen, M.
Submitted to the EMBL Data Library, August 1993
A;Title: Identification of the integration host factor genes of E. chrysanthemi
A;Reference number: S37139
A;Accession: S37141
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-8 <DOU>
A;Cross-references: EMBL:X74750; NID:G399669; PIDN:CAA52769.1; PID:G581108

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AF 2
Db 1 AF 2

RESULT 67
S68802
nitrate reductase (NADH) inhibitor - spinach (fragment)
C;Species: Spinacia oleracea (spinach)
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 30-Jan-1998
C;Accession: S68802
R;Bachmann, M.; Huber, J.L.; Liao, P.C.; Gage, D.A.; Huber, S.C.
FEBS Lett. 387, 127-131, 1996
A;Title: The inhibitor protein of phosphorylated nitrate reductase from spinach (spin
A;Reference number: S68802; MUID:96244508; PMID:8674533
A;Accession: S68802
A;Molecule type: protein
A;Residues: 1-8 <BAC>
A;Experimental source: leaves; strain cv. Bloomsdale

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LL 4
||
2 LL 3

RESULT 68

S16324
hypothetical protein 2 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
C:Accession: S16324
R:Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
EMBO J. 10, 1787-1791, 1991
A:Title: A novel class of plant proteins containing a homeodomain with a closely linked
A:Reference number: S16323; MUID:91266907; PMID:1675603
A:Accession: S16324
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <RUB>
A:Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g579259

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LL 4
||
5 LL 6

RESULT 69

A46306
spasmogenic toxin PNV1 - spider (Phoneutria nigriventer) (fragment)
C:Species: Phoneutria nigriventer
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999
C:Accession: A46306
R:Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.; Novello, J.
Toxicon 31, 377-384, 1993
A:Title: Biochemical characterization of a vascular smooth muscle contracting polypeptide
A:Reference number: A46306; MUID:93276438; PMID:8503129
A:Accession: A46306
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <MAR>

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2
||
2 AF 3

RESULT 70

JS0317
leucokinin VII - Madeira cockroach
C:Species: Leucophaea maderae (Madeira cockroach)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Accession: JS0317
R:Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 31-34, 1987
A:Title: Isolation, primary structure and synthesis of leucokinin VII and VIII: the first
A:Reference number: JS0317
A:Accession: JS0317
A:Molecule type: protein
A:Residues: 1-8 <HOL>
C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile act
C:Keywords: amidated carboxyl end; cephalomyotropic peptide
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2
||
3 AF 4

RESULT 71

S66646
cardioacceleratory protein 2b - tobacco hornworm
C:Species: Manduca sexta (tobacco hornworm)
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S66646
R:Huesmann, G.R.; Cheung, C.C.; Loi, P.K.; Lee, T.D.; Swiderek, K.M.; Tublitz, N.J.
PDBS Lett. 371, 311-314, 1995
A:Title: Amino acid sequence of CAP(2b), an insect cardioacceleratory peptide from t
A:Reference number: S66646; MUID:96013159; PMID:7556618
A:Accession: S66646
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <HUE>

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LY 5
||
2 LY 3

RESULT 72

A28719
thymic humoral factor gamma-2 - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1993
C:Accession: A28719
R:Burstein, Y.; Buchner, V.; Pecht, M.; Trainin, N.
Biochemistry 27, 4066-4071, 1988
A:Title: Thymic humoral factor gamma-2: purification and amino acid sequence of an i
A:Reference number: A28719; MUID:88326920; PMID:3261994
A:Accession: A28719
A:Molecule type: protein
A:Residues: 1-8 <BUR>

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
||
7 FL 8

RESULT 73

A42057
fibroblast growth factor receptor 1, secreted - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C:Accession: A42057
R:Werner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.
Mol. Cell. Biol. 12, 82-89, 1992
A:Title: Differential splicing in the extracellular region of fibroblast growth fact
A:Reference number: A42057; MUID:92107200; PMID:1309595
A:Accession: A42057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <WER>
A:Cross-references: GB:M80363
C:Keywords: growth factor receptor

Query Match 28.6%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4
||
Db 2 LL 3

RESULT 74
PN0043
phosphatidylethanol amine-binding protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
C;Accession: PN0043
R;Kato, H.
Kawasaki Igakkaishi 22, 245-259, 1996
A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro
A;Reference number: PN0041
A;Accession: PN0043
A;Molecule type: protein
A;Residues: 1-8 <KAR>
A;Experimental source: neuroblastoma cell
C;Comment: The molecular mass is 23,500 and the pI is 4.8. The amino-terminus is blocked
C;Keywords: brain

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LY 5
||
Db 1 LY 2

RESULT 75
A35180
neutral proteinase (EC 3.4.4.-), calcium-activated - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 21-Mar-1996
C;Accession: A35180
R;Yoshihara, Y.; Ueda, H.; Fujii, N.; Shide, A.; Yajima, H.; Satoh, M.
J. Biol. Chem. 265, 5809-5815, 1990
A;Title: Purification of a novel type of calcium-activated neutral protease from rat bra
A;Reference number: A35180; MUID:90202830; PMID:2318836
A;Accession: A35180
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <YOS>
C;Keywords: hydrolase

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4
||
Db 2 LL 3

Search completed: November 25, 2003, 19:36:12
Job time : 5.80233 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 2.48256 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-28

Perfect score: 7

Sequence: 1 AFLYQE 7

Scoring table: OIIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	42.9	9	1	MOSF_CLYQA
2	3	42.9	15	1	APP3_MALPA
3	3	42.9	15	1	PGF1_CANFA
4	3	42.9	16	1	P22_NAJSP
5	3	42.9	17	1	EPG_THEQA
6	3	42.9	17	1	PH3_PERAM
7	3	42.9	20	1	AF2L_MALPA
8	2	28.6	4	1	FLRF_HIRME
9	2	28.6	4	1	FLRN_ATEL
10	2	28.6	6	1	LOK1_LOCMI
11	2	28.6	7	1	ALL2_CARMA
12	2	28.6	7	1	ALL3_CARMA
13	2	28.6	7	1	ALL4_CARMA
14	2	28.6	7	1	ALL5_CARMA
15	2	28.6	7	1	FAR1_HELTI
16	2	28.6	7	1	FAR1_MACRS
17	2	28.6	7	1	FAR1_PROCL
18	2	28.6	7	1	FAR2_PROCL
19	2	28.6	7	1	GRFP_MOUSE
20	2	28.6	7	1	PH2_LYCES
21	2	28.6	7	1	UN06_PINPS
22	2	28.6	8	1	ALL2_CARMA
23	2	28.6	8	1	ALL6_CYPDO
24	2	28.6	8	1	ALL7_CARMA
25	2	28.6	8	1	ALL8_CARMA
26	2	28.6	8	1	ALL9_CARMA
27	2	28.6	8	1	B44K_FORGI
28	2	28.6	8	1	CUP_THICU
29	2	28.6	8	1	COW2_CONFU
30	2	28.6	8	1	CPD1_ENTFA
31	2	28.6	8	1	FAR1_PANRE
32	2	28.6	8	1	FAR1_PENNO
33	2	28.6	8	1	FAR2_MACRS

34	2	28.6	8	1	FAR3_HOMAM
35	2	28.6	8	1	FAR4_HOMAM
36	2	28.6	8	1	LCK1_LEUMA
37	2	28.6	8	1	ICK7_LEUMA
38	2	28.6	8	1	NPB_BOVIN
39	2	28.6	8	1	NS3_MYCTU
40	2	28.6	8	1	ORMV_ORCLI
41	2	28.6	8	1	RSI_ERWCH
42	2	28.6	8	1	UH09_RAT
43	2	28.6	8	1	UPA1_HUMAN
44	2	28.6	9	1	AL10_CARMA
45	2	28.6	9	1	AL11_CARMA
46	2	28.6	9	1	BUK_CLOPA
47	2	28.6	9	1	CCAP_CARMA
48	2	28.6	9	1	FAR2_PANRE
49	2	28.6	9	1	FAR3_MACRS
50	2	28.6	9	1	FAR6_MACRS
51	2	28.6	9	1	FAR8_MACRS
52	2	28.6	9	1	FARP_CALSI
53	2	28.6	9	1	FIBB_PAPAN
54	2	28.6	9	1	FIBB_PAPHA
55	2	28.6	9	1	FIBB_THEGE
56	2	28.6	9	1	NEUO_CAYPO
57	2	28.6	9	1	NEUX_HUMAN
58	2	28.6	9	1	RE42_LITRU
59	2	28.6	9	1	TAL1_PICUA
60	2	28.6	9	1	TAL3_PICUA
61	2	28.6	9	1	TKC1_CALVO
62	2	28.6	9	1	ULAE_HUMAN
63	2	28.6	9	1	UPA7_HUMAN
64	2	28.6	10	1	CU30_LOCMI
65	2	28.6	10	1	FAR7_MACRS
66	2	28.6	10	1	FARP_LOCMI
67	2	28.6	10	1	FARP_MANSE
68	2	28.6	10	1	LCMS_LEUMA
69	2	28.6	10	1	PORB_METTM
70	2	28.6	10	1	Q20B_COMTE
71	2	28.6	10	1	TEMK_RANTE
72	2	28.6	11	1	CSI5_BACSU
73	2	28.6	11	1	MHBI_KLEPN
74	2	28.6	11	1	RE41_LITRU
75	2	28.6	11	1	TKC2_CALVO
76	2	28.6	11	1	TKN1_UPSIN
77	2	28.6	11	1	TKN1_UPERU
78	2	28.6	11	1	TKN_ELEMO
79	2	28.6	11	1	ULAG_HUMAN
80	2	28.6	12	1	CD11_LITXA
81	2	28.6	12	1	CD14_LITXA
82	2	28.6	12	1	FRE1_LITIN
83	2	28.6	12	1	GRAR_RANRU
84	2	28.6	12	1	PA21_MICFM
85	2	28.6	12	1	PA2B_VIPBO
86	2	28.6	13	1	CD71_LITWE
87	2	28.6	13	1	CHEP_PARID
88	2	28.6	13	1	CRBL_ICASP
89	2	28.6	13	1	CRBL_VESAN
90	2	28.6	13	1	CRBL_VESCR
91	2	28.6	13	1	CRBL_VESLE
92	2	28.6	13	1	CRBL_VESMA
93	2	28.6	13	1	CRBL_VESMA
94	2	28.6	13	1	CRBL_VESXA
95	2	28.6	13	1	CRBL_VESXA
96	2	28.6	13	1	CRBL_VESXA
97	2	28.6	13	1	CRBL_VESXA
98	2	28.6	13	1	CRBL_VESXA
99	2	28.6	13	1	CRBL_VESXA
100	2	28.6	13	1	CRBL_VESXA

ALIGNMENTS

RESULT 1

```

MOSF_CLYJA
ID MOSF_CLYJA STANDARD; PRT; 9 AA.
AC P19853;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE [Phe-6]-mosact.
OS Clypeaster japonicus (Sand dollar).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroidea;
OC Clypeasteridae; Clypeaster.
OX NCBI_TaxID=7644;
RN [1]
RP SEQUENCE.
RC TISSUE=Egg jelly;
RA Suzuki N., Kurita M., Yoshino K.I., Kajiura H., Nomura K.,
RA Yamaguchi M.;
RT "Purification and structure of mosact and its derivatives from the
RT egg jelly of the sea urchin Clypeaster japonicus.";
RL Zool. Sci. 4:649-656(1987).
CC -!- FUNCTION: Stimulates sperm respiration and motility.
DR PIR; JN0027; JN0027.
SQ SEQUENCE 9 AA; 924 MW; 93245729CDC5BAB5 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APL 3
Db |||
5 APL 7

RESULT 2
APP3_MALPA
ID APP3_MALPA STANDARD; PRT; 15 AA.
AC P83137;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antifungal protein 3 (CW-3) (Fragment).
OS Malva parviflora (Little mallow) (Cheeseweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.
OX NCBI_TaxID=145753;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Seed;
RX MEDLINE=21199399; PubMed=11302747;
RA Wang X., Bunkers G.J., Walters M.R., Thoma R.S.;
RT "Purification and characterization of three antifungal proteins from
RT cheeseweed (Malva parviflora)";
RL Biochem. Biophys. Res. Commun. 282:1224-1228(2001).
CC -!- FUNCTION: Possesses antifungal activity against P.infestans but
CC not F.graminearum.
CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC concentration.
DR GO; GO:0003799; F:antifungal peptide activity; IDA.
DR GO; GO:0007275; P:development; NAS.
KW Fungicide; Antibiotic.
FT NON TER 15
SQ SEQUENCE 15 AA; 2016 MW; 01D9CA069F1A52DB CRC64;

Query Match 42.9%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YQE 7
Db |||
8 YQE 10

```

```

RESULT 3
FGF1_CANFA
ID FGF1_CANFA STANDARD; PRT; 15 AA.
AC P18651;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heparin-binding growth factor 1 (HBGF-1) (Acidic fibroblast growth
DE factor) (AFGF) (Alpha-endothelial cell growth factor) (Fragment).
GN FGF1 OR FGF-1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=89231704; PubMed=2714282;
RA Quinkler W., Maasberg M., Bernotat-Danielowski S., Luethke N.,
RA Sharma H.S., Schaper W.;
RT "Isolation of heparin-binding growth factors from bovine, porcine and
RT canine hearts.";
RL Eur. J. Biochem. 181:67-73(1989).
CC -!- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS
CC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN
CC VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
CC CONCENTRATION OF THESE 2 GROWTH FACTORS.
CC -!- SUBUNIT: Monomer.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN, ALTHOUGH LESS STRONGLY
CC THAN DOES HBGF.
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
DR PIR; S03955; S03955.
DR InterPro; IPR002348; IL1_HBGF.
DR PROSITE; PS00247; HBGF_FGF; PARTIAL.
KW Growth factor; Mitogen; Angiogenesis; Heparin-binding.
FT NON TER 15
SQ SEQUENCE 15 AA; 1732 MW; 53CC9A3CADDDDAA1 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLY 5
Db |||
7 LLY 9

RESULT 4
PA2_NAJSP
ID PA2_NAJSP STANDARD; PRT; 16 AA.
AC Q10756;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase)
DE (Muscarinic inhibitor) (Fragment).
OS Naja sputatrix (Malayan spitting cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Naja.
OX NCBI_TaxID=33626;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=96195757; PubMed=8638927;
RA Miyoshi S.-I., Tu A.T.;
RT "Phospholipase A2 from Naja naja sputatrix venom is a muscarinic
RT acetylcholine receptor inhibitor.";
RL Arch. Biochem. Biophys. 328:17-25(1996).
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides. Blocks neuromuscular
CC transmission at the postsynaptic site. Binds to the muscarinic
CC acetylcholine receptor.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-

```

CC acylglycerophosphocholine + a fatty acid anion.
CC -1- COPACITOR: Binds 1 calcium ion (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP I
CC SUBFAMILY.
DR PIR; S65520; S65520.
DR HSP; P00598; IPOA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PROSITE; PS00119; PA2_HIS; PARTIAL.
DR PROSITE; PS00118; PA2_HIS; PARTIAL.
KW Hydrolase; Lipid degradation; Calcium; Toxin; Neurotoxin;
KW postsynaptic neurotoxin; Acetylcholine receptor inhibitor.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1969 MW; 9AC1F9834BB585F0 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6
Db 2 LYQ 4

RESULT 5
EFG_THEAQ STANDARD; PRT; 17 AA.
AC Q01597;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (Fragment).
GN FUS1 OR FUS.
OS Thermus aquaticus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=271;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP 00276;
RX MEDLINE=92362620; PubMed=1499561;
RA Voss R.H., Hartmann R.K., Lippmann C., Alexander C., Jahn O.,
RA Erdmann V.;
RT "Sequence of the tufta gene encoding elongation factor EF-Tu from
RT Thermus aquaticus and overproduction of the protein in Escherichia
RT coli.";
RL Eur. J. Biochem. 207:839-846(1992).
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLLOCATION
CC OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
CC RIBOSOME.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; X66322; CAA46997.1; -.
DR HANAP; MF_00054; -; 1.
DR InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFACOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON TER 1 1
SQ SEQUENCE 17 AA; 2094 MW; EA46E1EF05F86EID CRC64;

Query Match 42.9%; Score 3; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YQE 7
Db 2 YQE 4

RESULT 6
PH3_PERAM STANDARD; PRT; 17 AA.
AC P82636;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peptide hormone 3 (Pea-VEAacid 1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=20140865; PubMed=10676456;
RA Predel R., Eckert M., Holman G.M.;
RT "The unique neuropeptide pattern in abdominal perisymphathetic organs
RT of insects.";
RL Ann. N.Y. Acad. Sci. 897:282-290(1999).
CC -1- FUNCTION: UNKNOWN.
CC -1- MASS SPECTROMETRY: MW=1651.35; METHOD=MALDI.
KW Neuropeptide.
SQ SEQUENCE 17 AA; 1807 MW; 2374AC8B1F86E8EB CRC64;

Query Match 42.9%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3
Db 1 AFL 3

RESULT 7
AF2L_MALPA STANDARD; PRT; 20 AA.
AC P83143;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antifungal protein 2 large subunit (CW-2) (Fragment).
OS Malva parviflora (little mallow) (Cheeseweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.
OX NCBI_TaxID=145753;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Seed;
RX MEDLINE=20568734; PubMed=11118343;
RA Wang X., Bunkers G.J.;
RT "Potent heterologous antifungal proteins from cheeseweed (Malva
RT parviflora).";
RL Biochem. Biophys. Res. Commun. 279:669-673(2000).
CC -1- FUNCTION: Possesses antifungal activity against P.infestans but
CC not F.graminearum.
CC -1- SUBUNIT: Heterodimer of a large and a small subunit.
CC -1- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC concentration.
DR GO; GO:0003799; F:antifungal peptide activity; IDA.
KW Fungicide; Antibiotic.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2603 MW; 6E766A5E342036DA CRC64;

```

Query Match      42.9%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YOE 7
DB 8 YOE 10

RESULT 8
FLRF_HIRME STANDARD; PRT; 4 AA.
AC P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FLRFamide.
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arvachobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421, 27815;
RN [1]
SEQUENCE.
RP SPECIES=H.medicalinalis;
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rhamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
RN [2]
SEQUENCE.
RP SPECIES=H.trivolvis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRamide-related peptides from the kidney of the snail, Helisoma
trivolvis.";
RL Peptides 15:31-36(1994).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4
SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
DB 1 FL 2

RESULT 9
FLRN_ANTLR FLRN_ANTLR STANDARD; PRT; 4 AA.
AC P58707;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Antho-RNamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=90319122; PubMed=1973541;
RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Reimscheid R.K., Nothacker H.-P., Staley A.L.;
RT "Isolation of L-3-phenylactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
anemone neuropeptide containing an unusual amino-terminal blocking
group.";
RN

Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414 (1990).
-!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron-specific.
CC -!- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
DR PIR; A35779; A35779.
KW Neuropeptide; Amidation.
FT MOD_RES 1 4
FT MOD_RES 4 1
SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
DB 1 FL 2

RESULT 10
LOKL_LOCMI STANDARD; PRT; 6 AA.
AC P41491;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustakinin I.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
SEQUENCE.
RP TISSUE=Corpora cardiaca;
RX MEDLINE=92262851; PubMed=1585017;
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
RA de Loof A.;
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,
RT isolation, primary structure and synthesis.";
RL Regul. Pept. 37:49-57(1992).
CC -!- FUNCTION: Myotropic peptide. May be important in the stimulation
CC of ion transport and inhibition of diuretic activity in Malpighian
CC tubules.
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PIR; A61068; A61068.
KW Neuropeptide; Amidation.
FT MOD_RES 6 6
SQ SEQUENCE 6 AA; 654 MW; 586365A5B9CDB000 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2
DB 1 AF 2

RESULT 11
ALL2_CARMA STANDARD; PRT; 7 AA.
AC P81805;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 2.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]

```

RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 770 MW; 672879CDBC5DB70 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AF 2
 ||
 Db 4 AF 5

RESULT 12
 ALL3_CARMA STANDARD; PRT; 7 AA.
 AC P81806;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 3.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Multigene family.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 796 MW; 672879CDBC476B70 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AF 2
 ||
 Db 4 AF 5

RESULT 13
 ALL4_CARMA STANDARD; PRT; 7 AA.
 AC P81807;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 4.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.

RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Multigene family.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 782 MW; 672879CDBC476AC0 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AF 2
 ||
 Db 4 AF 5

RESULT 14
 ALL5_CARMA STANDARD; PRT; 7 AA.
 AC P81808;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 5.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 781 MW; 672879CDBC476420 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AF 2
 ||
 Db 4 AF 5

RESULT 15
 FARI_HELTI STANDARD; PRT; 7 AA.
 AC P41871;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide GDFPLRF-amide.
 OS Helisoma trivolvis (Snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Basommatophora;
 OC Lymnaeidae; Planorbidae; Helisoma.
 OX NCBI_TaxID=27815;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRamide-related peptides from the kidney of the snail, Helisoma
 trivolvis";
 RL Peptides 15:31-36(1994).
 CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
 CC -!- THE KIDNEY, MANTLE AND SKIN.
 CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FL 3
 Db 4 FL 5
 RESULT 16
 FARP1_PROCL
 ID FARP1_PROCL STANDARD; PRT; 7 AA.
 AC P38274;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRamide-like neuropeptide FLPI (DRNFLRF-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonoidea; Palaemonidae; Macrobrachium.
 OX NCBI_TaxID=79674;
 [1]_SEQUENCE, AND MASS SPECTROMETRY.
 RP TISSUE=Eyestalk;
 RA Sithigorngul P., Sarathongkum W., Jaideechoey S., Longyant S.,
 RA Sithigorngul W.;
 RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant
 RT freshwater prawn Macrobrachium rosenbergii";
 RL Comp. Biochem. Physiol. 120B:587-595(1998).
 CC -!- MASS SPECTROMETRY: MW=965.7; METHOD=WALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR GO:0007218; P:neuropeptide signaling pathway; TAS.
 KW Neuropeptide; Amidation.
 FT MOD RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FL 3
 Db 4 FL 5
 RESULT 17
 FARP1_PROCL
 ID FARP1_PROCL STANDARD; PRT; 7 AA.
 AC P38459;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Cardioexcitatory FMRFamide homolog NF1.
 CC Procamburus clarkii (Red swamp crayfish).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;

OC Astacoidea; Cambaridae; Procamburus.
 OX NCBI_TaxID=6728;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Pericardial organs;
 RX MEDLINE=93248032; PubMed=8387183;
 RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;
 RT "Isolation of two FMRFamide-related peptides from crayfish
 RT pericardial organs";
 RL Peptides 14:137-143(1993).
 CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
 CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
 CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540420 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FL 3
 Db 4 FL 5
 RESULT 18
 FARP2_PROCL
 ID FARP2_PROCL STANDARD; PRT; 7 AA.
 AC P38498;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Cardioexcitatory FMRFamide homolog DF2.
 OS Procamburus clarkii (Red swamp crayfish).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Astacoidea; Cambaridae; Procamburus.
 OX NCBI_TaxID=6728;
 [1]_SEQUENCE.
 RP TISSUE=Pericardial organs;
 RX MEDLINE=93248032; PubMed=8387183;
 RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;
 RT "Isolation of two FMRFamide-related peptides from crayfish
 RT pericardial organs";
 RL Peptides 14:137-143(1993).
 CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
 CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
 CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FL 3
 Db 4 FL 5
 RESULT 19
 GFRP_MOUSE
 ID GFRP_MOUSE STANDARD; PRT; 7 AA.
 AC P99025;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
 GN GCHFR OR GFRP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE.
 RC TISSUE=Liver;
 RC Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
 RA Cowthorne M.,
 RA Submitted (AUG-1998) to the SWISS-PROT data bank.
 RL CC -!- FUNCTION: MEDIATES TETRAHYDROBIOTERIN INHIBITION OF GTP
 CC CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
 CC (BY SIMILARITY).
 CC -!- SUBUNIT: Homodimer (By similarity).
 DR SWISS-2DPAGE; P99025; MOUSE.
 FT INIT_MET 0 7
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 LL 4
 ||
 Db 3 LL 4
 RESULT 20
 PPH2 LYCES
 ID -PPH2 LYCES STANDARD; PRT; 7 AA.
 AC P83379;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Purple acid phosphatase isozyme LeSAP2 (EC 3.1.3.2) (Fragment).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridaceae; Lamiales; Solanales; Solanaceae; Solanum.
 OC NCBI_TaxID=4081;
 RN [1]
 RN SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND
 RP GLYCOSYLATION.
 RC STRAIN=cv. Moneymaker; TISSUE=Seed;
 RX MEDLINE=22361242; PubMed=12473124;
 RA Bozzo G.G., Ragnothama K.G., Plaxton W.C.;
 RT "Purification and characterization of two secreted purple acid
 RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon
 RT esculentum) cell cultures."
 RL Eur. J. Biochem. 269:6278-6286 (2002).
 CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
 CC alcohol + phosphate.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: Glycosylated.
 CC -!- MISCELLANEOUS: In L. esculentum there are at least two isozymes of
 CC purple acid phosphatase.
 KW Hydrolase; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 810 MW; 672AA862C9C729A0 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 FL 3
 ||

Db 1 FL 2
 RESULT 21
 UN06 PINPS STANDARD; PRT; 7 AA.
 ID -UN06 PINPS STANDARD; PRT; 7 AA.
 AC P81675;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of needles (N141) (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OC NCBI_TaxID=71647;
 RN [1]
 RN SEQUENCE.
 RP TISSUE=Needle;
 RC MEDLINE=99274088; PubMed=10344291;
 RX Costa P., Pionneau C., Bauw G., Dubos C., Bahrmann N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins."
 RL Electrophoresis 20:1098-1108 (1999).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
 FT NON_TER 1
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 823 MW; 69D7672448B5740 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 LY 5
 ||
 Db 1 LY 2
 RESULT 22
 AL12 CARMA
 ID -AL12 CARMA STANDARD; PRT; 8 AA.
 AC P81815;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinus maenas 12.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
 OC NCBI_TaxID=6759;
 RN [1]
 RN SEQUENCE.
 RP TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RC MEDLINE=98121193; PubMed=9461295;
 RX Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas."
 RL Eur. J. Biochem. 250:727-734 (1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Multigene family.
 SQ SEQUENCE 8 AA; 913 MW; 672879CDBC569AB7 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AF 2
 ||
 Db 5 AF 6

```

RESULT 23
ID ALL6 CYDPO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Cydiastatin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9328229;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LY 5
DB 3 LY 4

RESULT 24
ID ALL7 CARMA STANDARD; PRT; 8 AA.
AC P81809; P81804; P81810;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Carcinustatin 7 [Contains: Carcinustatin 6; Carcinustatin 1].
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 825 MW; 922879CDBC4775BD CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1.AF 2
DB 1.AF 2

```

```

DB 5 AF 6

RESULT 25
ID ALL8 CARMA STANDARD; PRT; 8 AA.
AC P81811;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 8.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 795 MW; 922879CDBC47687D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2
DB 5 AF 6

RESULT 26
ID ALL9 CARMA STANDARD; PRT; 8 AA.
AC P81812;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 9.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 781 MW; 7C2879CDBC476878 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 AF 2
 DB 5 AF 6

RESULT 27

B44K_PORGI STANDARD; PRT; 8 AA.
 AC P81886;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 44 kDa immunogenic protein (Fragment).
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OX NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE
 RC STRAIN=VFB 3492;
 RX MEDLINE=20198497; PubMed=10731616;
 RA Norris J.M., Love D.N.;
 RT "Serum antibody responses of cats to soluble whole cell antigens of
 feline Porphyromonas gingivalis.";
 RL Vet. Microbiol. 73:37-49(2000).
 CC -!- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
 KW Antigen.
 FT NON TER
 SQ SEQUENCE 8 AA; 989 MW; 9554540326CB476D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YQ 6
 DB 3 YQ 4

RESULT 28

CLP_THICU STANDARD; PRT; 8 AA.
 AC P80488;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Chemolithotroph-specific protein (Fragment).
 OS Thiobacillus cuprinus.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Comamonadaceae; Thiomonas.
 OX NCBI_TaxID=36860;
 RN [1]
 RP SEQUENCE
 RC STRAIN=DSM 5494;
 RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
 RL Submitted (SEP-1995) to the SWISS-PROT data bank.
 CC -!- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
 CHEMOLITHOTROPHICALLY.
 FT NON TER
 SQ SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QE 7
 DB 5 QE 6

RESULT 29

COW2_CONFU STANDARD; PRT; 8 AA.
 ID COW2_CONFU

P58785;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leu-contryphan-P.
 OS Conus purpurascens (Purple cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=41690;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC STRAIN=Clipperton Island; TISSUE=Venom;
 RX MEDLINE=9938839; PubMed=10461743;
 RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
 RA Olivera B.M.;
 RT "A novel D-leucine-containing Conus peptide: diverse conformational
 dynamics in the contryphan family.";
 RL J. Pept. Res. 54:93-99(1999).

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
 CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
 KW Toxin; Hydroxylation; D-amino acid.
 FT DISULFID 2 8
 FT MOD RES 4 4 D-LEUCINE.
 FT MOD RES 4 4
 SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LL 4
 DB 4 LL 5

RESULT 30

CPD1_ENTFA STANDARD; PRT; 8 AA.
 AC P13269;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CPD1.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=95040388; PubMed=6436978;
 RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
 RA Craig R.A., Clewell D.B.;
 RT "Isolation and structure of bacterial sex pheromone, CPD1.";
 RL Science 226:849-850(1984).
 CC -!- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 BACTERIOCIN PLASMID PPD1.
 KW Pheromone.
 SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
 DB 1 FL 2

RESULT 31

FAR1_PANRE STANDARD; PRT; 8 AA.
 ID FAR1_PANRE
 AC P41872;

```

DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRamide-like neuropeptide PF1 (SDPNFLRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE.
RX MEDLINE=93027659; PubMed=1408999;
RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
RA Garrison R.D., Williams J.F., Friedman A.R.;
RT "Two FMRamide-like peptides from the free-living nematode
RL Panagrellus redivivus."
RL Peptides 13:209-214(1992).
CC -!- FUNCTION: MYOACTIVE.
CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED
CC -!- CAUDALLY TO THE BASE OF THE PHARYNX.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 995 MW; C6D40729C4576AB5 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
Db 5 FL 6

RESULT 32
FAR1 PENMO STANDARD; PRT; 8 AA.
ID FAR1 PENMO
AC P83316;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLPI (GDRNFLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkasem C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540AA8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
Db 5 FL 6

RESULT 33
FAR2 MACRS STANDARD; PRT; 8 AA.
ID FAR2 MACRS
AC P83275;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLF2 (ADKNFLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RA Sithigorngul P., Saraithongkum W., Jaideechoey S., Longyant S.,
RA Sithigorngul W.;
RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant
RT freshwater prawn Macrobrachium rosenbergii."
RL Comp. Biochem. Physiol. 120B:587-595(1998).
CC -!- MASS SPECTROMETRY: MW=1009.4; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1010 MW; 9CD40729C4433AAD CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
Db 5 FL 6

RESULT 34
FAR3 HOMAM STANDARD; PRT; 8 AA.
ID FAR3 HOMAM
AC P41486;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRamide-like neuropeptide 3 (FLI 3) (F2).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6706;
RN [1]
RP SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=88116164; PubMed=34297114;
RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
RT "Purification and characterization of FMRamide-like immunoreactive
RT substances from the lobster nervous system: isolation and sequence
RT analysis of two closely related peptides."
RL J. Comp. Neurol. 266:16-26(1987).
CC -!- MISCELLANEOUS: PERICARDIAL ORGANS RELEASE THIS PEPTIDE WITH 100 MM
CC -!- POTASSIUM IN THE PRESENCE OF CALCIUM.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3

```

```

Db          5 FL 6      ||
              1 AF 2
              ||
              3 AF 4

RESULT 35
FAR4_HOMAM
ID_FAR4_HOMAM STANDARD; PRT; 8 AA.
AC P41487;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide 4 (FLI 4) (F1).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Fleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6706;
RN [1]
RP SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=88116164; PubMed=3429714;
RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
RT "Purification and characterization of FMRFamidelike immunoreactive
RT substances from the lobster nervous system: isolation and sequence
RT analysis of two closely related peptides.";
RL J. Comp. Neurol. 266:16-26 (1987)
CC -!- FUNCTION: CAN ACT AS A MODULATOR OF EXOSKELETAL AND CARDIAC
CC NEUROMUSCULAR JUNCTIONS.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 1067 MW; DDD40729C4540451 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          2 FL 3      ||
              1 AF 2
              ||
              3 AF 4

RESULT 36
LCK1_LEUMA
ID_LCK1_LEUMA STANDARD; PRT; 8 AA.
AC P21140;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin I (L-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:205-211 (1986).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 893 MW; DC6365B449CDC76A CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          2 FL 3      ||
              1 AF 2
              ||
              3 AF 4

RESULT 37
LCK7_LEUMA
ID_LCK7_LEUMA STANDARD; PRT; 8 AA.
AC P19989;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Leucokinin VII (L-VII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and
RT VIII: the final members of this new family of cephalomyotrophic
RT peptides isolated from head extracts of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:31-34 (1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
KW PIR; JS0317; JS0317.
FT MOD RES 8
SQ SEQUENCE 8 AA; 866 MW; DC6365A5B9CDC76A CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 AF 2      ||
              ||
              3 AF 4

RESULT 38
NPB_BOVIN
ID_NPB_BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovioidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761 (1985).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
KW PIR; B24749; B24749.
FT MOD RES 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

```

```
Query Match      28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FL 3
Db      1 FL 2

RESULT 39
NS3_MYCTU
ID NS3_MYCTU STANDARD; PRT; 8 AA.
AC P81I52;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30 kDa non-secretory protein 3 (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE.
RC STRAIN=H37Rv;
RA Praead H.K., Annapurna P.S.;
RL Submitted (DEC-1997) to the SWISS-PROT data bank.
CC -!- CAUTION: We are unable to find this protein in the translation of
CC the genome of strain H37Rv.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 919 MW; 8D3DC40B19CDC2D2 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AF 2
Db      3 AF 4

RESULT 40
ORMY_ORCLI
ID ORMY_ORCLI STANDARD; PRT; 8 AA.
AC P82A55;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Orcomytropin (OMT).
OS Orconectes limosus (Spinycheek crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidea; Cambaridae; Orconectes.
OX NCBI_TaxID=28379;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Hindgut;
RX MEDLINE=20411310; PubMed=10952880;
RA Dircksen H., Burdick S., Sauter A., Keller R.;
RT "Two orokins and the novel octapeptide orcomytropin in the hindgut
RT of the crayfish Orconectes limosus; identified myostimulatory
RT neuropeptides originating together in neurones of the terminal
RT abdominal ganglion."
RL J. Exp. Biol. 203:2807-2818(2000).
CC -!- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND
CC AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED
CC BY ABDOMINAL GANGLIONIC NEURONS.
CC -!- MASS SPECTROMETRY: MW=904.8; METHOD=FMAB.
KW Amidation; Neuropeptide.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 905 MW; 87C861B1A9CDDAA9 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AF 2
Db      3 AF 4

RESULT 41
RS1_ERWCH
ID RS1_ERWCH STANDARD; PRT; 8 AA.
AC P37985;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 30S ribosomal protein S1 (Fragment).
GN RPSA.
OS Erwinia chrysanthemi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3937;
RA Doullie A., Toussaint A., Faelen M.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BINDS MRNA; THUS FACILITATING RECOGNITION OF THE
CC INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT
CC SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X74750; CAA52769.1; -.
DR PIR; S37141; S37141.
KW Ribosomal protein; Repeat; RNA-binding.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 837 MW; 9E18733DC5B339CD CRC64;

Query Match      28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AF 2
Db      1 AF 2

RESULT 42
UH09_RAT
ID UH09_RAT STANDARD; PRT; 8 AA.
AC P56575;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
```

CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 1029 MW; 980775A6C4140B06 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 QE 7
 Db 1 QE 2
 RESULT 43
 UPAL_HUMAN
 ID UPAL_HUMAN STANDARD; PRT; 8 AA.
 AC P30087;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=9302937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Rissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.9, ITS MW IS: 65 kDa.
 DR SWISS-2DPAGE; P30087; HUMAN.
 FT NON_TER 1 1
 FT UNSURE 8 8
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 QE 7
 Db 2 QE 3
 RESULT 44
 AL10_CARMA
 ID AL10_CARMA STANDARD; PRT; 9 AA.
 AC P81813;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 10.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).

CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 963 MW; 372D79CDBC4776C7 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AF 2
 Db 6 AF 7
 RESULT 45
 AL11_CARMA
 ID AL11_CARMA STANDARD; PRT; 9 AA.
 AC P81814;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 11.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 927 MW; 832D79CDBC46D861 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AF 2
 Db 6 AF 7
 RESULT 46
 BUK_CLOPA
 ID BUK_CLOPA STANDARD; PRT; 9 AA.
 AC P81337;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Butyrate kinase (EC 2.7.2.7) (BK) (CP 38) (Fragment).
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=W5;
 RX MEDLINE=98291870; PubMed=9629918;
 RA Flengsrud R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum W5.";
 RL Electrophoresis 19:802-806(1998).

CC -!- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl phosphate to butyrate (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + 2-butanolate = ADP + butanoyl phosphate.
 CC -!- PATHWAY: Involved in the acidogenic phase of fermentation.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the acetokinase family.

DR HAMAP; MF_00542; -; 1.
 DR InterPro; IPR000890; Acetate kin.
 DR PROSITE; PS01075; ACETATE KINASE 1; PARTIAL.
 DR PROSITE; PS01076; ACETATE_KINASE_2; PARTIAL.
 KW Transferase; Kinase.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1104 MW; 055D4050572732B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LL 4
 DB 4 LL 5

RESULT 47

CCAP_CARMA STANDARD; PRT; 9 AA.
 AC P38556;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cardioactive peptide (CCAP).
 OS Cardinus maenas (Common shore crab) (Green crab),
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
 OS Tenebrio molitor (Yellow mealworm), and
 OS Spodoptera eridania (Southern armyworm).
 OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759, 7130, 7067, 37547;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=C.maenas; TISSUE=Pericardial organs;
 RC Stangler J., Halbach C., Beyreuther K., Keller R.;
 RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the shore crab Cardinus maenas.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=M.sexata;
 RX MEDLINE=93050243; PubMed=1426284;
 RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
 RT "Primary structure of a cardioactive neuropeptide from the tobacco hawkmoth, Manduca sexta.";
 RL FEBS Lett. 313:165-168(1992).
 RN [3]
 RP SEQUENCE.

RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
 RX MEDLINE=94176032; PubMed=8129851;
 RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M., Schooley D.A.;
 RT "Isolation and identification of a cardioactive peptide from Tenebrio molitor and Spodoptera eridania.";
 RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
 CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
 CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED INTO THE HEMOLYPH.

DR PIR; A26363; A26363.
 DR PIR; S27233; S27233.
 KW Neuropeptide; Amidation.
 FT DISULFID 3 9
 FT MOD_RES 9 9
 FT SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

AMIDATION.

Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2
 DB 5 AF 6

RESULT 48

FAR2_PANRE STANDARD; PRT; 9 AA.
 AC P41873;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide PF2 (SADPNFLRF-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=93027659; PubMed=1408999;
 RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D., Garrison R.D., Williams J.F., Friedman A.R.;
 RT "Two FMRFamide-like peptides from the free-living nematode Panagrellus redivivus.";
 RL Peptides 13:209-214(1992).
 CC -!- FUNCTION: MYOACTIVE.
 CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED CAUDALLY TO THE BASE OF THE PHARYNX.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 9
 SQ SEQUENCE 9 AA; 1066 MW; DA0B0729C4576AAD CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
 DB 6 FL 7

RESULT 49

FAR3_MACRS STANDARD; PRT; 9 AA.
 AC P83276;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRFamide-like neuropeptide FLP3 (NYDKNFLRF-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonoidea; Palaemonidae; Macrobrachium.
 OX NCBI_TaxID=79674;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RA Sithigongul P., Saraithongkum W., Jaidechoey S., Longyant S., Sithigongul W.;
 RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
 RL Comp. Biochem. Physiol. 120B:587-595(1998).
 CC -!- MASS SPECTROMETRY: MW=1215.4; METHOD=WALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
 CC GO: GO:0007218; P:neuropeptide signaling pathway; TAS.
 KW Neuropeptide; Amidation.

FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1216 MW; 18220729C4433ABB CRC64;
Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FL 3
||
Db 6 FL 7

RESULT 50
FAR6_MACRS
ID FAR6_MACRS STANDARD; PRT; 9 AA.
AC P83279;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP6 (DGGNFLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21107394; PubMed=11179812;
RA Sithigorngul P., Saraithongkum W., Longyant S., Panchan N.,
RA Sithigorngul W., Petsom A.;
RT "Three more novel FMRamide-like neuropeptide sequences from the
RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL Peptides 22:191-197(2001).
CC -!- MASS SPECTROMETRY: MW=1080.7; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1081 MW; 26800729C4540878 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FL 3
||
Db 6 FL 7

RESULT 51
FAR8_MACRS
ID FAR8_MACRS STANDARD; PRT; 9 AA.
AC P83281;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP8 (VSHNNFLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21107394; PubMed=11179812;
RA Sithigorngul P., Saraithongkum W., Longyant S., Panchan N.,
RA Sithigorngul W., Petsom A.;
RT "Three more novel FMRamide-like neuropeptide sequences from the
RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL Peptides 22:191-197(2001).

CC -!- MASS SPECTROMETRY: MW=1133.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1133 MW; 845A0729C44441F5 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FL 3
||
Db 6 FL 7

RESULT 52
FARP_CALSI
ID FARP_CALSI STANDARD; PRT; 9 AA.
AC P38495;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRamide-like neuropeptide.
OS Callinectes sapidus (Blue crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Callinectes.
OX NCBI_TaxID=6763;
RN [1]
RP SEQUENCE.
RX MEDLINE=92270479; PubMed=1815216;
RA Krajniak K.G.;
RT "The identification and structure-activity relations of a
RT cardioactive FMRamide-related peptide from the blue crab Callinectes
RT sapidus.";
RL Peptides 12:1295-1302(1991).
CC -!- FUNCTION: CARDIOACTIVE PEPTIDE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1159 MW; 134F0729D5A4045B CRC64;
Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FL 3
||
Db 6 FL 7

RESULT 53
FIBB_PAPAN
ID FIBB_PAPAN STANDARD; PRT; 9 AA.
AC P19344;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,

```

RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC PIR; D28854; D28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1076 MW; DDF6409C7287B06 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QE 7
DB 2 QE 3

RESULT 54
FIBB_PAPHA STANDARD; PRT; 9 AA.
AC P19343;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OC NCBI_TaxID=9557;
RN [1]
SQ SEQUENCE.
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC PIR; F28854; F28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 977 MW; DDFE7879C7287B06 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QE 7
DB 2 QE 3

RESULT 56
NEUU_CAVPO STANDARD; PRT; 9 AA.
AC P34966;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuromedin U-9 (NmU-9).
GN NMU.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OC NCBI_TaxID=10141;
RN [1]
SQ SEQUENCE.
RC TISSUE=Small intestine;
RA Murphy R., Turner C.A., Furness J.B., Parker L., Giraud A.;
RT "Isolation and microsequence analysis of a novel form of neuromedin U
RT from guinea pig small intestine.";
RL Peptides 11:613-617(1990).
```

```

DB 2 QE 3

RESULT 55
FIBB_THEGE STANDARD; PRT; 9 AA.
AC P19342;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Theropithecus gelada (Gelada baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Theropithecus.
OC NCBI_TaxID=9565;
RN [1]
SQ SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC PIR; F28854; F28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 977 MW; DDFE7879C7287B06 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QE 7
DB 2 QE 3

RESULT 56
NEUU_CAVPO STANDARD; PRT; 9 AA.
AC P34966;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuromedin U-9 (NmU-9).
GN NMU.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OC NCBI_TaxID=10141;
RN [1]
SQ SEQUENCE.
RC TISSUE=Small intestine;
RA Murphy R., Turner C.A., Furness J.B., Parker L., Giraud A.;
RT "Isolation and microsequence analysis of a novel form of neuromedin U
RT from guinea pig small intestine.";
RL Peptides 11:613-617(1990).
```

CC -!- FUNCTION: STIMULATES UTERINE SMOOTH MUSCLE CONTRACTION AND CAUSES
 CC -!- SELECTIVE VASOCONSTRICTION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE NMU FAMILY.
 DR InterPro: IPR001942; NMU.
 DR Pfam: PF02070; NMU; 1.
 DR PROSITE: PS00967; NMU; 1.
 KW Amidation; Hormone.
 FT MOD RES 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1169 MW; 1ECF177409C729DB CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FL 3
 DB 3 FL 4
 RESULT 57
 NEUX_HUMAN
 ID NEUX_HUMAN STANDARD; PRT; 9 AA.
 AC P04277;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neutensin-related peptide (NRP) (Kinetensin).
 OS Homo sapiens (Human),
 OS Bos taurus (Bovine), and
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606, 9913, 9986;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Human;
 RX MEDLINE=86242190; PubMed=3087352;
 RA Mogard M.H., Kobayashi R., Chen C.F., Lee T.D., Reeve J.R. Jr.,
 RA Shively J.E., Walsh J.H.;
 RT "The amino acid sequence of kinetensin, a novel peptide isolated from
 RT pepsin-treated human plasma: homology with human serum albumin,
 RT neutensin and angiotensin.";
 RL Biochem. Biophys. Res. Commun. 136:983-988(1986).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=Human, Bovine, and Rabbit;
 RX MEDLINE=87194805; PubMed=2437111;
 RA Carraway R.E., Mitra S.P., Cochrane D.E.;
 RT "Structure of a biologically active neutensin-related peptide
 RT obtained from pepsin-treated albumin(s).";
 RL J. Biol. Chem. 262:5968-5973(1987).
 CC -!- FUNCTION: REGULATION OF FAT DIGESTION, LIPID ABSORPTION, AND
 CC BLOOD FLOW (POTENTIAL).
 CC PIR: A38885; ABOS.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0005180; F:peptide hormone; NAS.
 DR GO: GO:0007599; P:hemosatosis; IDA.
 DR GO: GO:0006629; P:lipid metabolism; NAS.
 KW Hormone.
 SQ SEQUENCE 9 AA; 1172 MW; C804DB4761F4140D CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FL 3
 DB 8 FL 9
 RESULT 58
 RE42_LITRU

ID RE42_LITRU STANDARD; PRT; 9 AA.
 AC P82075; P82093;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Rubellidin 4.2/4.3.
 OS Litoria rubella (Desert tree frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hyliidae;
 CC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion.
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
 CC activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- PTM: Rubellidin 4.2 seems to differ from Rubellidin 4.3 by its C-
 CC terminal amidation.
 CC -!- MASS SPECTROMETRY: MW=883; METHOD=FAB.
 KW Amphibian defense peptide; Amidation.
 FT MOD RES 9
 SQ SEQUENCE 9 AA; 884 MW; 2C2D77205AA72728 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LL 4
 DB 3 LL 4
 RESULT 59
 TAL1_PICJA
 ID TAL1_PICJA STANDARD; PRT; 9 AA.
 AC P17440;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transaldolase I (EC 2.2.1.2) (Fragment).
 OS Pichia jadinii (Yeast) (Candida utilis).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Pichia.
 OX NCBI_TaxID=4903;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77110646; PubMed=556924;
 RA Sun S.C., Joris L., Tsolas O.;
 RT "Purification of crystallization of transaldolase isozyme I and
 RT evidence for different genetic origin of isozymes I and III in
 RT Candida utilis.";
 RL Arch. Biochem. Biophys. 178:69-78(1977).
 CC -!- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF
 CC METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
 CC -!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
 CC 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
 CC -!- PATHWAY: Pentose phosphate pathway; nonoxidative part.

CC -|- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.
 DR PIR; A12872; A12872.
 DR InterPro; IPR001585; Transaldolase.
 DR PROSITE; PS00958; TRANSALDOLASE_2; PARTIAL.
 DR PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
 KW Transferase; Pentose shunt.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1008 MW; 274F31AF0EB1E058 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LL 4
 ||
 8 LL 9

Db

RESULT 60
 TAL3 PICJA
 ID TAL3 PICJA STANDARD; PRT; 9 AA.
 AC P1741;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transaldolase III (EC 2.2.1.2) (Fragment).
 OS Pichia jadinii (Yeast) (Candida utilis).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Pichia.
 OX NCBI_TaxID=4903;
 RN [1]
 RP MEDLINE=75145197; PubMed=1092268;
 RA Tsolas O., Sun S.C.;
 RT "Isolation of a peptide containing a histidyl-cysteiny sequence
 from the active center of transaldolase."
 Arch. Biochem. Biophys. 167:525-533(1975).
 CC -|- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF
 METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
 CC -|- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
 CC -|- PATHWAY: Pentose phosphate pathway; nonoxidative part.
 CC -|- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.
 DR PIR; A11497; A11497.
 DR InterPro; IPR001585; Transaldolase.
 DR PROSITE; PS00958; TRANSALDOLASE_2; PARTIAL.
 DR PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
 KW Transferase; Pentose shunt.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1033 MW; 325A31A44EB1E058 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LL 4
 ||
 8 LL 9

Db

RESULT 61
 TKC1 CALVO
 ID TKC1 CALVO STANDARD; PRT; 9 AA.
 AC P41517;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Callitachykinin I.
 OS Calliphora vomitoria (Blue blowfly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;

OC Calliphoridae; Calliphora.
 NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=95075727; PubMed=7984492;
 RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
 RA Naesel D.R.;
 RT "Callitachykinin I and II, two novel myotropic peptides isolated from
 the blowfly, Calliphora vomitoria, that have resemblances to
 tachykinins."
 RL Peptides 15:761-768(1994).
 CC -|- FUNCTION: MYOACTIVE PEPTIDE.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 9 9
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 981 MW; 2417C86B59CDC1B7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2
 ||
 4 AF 5

Db

RESULT 62
 ULAE HUMAN
 ID ULAE HUMAN STANDARD; PRT; 9 AA.
 AC P31931;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of liver tissue (Spot 115) (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94147969; PubMed=8313870;
 RA Hughes G.J., Futiger S., Paquet N., Pasquali C., Sanchez J.-C.,
 RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
 RT "Human liver protein map: update 1993."
 RL Electrophoresis 14:1216-1222(1993).
 CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 5.5, ITS MW IS: 11 kDa.
 CC SWISS-2DPAGE; P31931; HUMAN.
 DR NON_TER 1 1
 DR NON_TER 9 9
 SQ SEQUENCE 9 AA; 1096 MW; 477B3B173AE729C7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
 ||
 3 FL 4

Db

RESULT 63
 UP47 HUMAN
 ID UP47 HUMAN STANDARD; PRT; 9 AA.
 AC P30093;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 18) (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.05, ITS MW IS: 37 kDa.
DE SWISS-2DPAGE; P30093; HUMAN.
FT NON_TER 1
FT UNSURE 5
FT NON_TER 9
SQ SEQUENCE 9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YQ 6
DB 8 YQ 9

RESULT 64
CU30 LOCM1
ID CU30 LOCM1 STANDARD; PRT; 10 AA.
AC P11735;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Cuticle protein 30 (LM-30) (LM-ACP 30) (Fragment).
OS Locusta migratoria (Migratory locust)...
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RX MEDLINE=86108304; PubMed=3943519;
RA Hoejrup P., Andersen S.O., Roepstorff P.;
RT "Isolation, characterization, and N-terminal sequence studies of
RT cuticular proteins from the migratory locust, Locusta migratoria.";
RL Eur. J. Biochem. 154:153-159(1986).
CC -!- FUNCTION: COMPONENT OF THE CUTICLE OF MIGRATORY LOCUST WHICH
CC CONTAINS MORE THAN 100 DIFFERENT STRUCTURAL PROTEINS.
DR PIR; H24802; H24802.
KW Structural protein; Cuticle.
FT NON_TER 10
SQ SEQUENCE 10 AA; 969 MW; 4973E36B58772877 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LL 4
DB 2 LL 3

RESULT 65
FAR7 MACRS
ID FAR7 MACRS STANDARD; PRT; 10 AA.
AC P83260;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLF7 (GYGRNFLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

```

```

OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21107394; PubMed=11179812;
RA Sithigorngul P., Saraithongkum W., Longyant S., Panchan N.,
RA Sithigorngul W., Petsom A.;
RT "Three more novel FMRFamide-like neuropeptide sequences from the
RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL Peptides 22:191-197(2001).
CC -!- MASS SPECTROMETRY: MW=1244.9; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD_RES 10
FT SEQUENCE 10 AA; 1244 MW; 3CFE9C29C4540AA8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
DB 7 FL 8

RESULT 66
FARP LOCM1
ID FARP LOCM1 STANDARD; PRT; 10 AA.
AC P38553;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Schistoflrfamide (PDVDFLRF-amide) (Cardioexcitatory neuropeptide).
OS Locusta migratoria (Migratory locust), and
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004; 7010;
RN [1]
RP SEQUENCE.
RC SPECIES=L.migratoria; TISSUE=Brain;
RX MEDLINE=93324430; PubMed=7687352;
RA Schoofs L., Holman G.M., Paemen L., Veelaert D., Amelinckx M.,
RA de Loof A.;
RT "Isolation, identification, and synthesis of PDVDFLRFamide
RT (Schistoflrfamide) in Locusta migratoria and its association with the
RT male accessory glands, the salivary glands, the heart, and the
RT oviduct.";
RL Peptides 14:409-421(1993).
RN [2]
RP SEQUENCE.
RC SPECIES=S.gregaria; TISSUE=Thoracic nervous system;
RX MEDLINE=89248543; PubMed=2719702;
RA Robb S., Packman L.C., Evans P.D.;
RT "Isolation, primary structure and bioactivity of schistoflrf-amide, a
RT FMRF-amide-like neuropeptide from the locust, Schistocerca
RT gregaria.";
RL Biochem. Biophys. Res. Commun. 160:850-856(1989).
CC -!- FUNCTION: MUSCLE INHIBITING AGENT. INVOLVED IN THE NEURAL CONTROL
CC OF THE VISCERAL MUSCLES OF THE HEART, ACCESSORY GLANDS AND
CC OVIDUCT. MAY BE INVOLVED IN THE REGULATION OF SALIVA SECRETION.
CC -!- TISSUE SPECIFICITY: FOUND IN AXONS OF THE MALE ACCESSORY GLANDS,
CC THE SALIVARY GLANDS, THE HEART, AND THE OVIDUCT.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A32543; A32543.
KW Neuropeptide; Amidation.
FT MOD_RES 10

```

SQ SEQUENCE 10 AA; 1244 MW; D3C51729D2C1EAB2 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1e+04; 0; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
 ||
 7 FL 8

Db

RESULT 67
 FARP MANSE
 ID FARP MANSE STANDARD; PRT; 10 AA.
 AC P18523;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRamide-like neuropeptide.
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
 OC Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RZ SEQUENCE.
 RP MEDLINE=91045350; PubMed=2235684;
 RA Kingan T.G., Teplov D.B., Phillips J.M., Riehm J.P., Rao K.R.,
 RA Hildebrand J.G., Homberg U., Kammer A.E., Jardine I., Griffin P.R.,
 RA Hunt D.F.;
 RT "A new peptide in the FMRamide family isolated from the CNS of the
 RT hawkmoth, *Manduca sexta*,"
 RL Peptides 11:849-856(1990).
 CC -!- FUNCTION: INCREASES THE FORCE OF NEURALLY EVOKED CONTRACTIONS IN
 CC THE MAJOR POWER-PRODUCING FLIGHT MUSCLES. THE DORSAL LONGITUDINAL
 CC MUSCLES AND SO IS LIKELY TO PLAY A ROLE IN SUSTAINING OR PROMOTING
 CC FLIGHT BEHAVIOR PATTERNS.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR PIR; A43977; A43977.
 KW Amidation; Neuropeptide; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1247 MW; D3C45229D5B1F2D2 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1e+04; 0; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
 ||
 7 FL 8

Db

RESULT 68
 LQMS LEUMA
 ID LQMS LEUMA STANDARD; PRT; 10 AA.
 AC P21144; P41497;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leucomyosuppressin (LMS) (Lem-MS).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RZ SEQUENCE, AND SYNTHESIS.
 RP TI=SUB=HEAD;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of leucomyosuppressin,
 RT an insect neuropeptide that inhibits spontaneous contractions of the

RT cockroach hindgut.";
 RL Comp. Biochem. Physiol. 85C:329-333(1986).
 CC -!- FUNCTION: INHIBITS THE SPONTANEOUS CONTRACTIONS OF COCKROACH
 CC PROTODEUM (HINDGUT).
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1275 MW; D3C45229D2C1EAB2 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1e+04; 0; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
 ||
 7 FL 8

Db

RESULT 69
 PORB METTM
 ID PORB METTM STANDARD; PRT; 10 AA.
 AC P80501;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Pyruvate synthase subunit porB (EC 1.2.7.1) (Pyruvate oxidoreductase
 DE beta chain) (POR) (Pyruvic-ferredoxin oxidoreductase beta subunit)
 DE (Fragment).
 GN PORB.
 OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=79929;
 RN [1]
 RZ SEQUENCE.
 RP MEDLINE=97261844; PubMed=9108258;
 RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
 RT "Structures and functions of four anaerobic 2-oxoacid oxidoreductases
 RT in Methanobacterium thermoautotrophicum,";
 RL Eur. J. Biochem. 244:862-868(1997).
 CC -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
 CC CoA + CO(2) + reduced ferredoxin.
 CC -!- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
 CC GAMMA CHAIN.
 CC -!- MISCELLANEOUS: As a pH optimum of 10.0 and an optimal temperature
 CC of 80 degrees Celsius.
 KW Oxidoreductase.
 FT NON_TER 10 10
 FT SEQUENCE 10 AA; 1232 MW; 167011DAF6DB0760 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1e+04; 0; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
 ||
 8 FL 9

Db

RESULT 70
 Q2OB COMTE
 ID Q2OB COMTE STANDARD; PRT; 10 AA.
 AC P80465;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Quinolone 2-oxidoreductase, beta chain (EC 1.3.99.17) (Fragment).
 OS Comamonas testosteroni (Pseudomonas testosteroni).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Comamonadaceae; Comamonas.
 OX NCBI_TaxID=285;
 RN [1]
 RZ SEQUENCE.

```

RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RA Schach S., Tshisuka B., Fetzner S., Lings F.;
RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT quinoline and 3-methylquinoline degradation.";
RL Eur. J. Biochem. 232:536-544(1995).
CC -!- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-
CC 1,2-DIHYDROQUINOLINE.
CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isequinol-
CC 1(2H)-one + reduced acceptor.
CC -!- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)-quinoline; first
CC step.
CC -!- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
CC TWO GAMMA CHAINS (PROBABLY).
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1241 MW; C2E2C25DD9CDC769 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2
Db |||
5 AF 6

RESULT 71
TEMP RANTE
ID TEMP RANTE STANDARD; PRT; 10 AA.
AC P56923;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin K.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LL 4
Db |||
1 LL 2

RESULT 72
CS15 BACSU
ID CS15 BACSU STANDARD; PRT; 11 AA.
AC P81095;
DT 15-JUL-1998 (Rel. 36, Created)

```

```

DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cold shock protein CS15 (11 kDa cold shock protein) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE.
RC STRAIN=168 / JH642;
RA Graumann P.L., Schmid R., Marahiel M.A.;
RL Submitted (OCT-1997) to the SWISS-PROT data bank.
RN [2]
RP CHARACTERIZATION.
RC STRAIN=168 / JH642;
RX MEDLINE=96345629; PubMed=8755892;
RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
RT "Cold shock stress-induced proteins in Bacillus subtilis.";
RL J. Bacteriol. 178:4611-4619(1996).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- INDUCTION: In response to low temperature.
CC -!- CAUTION: Could not be found in the genome of B. subtilis 168.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEB6322C330 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
Db |||
9 FL 10

RESULT 73
MHBI KLEPN
ID MHBI KLEPN STANDARD; PRT; 11 AA.
AC P80580;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).
GN MHBI.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE.
RX MEDLINE=96349117; PubMed=8760924;
RA Robson N.D., Parrott S., Cooper R.A.;
RT "In vitro formation of a catabolic plasmid carrying Klebsiella
RT pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-
RT hydroxybenzoate.";
RL Microbiology 142:2115-2120(1996).
CC -!- CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.
KW Isomerase.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1387 MW; 1EE0E2DD49C9DSAB CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LY 5
Db |||
3 LY 4

RESULT 74
RE41 LITRU
ID RE41 LITRU STANDARD; PRT; 11 AA.
AC P82074;
DT 28-FEB-2003 (Rel. 41, Created)

```

Search completed: November 25, 2003, 19:28:25
Job time : 3.55399 secs

```
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 4.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1039; METHOD=FAE.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1040 MW; 84ED5CEC2877205A CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4
Db 8 LL 9

RESULT 75
TKC2_CALVO
ID TKC2_CALVO STANDARD; PRT; 11 AA.
AC P41518;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Callitachykinin II.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
RA Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
RT the blowfly, Calliphora vomitoria, that have resemblances to
RT tachykinins.";
RL Peptides 15:761-768(1994).
CC -!- FUNCTION: MYOACTIVE PEPTIDE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9CDD444 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AF 2
Db 6 AF 7
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 13.1453 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-28

Perfect score: 7
Sequence: 1 AFLYQE 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SPTREMBL 23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	57.1	11	7	Q9TQB3
2	4	57.1	15	8	P92818
3	4	57.1	17	5	Q17205
4	4	57.1	17	5	Q26832
5	4	57.1	17	5	Q9TVY3
6	4	57.1	17	5	Q9TVX7
7	4	57.1	20	2	Q32710
8	3	42.9	7	8	Q99182
9	3	42.9	8	2	Q93SP2
10	3	42.9	8	8	Q94VC1
11	3	42.9	8	8	Q8HR64
12	3	42.9	10	5	Q95NT8
13	3	42.9	10	6	Q9TRU6
14	3	42.9	10	13	Q90ZV8
15	3	42.9	11	7	O77912
16	3	42.9	11	7	O77883

17	3	42.9	12	4	Q9JMO9
18	3	42.9	12	8	Q8SEB7
19	3	42.9	12	8	Q9XNR6
20	3	42.9	13	2	Q49230
21	3	42.9	13	4	Q75905
22	3	42.9	13	4	Q14461
23	3	42.9	13	8	Q99188
24	3	42.9	13	8	Q94RE2
25	3	42.9	14	4	Q9UHM5
26	3	42.9	14	12	Q85718
27	3	42.9	15	2	Q9FB61
28	3	42.9	15	10	Q9SAP4
29	3	42.9	15	11	Q9QUY5
30	3	42.9	16	5	Q9TWN2
31	3	42.9	16	8	Q35214
32	3	42.9	16	8	P92070
33	3	42.9	16	11	Q8CIS2
34	3	42.9	17	2	Q9EUP4
35	3	42.9	17	4	Q9UJH1
36	3	42.9	17	5	Q17203
37	3	42.9	17	8	Q8HKG6
38	3	42.9	17	8	Q8HCD7
39	3	42.9	17	8	Q8HAS3
40	3	42.9	17	11	Q9QUJ4
41	3	42.9	17	11	Q9QZ24
42	3	42.9	17	13	Q9PRU8
43	3	42.9	18	4	Q9UC81
44	3	42.9	18	4	Q9UJ81
45	3	42.9	18	4	Q9UCR5
46	3	42.9	18	4	Q8NED1
47	3	42.9	18	5	Q26833
48	3	42.9	18	6	Q9TRG2
49	3	42.9	18	11	Q8VHM8
50	3	42.9	18	13	Q90912
51	3	42.9	19	2	Q44608
52	3	42.9	19	2	Q9AIE8
53	3	42.9	19	8	Q99736
54	3	42.9	19	10	Q41472
55	3	42.9	19	12	Q85671
56	3	42.9	19	13	Q9PS15
57	3	42.9	19	13	Q9PRN4
58	3	42.9	19	15	Q905H9
59	3	42.9	19	15	Q905K7
60	3	42.9	19	15	Q905H1
61	3	42.9	19	15	Q905F9
62	3	42.9	19	15	Q905E7
63	3	42.9	19	15	Q90RH0
64	3	42.9	19	15	Q905J9
65	3	42.9	19	15	Q90RH3
66	3	42.9	19	15	Q90SK3
67	3	42.9	19	15	Q90RG6
68	3	42.9	19	15	Q905D9
69	3	42.9	19	15	Q905G7
70	3	42.9	19	15	Q905G3
71	3	42.9	19	15	Q905J5
72	3	42.9	19	15	Q905H5
73	3	42.9	19	15	Q90R12
74	3	42.9	19	15	Q905F1
75	3	42.9	19	15	Q90RF3
76	3	42.9	19	15	Q905F5
77	3	42.9	19	15	Q905L1
78	3	42.9	19	15	Q90RF7
79	3	42.9	19	15	Q90RH7
80	3	42.9	19	15	Q90RG2
81	3	42.9	19	15	Q905E3
82	3	42.9	19	15	Q905I7
83	3	42.9	19	15	Q90RF0
84	3	42.9	19	15	Q905J1
85	3	42.9	19	15	Q905I3
86	3	42.9	20	2	Q9R4V8
87	3	42.9	20	2	Q9R4I1
88	3	42.9	20	2	Q9R4F1
89	3	42.9	20	2	Q52918

Q9umg9	homo sapien
Q8seb7	gratelopipia
Q9xnr6	pylataella i
Q49230	mycoplasma
Q75905	homo sapien
Q14461	homo sapien
Q99188	riivulus cau
Q94re2	leptomonas
Q9uhm5	homo sapien
Q85718	reovirus (t
Q9fb61	corynebacte
Q9sap4	solanum tub
Q9quy5	rattus sp.
Q8twn2	macrobodella
Q35214	oenothera b
P92070	euhadra her
Q9sap4	solanum tub
Q8cis2	mus musculus
Q9eup4	thermus the
Q9uji1	homo sapien
Q17203	bombyx mori
Q8hkg6	boophilus k
Q8hcd7	zea mays (m
Q8has3	zea mays (m
Q9quj4	mus sp. mep
Q9qz24	mus musculus
Q9pru8	gallus gall
Q9uc81	homo sapien
Q9uj81	homo sapien
Q9ucr5	homo sapien
Q8ned1	homo sapien
Q26833	trypanosoma
Q9rg2	oryctolagus
Q8vnm8	mus musculus
Q90912	gallus gall
Q44608	buchnera ap
Q9aie8	actinobacil
Q99736	lanius coli
Q41472	solanum tub
Q85671	reovirus (t
Q9ps15	gallus gall
Q9prn4	petromyzon
Q905h9	human immun
Q905k7	human immun
Q905h1	human immun
Q905f9	human immun
Q905e7	human immun
Q90rh0	human immun
Q905j9	human immun
Q90rh3	human immun
Q90sk3	human immun
Q90rg6	human immun
Q905d9	human immun
Q905g7	human immun
Q905g3	human immun
Q905j5	human immun
Q905h5	human immun
Q90r12	human immun
Q905f1	human immun
Q90rf3	human immun
Q905f5	human immun
Q905l1	human immun
Q90rf7	human immun
Q90rh7	human immun
Q90rg2	human immun
Q905e3	human immun
Q905i7	human immun
Q90rf0	human immun
Q905j1	human immun
Q905i3	human immun
Q9r4v8	streptococc
Q9r4i1	borderella
Q9r4f1	desulfovibr
Q52918	rhizobium m

90 Q9417 leuconostoc
 91 Q94m1 streptomyce
 92 Q46499 desulfovibr
 93 Q9bpu4 halocynthia
 94 Q9tw8 leptinotars
 95 Q9trv0 bos taurus
 96 Q95947 saccharomyc
 97 Q9mmf2 buteo rufin
 98 Q9t2q9 solanum tub
 99 Q9st52 vicia faba
 100 Q91x54 mus musculu

ALIGNMENTS

RESULT 1

Q9TQB3 PRELIMINARY; PRT; 11 AA.
 AC Q9TQB3;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE MHC class I related protein 1 (Fragment).
 GN MRI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98451457; PubMed=9780177;
 RA Regiert P., Wanner V., Bahram S.;
 RT "Genomics, isoforms, expression, and phylogeny of the MHC class I-
 RT related MRI Gene";
 RL J. Immunol. 161:4066-4077(1998).
 DR EMBL: AF039526; AAD02172.1; -.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1235 MW; 5E71A31E29CDD697 CRC64;

Query Match 57.1%; Score 4; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APLL 4
 Db 6 APLL 9

RESULT 2

P92818 PRELIMINARY; PRT; 15 AA.
 AC P92818;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE NADH dehydrogenase subunit-4L (Fragment).
 OS Paralichthys olivaceus (Flounder).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
 OC Pleuronectoidei; Paralichthyidae; Paralichthys.
 OX NCBI_TaxID=8255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Saitoh K.;
 RT "Characterization of cloned mitochondrial fragments from the Japanese
 RT flounder";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB000674; BAA20924.1; -.
 KW Mitochondrion.

FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1613 MW; D1BAA2018C95FE80 CRC64;

Query Match 57.1%; Score 4; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APLL 4
 Db 11 APLL 14

RESULT 3

Q17205 PRELIMINARY; PRT; 17 AA.
 AC Q17205;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE A.L6 protein (Fragment).
 GN A.L6.
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=703;
 RX MEDLINE=90040707; PubMed=2810362;
 RA Spoerel N.A., Nguyen H.T., Eickbush T.H., Kafatos F.C.;
 RT "Gene Evolution and Regulation in the Chorion Complex of Bombyx mori:
 RT Hybridization and Sequence Analysis of Multiple Developmentally Middle
 RT A/B Chorion Gene Pairs";
 RL J. Mol. Biol. 209:11-19(1989).
 DR EMBL: X15562; CAA33575.1; -.
 FT NON TER 17 17
 SQ SEQUENCE 17 AA; 1877 MW; 577145043395539D CRC64;

Query Match 57.1%; Score 4; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APLL 4
 Db 5 APLL 8

RESULT 4

Q26832 PRELIMINARY; PRT; 17 AA.
 AC Q26832;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE (TaTat 1.2) variant surface glycoprotein ELC gene (Fragment).
 OS Trypanosoma brucei
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=86278091; PubMed=2942540;
 RA Brown K.H., Brentano S.T., Donelson J.E.;
 RT "Mung bean nuclease cleaves preferentially at the boundaries of
 RT variant surface glycoprotein gene transpositions in trypanosome DNA";
 RL J. Biol. Chem. 261:10352-10358(1986).
 DR EMBL: M14020; AAA30305.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 17 AA; 1973 MW; 9E00FBD261B8FFBF CRC64;

Query Match 57.1%; Score 4; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 AFLL 4
Db 13 AFLL 16

RESULT 5
Q9TVY3
ID Q9TVY3 PRELIMINARY; PRT; 17 AA.
AC Q9TVY3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE A.L10 protein (Fragment).
GN A.L10 OR A.L5 OR A.L9.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=703;
RX MEDLINE=90040707; PubMed=2810362;
RA Spoerel N.A., Nguyen H.T., Eickbush T.H., Kafatos F.C.;
RT "Gene evolution and regulation in the chorion complex of Bombyx mori.
RT Hybridization and sequence analysis of multiple developmentally middle
RT A/B chorion gene pairs.";
RL J. Mol. Biol. 209:1-19(1989).
DR EMBL; X15565; CAA33581.1; -.
DR EMBL; X15561; CAA33573.1; -.
DR EMBL; X15564; CAA33579.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1907 MW; 577145043395439C CRC64;

Query Match 57.1%; Score 4; DB 5; Length 17;
Best Local Similarity 100.0%; Pred.No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
Db 5 AFLL 8

RESULT 6
Q9TVX7
ID Q9TVX7 PRELIMINARY; PRT; 17 AA.
AC Q9TVX7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE A.X3 protein (Fragment).
GN A.X3 OR A.L4 OR A.L13 OR A.R2 OR A.R3 OR A.X1 OR A.X2.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=703;
RX MEDLINE=90040707; PubMed=2810362;
RA Spoerel N.A., Nguyen H.T., Eickbush T.H., Kafatos F.C.;
RT "Gene evolution and regulation in the chorion complex of Bombyx mori.
RT Hybridization and sequence analysis of multiple developmentally middle
RT A/B chorion gene pairs.";
RL J. Mol. Biol. 209:1-19(1989).
DR EMBL; X15572; CAA33595.1; -.
DR EMBL; X15560; CAA33571.1; -.
DR EMBL; X15566; CAA33583.1; -.
DR EMBL; X15568; CAA33587.1; -.
DR EMBL; X15569; CAA33589.1; -.
DR EMBL; X15570; CAA33591.1; -.

Qy 1 AFLL 4
Db 5 AFLL 8

RESULT 7
Q32710
ID Q32710 PRELIMINARY; PRT; 20 AA.
AC Q32710;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Yhnf protein (Fragment).
GN YHNF.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97352552; PubMed=9208947;
RA Hoenke S., Schmid M., Dimroth P.;
RT "Sequence of a gene cluster from Klebsiella pneumoniae encoding
RT malonate decarboxylase and expression of the enzyme in Escherichia
RT coli.";
RL Eur. J. Biochem. 246:530-538(1997).
DR EMBL; U95087; AAC45462.1; -.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2108 MW; 86A17AAC8BF77BFA CRC64;

Query Match 57.1%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred.No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
Db 11 AFLL 14

RESULT 8
O99182
ID O99182 PRELIMINARY; PRT; 7 AA.
AC O99182;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Cytochrome oxidase I (Fragment).
GN COI.
OS Gnatholebias zonatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnatholebias.
OX NCBI_TaxID=135316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20072928; PubMed=10603257;
RA Murphy W.J., Thomson J.E., Collier G.E.;
RT "Phylogeny of the Neotropical killifish family Rivulidae
RT (Cyprinodontiformes, Aplocheiloidei) inferred from mitochondrial DNA
RT sequences.";
RL Mol. Phylogenet. Evol. 13:289-301(1999).
DR EMBL; AF002591; AAD01074.1; -.
KW Mitochondrion.

```

```

DR EMBL; X15571; CAA33593.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1901 MW; 5FD3450433955C8C CRC64;

Query Match 57.1%; Score 4; DB 5; Length 17;
Best Local Similarity 100.0%; Pred.No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
Db 5 AFLL 8

RESULT 7
Q32710
ID Q32710 PRELIMINARY; PRT; 20 AA.
AC Q32710;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Yhnf protein (Fragment).
GN YHNF.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97352552; PubMed=9208947;
RA Hoenke S., Schmid M., Dimroth P.;
RT "Sequence of a gene cluster from Klebsiella pneumoniae encoding
RT malonate decarboxylase and expression of the enzyme in Escherichia
RT coli.";
RL Eur. J. Biochem. 246:530-538(1997).
DR EMBL; U95087; AAC45462.1; -.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2108 MW; 86A17AAC8BF77BFA CRC64;

Query Match 57.1%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred.No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
Db 11 AFLL 14

RESULT 8
O99182
ID O99182 PRELIMINARY; PRT; 7 AA.
AC O99182;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Cytochrome oxidase I (Fragment).
GN COI.
OS Gnatholebias zonatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnatholebias.
OX NCBI_TaxID=135316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20072928; PubMed=10603257;
RA Murphy W.J., Thomson J.E., Collier G.E.;
RT "Phylogeny of the Neotropical killifish family Rivulidae
RT (Cyprinodontiformes, Aplocheiloidei) inferred from mitochondrial DNA
RT sequences.";
RL Mol. Phylogenet. Evol. 13:289-301(1999).
DR EMBL; AF002591; AAD01074.1; -.
KW Mitochondrion.

```

```

FT  NON_TER      1
SQ  SEQUENCE      7 AA;  899 MW;  672721F6CB572030 CRC64;

Query Match      42.9%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 LYQ 6
Db  2 LYQ 4

RESULT 9
Q93SP2 ID Q93SP2 PRELIMINARY; PRT; 8 AA.
AC Q93SP2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Quaternary ammonium compound-resistance protein Qacdelta1
DE (Fragment).
DE NCBI_TaxID=287;
GN QACDELTA1.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YMC704; TRANSPOSON=class I integron;
RA Lee K., Chong Y., Yum J.H., Yong D., Livermore D.M.;
RT "VIM-2 metallo-beta-lactamase gene-containing integron in a
RT Pseudomonas aeruginosa clinical isolate.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY029772; AAK50441.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 920 MW; FE2729C732C87336 CRC64;

Query Match      42.9%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 FLL 4
Db  6 FLL 8

RESULT 10
Q94VC1 ID Q94VC1 PRELIMINARY; PRT; 8 AA.
AC Q94VC1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COL.
OS Varanus rudicollis.
OG Mitochondrion.
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguilliformia; Varanidae; Varanus.
OX NCBI_TaxID=169851;
RN [1]
RP SEQUENCE FROM N.A.
RC Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL: AF407521; AAL10116.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1053 MW; FE2729D5A36411A6 CRC64;

Query Match      42.9%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY  2 FLL 4
Db  6 FLL 8

RESULT 11
Q8HR64 ID Q8HR64 PRELIMINARY; PRT; 8 AA.
AC Q8HR64;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Rps16 protein (Fragment).
DE NCBI_TaxID=152470;
GN RPS16.
OS Clivia caulescens.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
OC Clivia.
OX NCBI_TaxID=152470;
RN [1]
RP SEQUENCE FROM N.A.
RC Conrad F., Reeves G., Rourke J.P.;
RT "Phylogenetic relationships of the recently discovered species Clivia
RT mirabilis.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ519544; CAD59437.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 909 MW; 9FA8772729C732C9 CRC64;

Query Match      42.9%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 FLL 4
Db  4 FLL 6

RESULT 12
Q95NT8 ID Q95NT8 PRELIMINARY; PRT; 10 AA.
AC Q95NT8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome P450 (Fragment).
GN CYP6D3.
OS Musca domestica (House fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscidae;
OX Muscidae; Musca.
OX NCBI_TaxID=7370;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LPR;
RA Kasai S., Scott J.G.;
RT "5' flanking sequence of CYP6D3.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CS;
RA Kasai S., Scott J.G.;
RT "Cytochrome P450 CYP6D3 5' flanking sequence.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF283258; AAK69543.1; -.
DR EMBL: AF283259; AAK69544.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1190 MW; 550408A0572729C7 CRC64;

Query Match      42.9%; Score 3; DB 5; Length 10;

```

Best Local Similarity 100.0%; Pred. No. 4e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4

DB 4 FLL 6

RESULT 13

Q9TRU6 PRELIMINARY; PRT; 10 AA.
 AC Q9TRU6;
 DT 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
 DE GAP-3, GTPase-activating protein (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92112868; PubMed=1309786;
 RA Nice E.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,
 RA Burgess A.W.;
 RT "The purification of a Rap1 GTPase-activating protein from bovine
 RT brain cytosol."
 RL J. Biol. Chem. 267:1546-1553(1992).
 FT NON_TER 1
 FT NON_TER 10
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1149 MW; 59370A51A72321A7 CRC64;

Query Match 42.9%; Score 3; DB 6; Length 10;

Best Local Similarity 100.0%; Pred. No. 4e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4

DB 1 FLL 3

RESULT 14

Q90ZV8 PRELIMINARY; PRT; 10 AA.
 AC Q90ZV8;
 DT 01-DEC-2001 (TREMELrel. 19, Created)
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
 DE Adenylate Kinase (Fragment).
 OS Psittacus erithacus (grey parrot).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Psittaciformes; Psittacidae; Psittacus.
 OX NCBI_TaxID=57247;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shapiro L.H., Dumbacher J.P.;
 RT "Adenylate kinase intron 5: a new nuclear locus for avian
 RT systematics."
 RL Auk 118:248-255(2001)
 DR EMBL; AF307895; AAK43534.1; -.
 KW Kinase.
 FT NON_TER 1
 FT NON_TER 10
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1099 MW; 22847A272731B777 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 10;

Best Local Similarity 100.0%; Pred. No. 4e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLY 5

DB 7 LLY 9

RESULT 15

O77912 PRELIMINARY; PRT; 11 AA.
 AC O77912;
 DT 01-NOV-1998 (TREMELrel. 08, Created)
 DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
 DE MHC class II B locus 4 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci."
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050023; AAC41362.1; -.
 FT NON_TER 1
 FT NON_TER 11
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1288 MW; 87F42A0FB2D5AB45 CRC64;

Query Match 42.9%; Score 3; DB 7; Length 11;

Best Local Similarity 100.0%; Pred. No. 4.3e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 3

DB 1 AFL 3

RESULT 16

O77883 PRELIMINARY; PRT; 11 AA.
 AC O77883;
 DT 01-NOV-1998 (TREMELrel. 08, Created)
 DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
 DE MHC class II B locus 4 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci."
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF049992; AAC41331.1; -.
 FT NON_TER 1
 FT NON_TER 11
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1288 MW; 87F42A0FB2D5AB45 CRC64;

Query Match 42.9%; Score 3; DB 7; Length 11;

Best Local Similarity 100.0%; Pred. No. 4.3e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 3

DB 1 AFL 3

```

RESULT 17
Q9UMQ9
ID Q9UMQ9 PRELIMINARY; PRT; 12 AA.
AC Q9UMQ9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment).
GN FBP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20237676; PubMed=10773464;
RA Tillmann H., Stein S., Liehr T., Eschrich K.;
RT "Structure and chromosomal localization of the human and mouse muscle
RT fructose-1,6-bisphosphatase genes.";
RL Gene 247:241-253(2000).
RL EMBL; AJ238490; CAB53366.1; -.
KW Hydrolase.
KW NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1432 MW; 28E901A093072338 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLY 5
Db 9 LLY 11

RESULT 18
Q8SEB7
ID Q8SEB7 PRELIMINARY; PRT; 12 AA.
AC Q8SEB7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cytochrome oxidase subunit 3 (Fragment).
GN COX3.
OS Grateloupia sp.
OC Mitochondrion.
OC Eukaryota; Rhodophyta; Florideophyceae; Halymeniales; Halymeniaceae;
OC Grateloupia.
OX NCBI_TaxID=185958;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1, and 3;
RA Marston M.F., Villalard-Bohnack M.;
RT "Genetic variability and potential sources of Grateloupia doryphora
RT (Halymeniaceae, Rhodophyta), an invasive species in Rhode Island
RT waters (USA).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF414928; AAL85237.1; -.
DR EMBL; AF414929; AAL85239.1; -.
KW Mitochondrion.
KW NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1367 MW; 9CFAEBE91CB046C1 CRC64;

Query Match 42.9%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3
Db 2 AFL 4

```

```

RESULT 19
Q9XNR6
ID Q9XNR6 PRELIMINARY; PRT; 12 AA.
AC Q9XNR6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH:ubiquinone oxidoreductase subunit 3 (Fragment).
GN NAD3.
OS Pylaiella littoralis.
OC Mitochondrion.
OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales;
OC Acinetosporaceae; Pylaiella.
OX NCBI_TaxID=2885;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=roscoff;
RX MEDLINE=99346148; PubMed=10415341;
RA Oudot M.P., Kloareg B., Loiseaux-de Goer S.;
RT "The mitochondrial Pylaiella littoralis nad1 gene contains only the
RT N-terminal Fes-binding domain.";
RL Gene 235:131-137(1999).
RL EMBL; AF110139; AAD44051.1; -.
KW Mitochondrion; Ubiquinone.
KW NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1501 MW; 49750746424B5B13 CRC64;

Query Match 42.9%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4
Db 2 FLL 4

RESULT 20
Q49230
ID Q49230 PRELIMINARY; PRT; 13 AA.
AC Q49230;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical 1.6 kDa protein (Fragment).
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=G-37;
RA Peterson S.N.;
RT "Characterization and analysis of the Mycoplasma genitalium genome.";
RL Thesis (1992), University of North Carolina Medical School, USA.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=G-37;
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.C., Bott K.F., Hutchison C.A. III.;
RT "A survey of the Mycoplasma genitalium genome by using random
RT sequencing.";
RL J. Bacteriol. 175:7918-7930(1993).
DR EMBL; U01791; AAD10602.1; -.
KW Hypothetical protein.
KW NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; EC726B2670F6D2C1 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4
Db 2 FLL 4

```


OS Leptomonas seymouri.
 OG Mitochondrion.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leptomonas.
 OX NCBI_TaxID=5684;
 RN [1] SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RA Merlyak E.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kolesnikov A.A.;
 RT "Cyb and A6 gene transcribed and edited in polycistron."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ313532; CAC67493.1; -
 KW Mitochondrion.
 FT NON_TER 1
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1626 MW; 471B78F48BDCCEB7 CRC64;

Query Match 42.9%; Score 3; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLY 5

Db 10 LLY 12

RESULT 25

Q9UHM5 PRELIMINARY; PRT; 14 AA.
 AC Q9UHM5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Islet cell autoantigen ICA69 (Fragment).
 GN ICA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N.A.
 RP Friday R.P., Trucco M., Pietropaolo M.;
 RA "Refined genomic organization of the diabetes autoantigen ICA69 gene locus."
 RT locus.
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF147807; AAP2021.1; -
 FT NON_TER 1 1
 SQ SEQUENCE 14 AA; 1656 MW; 1AEB6ACD19E2F9CB CRC64;

Query Match 42.9%; Score 3; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6

Db 6 LYQ 8

RESULT 26

Q85718 PRELIMINARY; PRT; 14 AA.
 AC Q85718;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Reovirus serotype 1 S2 (Fragment).
 OS Reovirus (type 1 / strain Lang).
 OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
 OX NCBI_TaxID=10884;
 RN [1] SEQUENCE FROM N.A.
 RP

RX MEDLINE=83017877; PubMed=7123853;
 RA Gaillard R.K., Li J.K., Keene J.D., Joklik W.K.;
 RT "The sequences at the termini of four genes of the three reovirus serotypes."
 RL Virology 121:320-326(1982).
 DR EMBL; J02303; AAA47241.1; -
 DR InterPro; IPR004317; Sigma 1.2.
 DR Pfam; PF03084; Sigma 1.2; 1.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1516 MW; 52F79D201BF900C7 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 3

Db 5 AFL 7

RESULT 27

Q9FB61 PRELIMINARY; PRT; 15 AA.
 AC Q9FB61;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 23S rRNA adenine N-6-methyltransferase leader peptide (ErmLP) (Putative leader peptide).
 GN ErmLP.
 OS Corynebacterium diphtheriae,
 OS Corynebacterium striatum, and
 OS Corynebacterium jeikeium.
 OG Plasmid pNG2, and Plasmid pTP10.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1717, 43770, 38289;
 RN [1] SEQUENCE FROM N.A.
 RP SPECIES=C. diphtheriae; STRAIN=S601; PLASMID=pNG2;
 RC Tauch A., Bischoff N., Kalinowski J., Puhler A.;
 RA "Insights into the genetic organization of the Corynebacterium diphtheriae erythromycin resistance plasmid pNG2 deduced from its complete nucleotide sequence."
 RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RL [2] SEQUENCE FROM N.A.
 RP SPECIES=C. striatum; STRAIN=M82B; PLASMID=pTP10;
 RC MEDLINE=20194806; PubMed=10732668;
 RX Tauch A., Kriest S., Kalinowski J., Puhler A.;
 RA "The 51,409-bp R-plasmid pTP10 from the multiresistant clinical isolate Corynebacterium striatum M82B is composed of DNA segments initially identified in soil bacteria and in plant, animal, and human pathogens."
 RT Mol. Gen. Genet. 263:1-11(2000).
 RN [3] SEQUENCE FROM N.A.
 RP SPECIES=C. jeikeium; STRAIN=CJ21;
 RC Rosato A.E., Lee B.S., Nash K.A.;
 RA "Inducible macrolide resistance in Corynebacterium jeikeium."
 RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF492560; AAM12764.1; -
 DR EMBL; AF024666; AAG03358.1; -
 DR EMBL; AF338705; AAK28909.1; -
 KW Methyltransferase; Transferase; Plasmid.
 SQ SEQUENCE 15 AA; 1749 MW; CA41026982472410 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 3

Db 1


```

Db          7 AFL 9

RESULT 28
Q9SAP4
ID Q9SAP4 PRELIMINARY; PRT; 15 AA.
AC Q9SAP4
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Serine proteinase inhibitor (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Irish Cobbler;
RA Yamagishi K., Kikuta Y.;
RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; X70376; CAA49837.1; -.
FT NON TER 15
SQ SEQUENCE 15 AA; 1667 MW; 8093D41B4CA0D1EC CRC64;

Query Match 42.9%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4
Db 9 FLL 11

RESULT 29
Q9QUY5
ID Q9QUY5 PRELIMINARY; PRT; 15 AA.
AC Q9QUY5
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE Oligodendrocyte-specific UDP-galactose:ceramide galactosyltransferase
  (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=96085162; PubMed=8521863;
RA Schulte S., Scofield W.;
RT "UDP galactose:ceramide galactosyltransferase and glutamate/aspartate
  transporter. Copurification, separation and characterization of the two
  glycoproteins.";
RL Eur. J. Biochem. 233:947-953(1995).
SQ SEQUENCE 15 AA; 1657 MW; 84474749A06BFFCC CRC64;

Query Match 42.9%; Score 3; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3
Db 12 AFL 14

RESULT 30
Q9TNW2
ID Q9TNW2 PRELIMINARY; PRT; 16 AA.
AC Q9TNW2
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)

Db          7 AFL 9

Sialidase L (Fragment).
OS Macrobodella decora (North American leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniiformes; Hirudinidae; Macrobodella.
OX NCBI_TaxID=6405;
RN [1]
RP SEQUENCE.
RX MEDLINE=94308136; PubMed=8034634;
RA Chou M.Y., Li S.C., Kiso M., Hasegawa A., Li Y.T.;
RT "Purification and characterization of sialidase L, a NeuAc alpha 2--
  >3Gal-specific sialidase.";
RL J. Biol. Chem. 269:18821-18826(1994).
SQ SEQUENCE 16 AA; 1910 MW; 0822879C79EC6BE0 CRC64;

Query Match 42.9%; Score 3; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6
Db 7 LYQ 9

RESULT 31
Q35214
ID Q35214 PRELIMINARY; PRT; 16 AA.
AC Q35214
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE ATPase alpha subunit (16 aa) (Fragment).
OS Oenothera bertiana (Bertero's evening primrose).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Onagraceae; Oenothera.
OX NCBI_TaxID=3950;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86312871; PubMed=2875433;
RA Schuster W., Hiesel R., Isaac P.G., Leaver C.J., Brennicke A.;
RT "Transcript termini of messenger RNAs in higher plant mitochondria.";
RL Nucleic Acids Res. 14:5943-5954(1986).
DR EMBL; X04203; CAA27800.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 16 AA; 1820 MW; 118AC961C9322C91 CRC64;

Query Match 42.9%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3
Db 4 AFL 6

RESULT 32
P92070
ID P92070 PRELIMINARY; PRT; 16 AA.
AC P92070
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE NADH dehydrogenase subunit 6 (Fragment).
OS Euhadra herklotzi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Helicoidea; Bradybaenidae; Euhadra.
OX NCBI_TaxID=58912;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hepatopancreas;

```

RA Yamazaki N., Ueshima R., Terrett J.A., Yokobori S., Kaifu M.,
RA Segawa R., Kobayashi T., Numachi K., Ueda T., Nishikawa K.,
RA Watanabe K., Thomas R.H.;
RT "Evolution of pulmonate gastropod mitochondrial genomes: comparisons
of complete gene organization of Euhadra, Cepaea and Albinaria and
implications of unusual tRNA secondary structures.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z71694; CAA96364.1; -.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1936 MW; 258908495BFBFCAE CRC64;

Query Match 42.9%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
DB 10 FLL 12

RESULT 33
O8CIS2 PRELIMINARY; PRT; 16 AA.
ID Q8CIS2
AC Q8CIS2;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Plasminogen (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Liver;
RX PubMed=12149246;
RA Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
RA Farmer R.J., Miles L.A.;
RT "Localization of Regulatory Elements Mediating Constitutive and
Cytokine-stimulated Plasminogen Gene Expression.";
RL J. Biol. Chem. 277:38579-38588(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Liver;
RA Garcia Bannach F., Fowler B.J., Gutierrez A., Bugge T.H., Degen J.L.,
RA Farmer R.J., Miles L.A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY134430; AAL15805.1; -.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1922 MW; 647558FC6EDB15CC CRC64;

Query Match 42.9%; Score 3; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
DB 10 FLL 12

RESULT 34
Q9EUP4 PRELIMINARY; PRT; 17 AA.
ID Q9EUP4
AC Q9EUP4;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Cell division associated protein (Fragment).
GN DIVIVA.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.

OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KT8;
RA Spada S., Gilbert Y., Pembroke J.T., Wall J.G.;
RT "Cloning and characterisation of the ylmE homologue of Thermus
thermophilus";
RL DNA Seq. 11:5007-5014(2001).
DR EMBL; AJ297409; CAC21427.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2084 MW; 0C642E1D509D87E3 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YQE 7
DB 10 YQE 12

RESULT 35
Q9UJH1 PRELIMINARY; PRT; 17 AA.
ID Q9UJH1
AC Q9UJH1;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE DJ436M11.2 (Retinoschisis (X-linked, juvenile) 1 (XLRs1))
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Grafham D.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z94036; CAB40073.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2029 MW; 8100E1B78C52C7PB CRC64;

Query Match 42.9%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
DB 8 FLL 10

RESULT 36
Q17203 PRELIMINARY; PRT; 17 AA.
ID Q17203
AC Q17203;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE A.L2 protein (Fragment).
OS A.L2.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=703;
RX MEDLINE=90040707; PubMed=2810362;
RA Spoerel N.A., Nguyen H.T., Eickbush T.H., Kafatos F.C.;
RT "Gene Evolution and Regulation in the Chorion Complex of Bombyx mori:
Hybridization and Sequence Analysis of Multiple Developmentally Middle

RT A/B Chorion Gene Pairs";
 RL J. Mol. Biol. 209:1-19 (1989).
 DR EMBL; X15558; CRA33567.1; -.
 FT NON TER 17
 SQ SEQUENCE 17 AA; 1935 MW; 5FD34DA633955C9C CRC64;
 Query Match 42.9%; Score 3; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 AFL 4
 Db 7 AFL 9

RESULT 37
 Q8HKG6 PRELIMINARY; PRT; 17 AA.
 ID Q8HKG6
 AC Q8HKG6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 GN NDI.
 OS Boophilus kohlsi.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
 OX NCBI_TaxID=127004;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Campbell N.J.H., Murrell A., Barker S.C.;
 RT "The value of idiosyncratic markers and conserved tRNA sequences from
 RT the mitochondrial genome of hard ticks (Acari: Ixodida: Ixodidae) for
 RT phylogenetic inference."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY059201; AAL79405.1; -.
 KW Mitochondrion.
 FT NON TER 1
 SQ SEQUENCE 17 AA; 1989 MW; 0F9CD412E9843E0A CRC64;
 Query Match 42.9%; Score 3; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AFL 3
 Db 3 AFL 5

RESULT 38
 Q8HCD7 PRELIMINARY; PRT; 17 AA.
 ID Q8HCD7
 AC Q8HCD7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Zea mays (Maize).
 OG Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Mo17; TISSUE=Microspore;
 RA Betz S.K., Gallagher L.J., Chase C.D.;
 RT "Mitochondrial RNA editing truncates a chimeric open reading frame
 RT associated with S male sterility in maize."
 RL Curr. Genet. 0:0-0(2002).
 DR EMBL; AF536188; AAN40750.1; -.
 KW EMBL; AF536189; AAN40752.1; -.

DR EMBL; AF536190; AAN40754.1; -.
 KW Hypothetical protein; Mitochondrion.
 SQ SEQUENCE 17 AA; 1991 MW; 1A25865EB2CFA69E CRC64;
 Query Match 42.9%; Score 3; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AFL 3
 Db 10 AFL 12

RESULT 39
 Q8HAS3 PRELIMINARY; PRT; 17 AA.
 ID Q8HAS3
 AC Q8HAS3;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ORF17 (Hypothetical protein).
 OS Zea mays (Maize).
 OG Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Mo17; TISSUE=Microspore;
 RX MEDLINE=22378502; PubMed=12491012;
 RA Gallagher L.J., Betz S.K., Chase C.D.;
 RT "Mitochondrial RNA editing truncates a chimeric open reading frame
 RT associated with S male sterility in maize."
 RL Curr. Genet. 42:179-184(2002).
 DR EMBL; AF534133; AAN39280.1; -.
 KW EMBL; AF536191; AAN40756.1; -.
 KW Hypothetical protein; Mitochondrion.
 SQ SEQUENCE 17 AA; 2017 MW; 1A25864C22CFA69E CRC64;
 Query Match 42.9%; Score 3; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AFL 3
 Db 10 AFL 12

RESULT 40
 Q9QUJ4 PRELIMINARY; PRT; 17 AA.
 ID Q9QUJ4
 AC Q9QUJ4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Meprin-B peptide B2 (Fragment).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91373354; PubMed=1894622;
 RA Kounnas M.Z., Wolz R.L., Gorbea C.M., Bond J.S.;
 RT "Meprin-A and -B. Cell surface endopeptidases of the mouse kidney."
 RL J. Biol. Chem. 266:17350-17357(1991).
 FT NON TER 1
 FT NON TER 17
 SQ SEQUENCE 17 AA; 2165 MW; ACA591691044F20B CRC64;
 Query Match 42.9%; Score 3; DB 11; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLY 5
|||
Db 4 LLY 6

RESULT 41

Q9QZ24 ID Q9QZ24 PRELIMINARY; PRT; 17 AA.
AC Q9QZ24; 17 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE B7-Ag protein (Fragment).
GN CD80 OR B7-AG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99453732; PubMed=10524207;
RA Tone M., Nolan K.F., Walsh L.A., Tone Y., Thompson S.A.J.,
RA Waldmann H.;
RT "Structure and chromosomal location of mouse and human CD52 genes.";
RL Biochim. Biophys. Acta, Gene Struct. Expr. 1446:334-340(1999).
DR EMBL; AJ132360; CAB51320.1; --
DR MGD; MGI:101775; Cd80.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1932 MW; 8F2B5852E50DB8D7 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
|||
Db 4 FLL 6

RESULT 42

Q9PRU8 ID Q9PRU8 PRELIMINARY; PRT; 17 AA.
AC Q9PRU8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE P130=PHOSPHOPROTEINS TIGHTLY associated with V-Crk in VIVO (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=95105151; PubMed=7806494;
RA Sakai R., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Nishida J.,
RA Yazaki Y., Hirai H.;
RT "Characterization, partial purification, and peptide sequencing of p130, the main phosphoprotein associated with v-Crk oncoprotein.";
RL J. Biol. Chem. 269:32740-32746(1994).
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1861 MW; 379058CDE44F8879 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LLY 6
|||

Db 5 LYQ 7

RESULT 43

Q9UC81 ID Q9UC81 PRELIMINARY; PRT; 18 AA.
AC Q9UC81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE 34.5 kDa stone matrix protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95215817; PubMed=7701298;
RA Binette J.P., Binette M.B.;
RT "Sequencing of proteins extracted from stones.";
RL Scanning Microsc. 8:233-239(1994).
DR HSP; P02906; 1SBP.
SQ SEQUENCE 18 AA; 2246 MW; B6CB60E9AC339E35 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 6.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
|||
Db 16 LYQ 18

RESULT 44

Q9UJ81 ID Q9UJ81 PRELIMINARY; PRT; 18 AA.
AC Q9UJ81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CD52 protein (Fragment).
GN CD52.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99453732; PubMed=10524207;
RA Tone M., Nolan K.F., Walsh L.A., Tone Y., Thompson S.A.J.,
RA Waldmann H.;
RT "Structure and chromosomal location of mouse and human CD52 genes.";
RL Biochim. Biophys. Acta, Gene Struct. Expr. 1446:334-340(1999).
DR EMBL; AJ132359; CAB51285.1; --
FT NON_TER 18
SQ SEQUENCE 18 AA; 2166 MW; AC6C4590EDA71F29 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 6.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
|||
Db 6 FLL 8

RESULT 45

Q9UCR5 ID Q9UCR5 PRELIMINARY; PRT; 18 AA.
AC Q9UCR5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Mammary-derived growth factor 1, MDGF1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92118863; PubMed=1731916;
RA Bano M., Lupu R., Kidwell W.R., Lippman M.E., Dickson R.B.;
RT "Production and characterization of mammary-derived growth factor 1 in
mammary epithelial cell lines."
RL Biochemistry 31:610-616(1992).
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2060 MW; 720BIA09F9262ACC CRC64;

Query Match 42.9%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db 11 FLL 13

RESULT 46
QNEDI
ID Q8NED1 PRELIMINARY; PRT; 18 AA.
AC Q8NED1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Straussberg R.;
RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL, BC032027; RAH32027.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 2050 MW; E71A655E65FD253F CRC64;

Query Match 42.9%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db 2 FLL 4

RESULT 47
Q26833
ID Q26833 PRELIMINARY; PRT; 18 AA.
AC Q26833;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Iatf 1.2) variant surface glycoprotein BC gene (Fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86278091; PubMed=2942540;
RA Brown K.H., Brentano S.T., Donelson J.E.;
RT "Mung bean nuclease cleaves preferentially at the boundaries of
RT variant surface glycoprotein gene transpositions in trypanosome DNA.";

RL J. Biol. Chem. 261:10352-10358(1986).
DR EMBL, M14021; AAA30306.1; -.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2039 MW; 8EA0F51BD630BF8F CRC64;

Query Match 42.9%; Score 3; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 3
Db 13 AFL 15

RESULT 48
Q9TRG2
ID Q9TRG2 PRELIMINARY; PRT; 18 AA.
AC Q9TRG2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
DE C1-INHIBITOR-SERINE proteinase inhibitor (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=93264944; PubMed=8495195;
RA Aulak K.S., Davis A.E.III., Donaldson V.H., Harrison R.A.;
RT "Chymotrypsin inhibitory activity of normal C1-inhibitor and a p1 Arg
to His mutant: evidence for the presence of overlapping reactive
centers."
RL Protein Sci. 2:727-732(1993).
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; 1.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2134 MW; 6A74AE35AF54C5E CRC64;

Query Match 42.9%; Score 3; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db 16 FLL 18

RESULT 49
Q8VHM8
ID Q8VHM8 PRELIMINARY; PRT; 18 AA.
AC Q8VHM8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Interleukin 10 receptor 2 (Fragment).
GN IL10R2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
RT "The genomic structure and expression patterns of the gene encoding
RT the second chain of the murine interleukin 10 receptor, IL-10R2.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Hardy M.P., Hertzog P.J., Owczarek C.M.;

RT "The organization, transcriptional regulation and chromosomal
 RT localization of the locus encoding the gene for the murine type I
 RT interferon receptor, Ifnar2.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF440786; AAL40943.1; -.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 1888 MW; 8AC62D50E1523831 CRC64;
 Query Match 42.9%; Score 3; DB 11; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;
 QY 2 FLL 4
 Db 14 FLL 16
 RESULT 50
 Q90912 PRELIMINARY; PRT; 18 AA.
 AC Q90912;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Chicken embryonic myosin heavy chain, 3' end of mRNA, fragment 2
 DE (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83213464; PubMed=6304080;
 RA Freyer G.A., Robbins J.;
 RT "The analysis of a chicken myosin heavy chain cdna clone.";
 RL J. Biol. Chem. 258:7149-7154(1983).
 DR EMBL; K00815; AAA48969.1; -.
 FT NON_TER 1 1
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2039 MW; 38DDB38C4184436B CRC64;
 Query Match 42.9%; Score 3; DB 13; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;
 QY 2 FLL 4
 Db 7 FLL 9
 RESULT 51
 Q44608 PRELIMINARY; PRT; 19 AA.
 AC Q44608;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Shikimate dehydrogenase (Fragment).
 DE AROE.
 OS Buchnera aphidicola.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=9;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95212914; PubMed=7535281;
 RA Roubhakhsh D., Baumann P.;
 RT Characterization of a putative 23S-5S rRNA operon of Buchnera
 RT aphidicola (endosymbiont of aphids) unlinked to the 16S rRNA-encoding
 RT gene.";
 RL Gene 156:107-112(1995).

DR EMBL; U10497; AAA79126.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 19 AA; 2214 MW; 2C1A573F6A4D01D5 CRC64;
 Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;
 QY 2 FLL 4
 Db 2 FLL 4
 RESULT 52
 Q9AIE8 PRELIMINARY; PRT; 19 AA.
 AC Q9AIE8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Hypothetical 2.4 kDa protein.
 OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Actinobacillus.
 OX NCBI_TaxID=715;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=ATCC27088;
 RX MEDLINE=21125560; PubMed=11222596;
 RA Doree S.M., Mulks M.H.;
 RT "Identification of an Actinobacillus pleuropneumoniae consensus
 RT promoter structure.";
 RL J. Bacteriol. 183:1983-1989(2001).
 DR EMBL; AF275729; AAK18080.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 19 AA; 2379 MW; DCA788F5221B03DC CRC64;
 Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;
 QY 4 LYQ 6
 Db 8 LYQ 10
 RESULT 53
 O99736 PRELIMINARY; PRT; 19 AA.
 AC O99736;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Cytochrome oxidase subunit III (EC 1.9.3.1) (Cytochrome c oxidase
 DE polypeptide III) (Fragment).
 OS Lanius collurio.
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Corvoidea; Laniidae;
 OC Lanius.
 OX NCBI_TaxID=56324;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22459836; PubMed=12572620;
 RA Mindell D.P., Sorenson M.D., Dimcheff D.E.;
 RT "An extra nucleotide is not translated in mitochondrial ND3 of some
 RT birds and turtles.";
 RL Mol. Biol. Evol. 15:1568-1571(1998).
 CC -!- FUNCTION: SUBUNITS I, II AND III FORM THE FUNCTIONAL CORE OF THE
 CC ENZYME COMPLEX (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICCYTOCHROME
 CC C + 2 H(2)O.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.

```
DR      piam;  
FT      NON TE  
SQ      SEQUEN
```

ID Q905H9 PRELIMINARY; PRT; 19 AA.
AC Q905H9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
RN NCBI_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=96CG38;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410444; AAL10243.1; -.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2193 MW; 00430F35A7111915 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
Db 16 LYQ 18

RESULT 59
Q905K7 PRELIMINARY; PRT; 19 AA.
AC Q905K7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
RN NCBI_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=96CG14;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410437; AAL10215.1; -.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2176 MW; 3516A49DA9711856 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
Db 16 LYQ 18

RESULT 60
Q905H1 PRELIMINARY; PRT; 19 AA.
ID Q905H1
AC Q905H1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
RN NCBI_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=97CG275;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410446; AAL10251.1; -.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2250 MW; ED16A23424711905 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
Db 16 LYQ 18

RESULT 61
Q905F9 PRELIMINARY; PRT; 19 AA.
ID Q905F9;
AC Q905F9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
RN NCBI_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=97CG305;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410449; AAL10263.1; -.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2261 MW; 005A7947EB711915 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
Db 16 LYQ 18

RESULT 62
Q905E7 PRELIMINARY; PRT; 19 AA.
ID Q905E7
AC Q905E7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CG314;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RL Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410452; AAL10275.1; -.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2122 MW; 6B3BE70E0A662B9E CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6
Db 16 LYQ 18

RESULT 63
Q90RH0 PRELIMINARY; PRT; 19 AA.
ID Q90RH0
AC Q90RH0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96CG21;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
RA Hayami M., Ichimura H., Parra J.H.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RL Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127547; AAK84905.1; -.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2276 MW; 740E013424711914 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6
Db 16 LYQ 18

RESULT 64
Q905J9 PRELIMINARY; PRT; 19 AA.
ID Q905J9
AC Q905J9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).

OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96CG22;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RL Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410439; AAL10223.1; -.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2120 MW; 7413BAD4EA711B9E CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6
Db 16 LYQ 18

RESULT 65
Q90RH3 PRELIMINARY; PRT; 19 AA.
ID Q90RH3
AC Q90RH3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96CG17;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
RA Hayami M., Ichimura H., Parra J.H.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RL Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127546; AAK84901.1; -.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2120 MW; 7413BAD4EA711B9E CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6
Db 16 LYQ 18

RESULT 66
Q905K3 PRELIMINARY; PRT; 19 AA.
ID Q905K3
AC Q905K3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).

```
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96CG34;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF10438; AAL10219.1; -.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2260 MW; 7415E9997A711914 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
Db 16 LYQ 18

RESULT 67
Q90RG6 PRELIMINARY; PRT; 19 AA.
AC Q90RG6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96CG34;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
RA Hayami M., Ichimura H., Parra J.H.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127548; AAK84308.1; -.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2264 MW; 7413AAD274711851 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
Db 16 LYQ 18

RESULT 68
Q90SD9 PRELIMINARY; PRT; 19 AA.
AC Q90SD9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CG316;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410454; AAL10283.1; -.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2160 MW; 740C7E5DA9711914 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
Db 16 LYQ 18

RESULT 69
Q905G7 PRELIMINARY; PRT; 19 AA.
AC Q905G7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CG281;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410447; AAL10255.1; -.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2332 MW; 740E13BF24662914 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
Db 16 LYQ 18

RESULT 70
Q905G3 PRELIMINARY; PRT; 19 AA.
AC Q905G3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
```

```

[1]
RN SEQUENCE FROM N.A.
RC STRAIN=97CG284;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410448; AAL10259.1; -.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2262 MW; 740E013424711851 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6
Db 16 LYQ 18

RESULT 71
Q905J5 ID Q905J5 PRELIMINARY; PRT; 19 AA.
AC Q905J5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96CG23;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410440; AAL10227.1; -.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2304 MW; 740E0B1C24711851 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6
Db 16 LYQ 18

RESULT 72
Q905H5 ID Q905H5 PRELIMINARY; PRT; 19 AA.
AC Q905H5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]

```

```

RN SEQUENCE FROM N.A.
RC STRAIN=97CG152;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410445; AAL10247.1; -.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2187 MW; 7416A234246A7000 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6
Db 16 LYQ 18

RESULT 73
Q90RI2 ID Q90RI2 PRELIMINARY; PRT; 19 AA.
AC Q90RI2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96CG11;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
RA Hayami M., Ichimura H., Parra J.H.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127544; AAK84895.2; -.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2305 MW; F0B4722C24711905 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6
Db 16 LYQ 18

RESULT 74
Q905F1 ID Q905F1 PRELIMINARY; PRT; 19 AA.
AC Q905F1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CG313;

```

RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.,
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville,"
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410451; AAL10271.1; -.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2248 MW; 7413BAD374711914 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
Db 16 LYQ 18

RESULT 75

Q90RF3 PRELIMINARY; PRT; 19 AA.
AC Q90RF3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
CX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CG282;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
RA Hayami M., Ichimura H., Parra J.H.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville,"
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127551; AAK84918.1; -.
FT NON_TER 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2185 MW; 69D3ABD5FA711911 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
Db 16 LYQ 18

Search completed: November 25, 2003, 19:34:09
Job time : 16.1453 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 17.8663 Seconds
(without alignments)
62.189 Million cell updates/sec

Title: US-09-641-801-28

Perfect score: 7

Sequence: 1 AFLYQOE 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :
1: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	22	Colostrinin derive
2	7	100.0	7	22	Colostrinin peptid
3	7	100.0	7	22	Colostrinin peptid
4	7	100.0	7	22	Ewe colostrinin pe
5	7	100.0	7	23	Colostrinin consti
6	7	100.0	7	23	Colostrinin consti
7	7	100.0	7	23	Neural cell regula
8	7	100.0	7	23	Antiviral composi
9	7	100.0	9	22	Ewe colostrinin pe

10	7	100.0	11	23	AAU83297	Antiviral composi
11	7	100.0	12	23	AAU83299	Antiviral composi
12	7	100.0	12	23	AAU83300	Antiviral composi
13	7	100.0	13	23	AAU83302	Antiviral composi
14	7	100.0	13	23	AAU83305	Antiviral composi
15	7	100.0	13	23	AAU83309	Antiviral composi
16	7	100.0	14	23	AAU83316	Antiviral composi
17	7	100.0	14	23	AAU83325	Antiviral composi
18	7	100.0	15	23	AAU83327	Antiviral composi
19	7	100.0	16	23	AAU83335	Antiviral composi
20	7	100.0	16	23	AAU83336	Antiviral composi
21	7	100.0	19	23	AAU83341	Antiviral composi
22	6	85.7	9	23	AAU83290	Antiviral composi
23	6	85.7	13	22	AAU83277	Colostrinin derive
24	6	85.7	13	22	AAU83250	Colostrinin peptid
25	6	85.7	13	22	AAU83252	Colostrinin peptid
26	6	85.7	13	22	AAU83338	Ewe colostrinin pe
27	6	85.7	13	23	AAU83259	Colostrinin consti
28	6	85.7	13	23	AAU831065	Colostrinin consti
29	6	85.7	13	23	AAU831068	Neural cell regula
30	6	85.7	13	23	AAU83314	Antiviral composi
31	6	85.7	14	23	AAU83320	Antiviral composi
32	6	85.7	15	23	AAU83332	Antiviral composi
33	6	85.7	16	23	AAU83339	Antiviral composi
34	6	85.7	19	20	AAU83233	Casein antimicrobi
35	5	71.4	6	23	AAU831810	Human butyrylcholi
36	5	71.4	7	22	AAU83190	Colostrinin peptid
37	5	71.4	8	22	AAU83200	Modified colostrin
38	5	71.4	16	23	AAU83337	Antiviral composi
39	4	57.1	5	17	AAU8316494	Linear thrombin re
40	4	57.1	6	22	AAU831616	Human olfactory re
41	4	57.1	6	22	AAU832026	Amino acid sequenc
42	4	57.1	6	22	AAU833034	Amino acid sequenc
43	4	57.1	6	22	AAU833043	Amino acid sequenc
44	4	57.1	6	22	AAU833065	Amino acid sequenc
45	4	57.1	6	22	AAU833106	Amino acid sequenc
46	4	57.1	6	22	AAU833108	Amino acid sequenc
47	4	57.1	6	24	AAU83261	Olfactory receptor
48	4	57.1	6	24	AAU83261	Peptide binding to
49	4	57.1	6	24	AAU83271	Peptide binding to
50	4	57.1	6	24	AAU83271	Peptide binding to
51	4	57.1	6	24	AAU83291	Poliovirus-binding
52	4	57.1	6	24	AAU83293	Poliovirus-binding
53	4	57.1	6	24	AAU83312	Peptide binding to
54	4	57.1	7	17	AAU83280	Peptide binding to
55	4	57.1	9	15	AAU838067	Hepatitis B virus-
56	4	57.1	9	20	AAU835635	Immunogenic peptid
57	4	57.1	9	20	AAU835635	Immunogenic peptid
58	4	57.1	9	20	AAU835635	Immunogenic peptid
59	4	57.1	9	21	AAU835635	Immunogenic peptid
60	4	57.1	9	21	AAU835635	Immunogenic peptid
61	4	57.1	9	21	AAU835635	Immunogenic peptid
62	4	57.1	9	22	AAU835635	Immunogenic peptid
63	4	57.1	9	22	AAU835635	Immunogenic peptid
64	4	57.1	9	22	AAU835635	Immunogenic peptid
65	4	57.1	9	22	AAU835635	Immunogenic peptid
66	4	57.1	9	22	AAU835635	Immunogenic peptid
67	4	57.1	9	22	AAU835635	Immunogenic peptid
68	4	57.1	9	22	AAU835635	Immunogenic peptid
69	4	57.1	9	22	AAU835635	Immunogenic peptid
70	4	57.1	9	22	AAU835635	Immunogenic peptid
71	4	57.1	9	22	AAU835635	Immunogenic peptid
72	4	57.1	9	22	AAU835635	Immunogenic peptid
73	4	57.1	9	22	AAU835635	Immunogenic peptid
74	4	57.1	9	22	AAU835635	Immunogenic peptid
75	4	57.1	9	22	AAU835635	Immunogenic peptid
76	4	57.1	9	22	AAU835635	Immunogenic peptid
77	4	57.1	9	22	AAU835635	Immunogenic peptid
78	4	57.1	9	22	AAU835635	Immunogenic peptid
79	4	57.1	9	22	AAU835635	Immunogenic peptid
80	4	57.1	9	22	AAU835635	Immunogenic peptid
81	4	57.1	9	22	AAU835635	Immunogenic peptid
82	4	57.1	9	22	AAU835635	Immunogenic peptid

83 4 57.1 9 23 ABJ16319 Zinc transporter p
84 4 57.1 9 23 ABJ16343 Zinc transporter p
85 4 57.1 9 23 ABJ16358 Zinc transporter p
86 4 57.1 9 23 ABJ16392 Zinc transporter p
87 4 57.1 9 23 ABJ16476 Zinc transporter p
88 4 57.1 9 23 ABJ16485 Zinc transporter p
89 4 57.1 9 23 ABJ16523 Zinc transporter p
90 4 57.1 9 23 ABJ16785 Zinc transporter p
91 4 57.1 9 23 ABJ16893 CTL epitope HLA pe
92 4 57.1 9 23 ABJ16958 CTL epitope HLA pe
93 4 57.1 9 23 ABJ17016 CTL epitope HLA pe
94 4 57.1 9 23 ABJ17089 CTL epitope HLA pe
95 4 57.1 9 23 ABJ17173 CTL epitope HLA pe
96 4 57.1 9 23 ABJ17204 CTL epitope HLA pe
97 4 57.1 9 23 ABJ17281 CTL epitope HLA pe
98 4 57.1 9 23 ABJ17385 Human cancer-relat
99 4 57.1 9 24 ABR17411 Human cancer-relat
100 4 57.1 9 24 ABR17411 Human cancer-relat

ALIGNMENTS

RESULT 1
AAB72273
ID AAB72273 standard; peptide; 7 AA.
XX AC AAB72273;
XX DT 14-MAY-2001 (first entry)
XX DE Colostrinin derived cytokine inducing peptide SEQ ID 28.
XX KW Colostrinin; immune response; cytokine; blood cell proliferation;
XX KW central nervous system disorder; neurological disorder; mental disorder;
XX KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
XX KW neurosis; infection.
XX OS Synthetic.
XX PN WO200111937-A2.
XX XX WO200111937-A2.
XX PD 22-FEB-2001.
XX PF 17-AUG-2000; 2000WO-US22818.
XX PR 17-AUG-1999; 99US-0149311.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PA (REG-) REGEN THERAPEUTICS PLC.
XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX DR WPI; 2001-202804/20.
XX XX Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator -
XX FS Claim 1; Page 34; 50pp; English.
XX CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The
CC peptides have immune response modulatory activity, and are capable of
CC inducing cytokines. Colostrinin and its derived peptides are useful for
CC inducing cytokine production, for modulating an immunological response
CC and for inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.

XX SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AFLLYQE 7
DB 1 AFLLYQE 7
RESULT 2
AAB72526
ID AAB72526 standard; Peptide; 7 AA.
XX AC AAB72526;
XX DT 09-MAY-2001 (first entry)
XX DE Colostrinin peptide #27.
XX KW Dermatological; oxidative stress regulator; colostrinin.
XX OS Unidentified.
XX PN WO200112650-A2.
XX XX WO200112650-A2.
XX PD 22-FEB-2001.
XX PF 17-AUG-2000; 2000WO-US22665.
XX PR 17-AUG-1999; 99US-0149310.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Stanton GJ, Hughes TK, Boldogh I;
XX DR WPI; 2001-218342/22.
XX XX Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -
XX FS Claim 6; Page 26; 48pp; English.
XX CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.
XX SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AFLLYQE 7
DB 1 AFLLYQE 7
RESULT 3
AAB72558
ID AAB72558 standard; Peptide; 7 AA.
XX AC AAB72558;
XX DT 09-MAY-2001 (first entry)
XX XX

```

DE Colostrinin peptide #27.
KW Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX
OS Unidentified.
XX
PN WO200112651-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22774.
XX
PR 17-AUG-1999; 99US-0149633.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Boldogh I;
XX
XX WPI; 2001-226545/23.
XX
PT Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating
PT damaged neural cells in a patient .
XX
PS Claim 6; Page 22; 35pp; English.
XX
CC The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLLYQE 7
Db |||||
1 AFLLYQE 7

RESULT 4
AAB59337
ID AAB59337 standard; Peptide; 7 AA.
AC AAB59337;
XX
DT 21-MAR-2001 (first entry)
XX
DE Ewe colostrinin peptide fragment C-12.
XX
KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
OS Ovis sp.
XX
PN WO200075173-A2.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-GB02128.
XX
PR 02-JUN-1999; 99GB-0012852.
XX
PA (REGG-) REGEN THERAPEUTICS PLC.
XX
PI Georgiades JA;
XX
XX WPI; 2001-071058/08.
XX
PT Peptides having an N-terminal amino acid sequence isolated from

colostrinin for treating e.g. disorders of the central nervous system
and immune system, viral and bacterial infections, and diseases
characterized by amyloid plaques -
Claim 7; Page 27; 63pp; English.
The present invention provides the sequences of a number of peptides
found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
fragment of colostrum. These peptides can be used in the treatment of
central nervous system disorders such as senile dementia, Parkinson's
disease, Alzheimer's disease, psychosis and neurosis, immune system
disorders such as bacterial and viral infections, to improve the
development of a child's immune system, as a dietary supplement, and to
promote the dissolution of beta-amyloid plaques.
Sequence 7 AA;
Query Match 100.0%; Score 7; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLLYQE 7
Db |||||
1 AFLLYQE 7

RESULT 5
AAE20255
ID AAE20255 standard; peptide; 7 AA.
AC AAE20255;
XX
DT 18-JUN-2002 (first entry)
XX
DE Colostrinin constituent peptide #27.
XX
KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnary.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 7 /note= "Optionally C-terminal amide"
FT FT
XX
PN WO200213850-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US22776.
XX
PR 17-AUG-2000; 2000WO-US22776.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX
XX WPI; 2002-269151/31.
XX
PT Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog -
XX
PS Claim 6; Page 26; 51pp; English.
XX
CC The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/

```

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidizing species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 7; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AFLLYQE 7
 Db 1 AFLLYQE 7

RESULT 6
 AAM51062
 ID AAM51062 standard; Peptide; 7 AA.

XX AC AAM51062;
 XX DT 30-MAY-2002 (first entry)
 XX DE Colostrinin constituent peptide (casein amino acids 202-208).
 XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;
 XX KW blood cell regulator; cytokine inducer; beta-casein; human.
 XX OS Homo sapiens.

XX Key Location/Qualifiers
 XX FT Modified-site 7 /note= "optional C-terminal amidation"
 XX FT
 XX PN WO200213849-A1.

XX XX 21-FEB-2002.
 XX XX 17-AUG-2000; 2000WO-US22775.
 XX XX 17-AUG-2000; 2000WO-US22775.
 XX XX (TEXA) UNIV TEXAS SYSTEM.
 XX XX (REGE-) REGEN THERAPEUTICS PLC.

XX XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 XX blood cell regulator selected from colostrinin, its constituent peptide
 XX and/or analogue -

XX PS Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified
 CC as having a beta-casein homologue precursor, and corresponds to
 CC casein amino acids 202-208. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ
 CC or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patient. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide.

XX SQ Sequence 7 AA;
 Query Match 100.0%; Score 7; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AFLLYQE 7
 Db 1 AFLLYQE 7

RESULT 7
 AAO14604
 ID AAO14604 standard; peptide; 7 AA.

XX AC AAO14604;
 XX DT 27-MAY-2002 (first entry)
 XX DE Neural cell regulatory colostrinin peptide 27.
 XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
 XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 XX KW neural cell treatment.

XX OS Unidentified.
 XX Key Location/Qualifiers
 XX FT Modified-site 7 /note= "Optional C-terminal amide"
 XX FT

XX PN WO200213851-A1.
 XX XX 21-FEB-2002.
 XX XX 17-AUG-2000; 2000WO-US22777.
 XX XX 17-AUG-2000; 2000WO-US22777.
 XX XX (TEXA) UNIV TEXAS SYSTEM.

XX XX Boldogh I, Stanton JG, Hughes TK;
 XX XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 XX regulator selected from colostrinin, its constituent peptide and/or
 XX analog -

XX PS Claim 7; Page 22; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cell morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention.

SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLYQE 7

Db 1 AFLLYQE 7

RESULT 8

AAU83286
ID AAU83286 standard; Peptide; 8 AA.

XX AC AAU83286;

DT 23-APR-2002 (first entry)

DE Antiviral composition peptide-A, fragment #4.

XX Virucide; Immunostimulant; interleukin-8; viral infection;

KW monocyte chemotactic protein 1; immune system.

OS Synthetic.

XX US2002004579-A1.

PN 10-JAN-2002.

XX 17-JAN-2001; 2001US-0764017.

XX 22-OCT-1996; 96US-0735236.

PR 25-JUN-1999; 99US-0344095.

XX (ADVI-) ADVANCED VIRAL RES CORP.

XX Friedland B, Hirschman SZ, Taraporewala IB;

XX WPI; 2002-163727/21.

XX New peptides compositions, useful for treating viral infections and

PT stimulating the immune system -

PS Disclosure; Page 7; 37pp; English.

XX The invention relates to a new peptide composition comprising a specified peptide sequence. The composition comprises nucleotide-peptide comprising a peptide linked through a serine residue and diphosphodiester to a nucleotide; or peptides with about 31 amino acid residues capable of stimulating production of interleukin-8 in cultured cells; or peptides with about 31 amino acid residues capable of stimulating production of monocyte chemotactic protein 1 in cultured cells. The peptides are useful for treating viral infections and stimulating the immune system.

CC AAU83282-AAU83401 represent peptides used in the composition of the invention.

XX Sequence 8 AA;

Query Match 100.0%; Score 7; DB 23; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLYQE 7

Db 1 AFLLYQE 7

RESULT 9

AAU83286
ID AAU83286 standard; Peptide; 9 AA.

XX AAB59356;

DT 21-MAR-2001 (first entry)

DE Ewe colostrin peptide fragment derived sequence #16.

XX Sheep; colostrin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX Ovis sp.

XX WO200075173-A2.

XX 14-DEC-2000.

XX 02-JUN-2000; 2000WO-GB02128.

XX 02-JUN-1999; 99GB-0012852.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-071058/08.

XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrin for treating e.g. disorders of the central nervous system

PT and immune system, viral and bacterial infections, and diseases

PT characterized by amyloid plaques -

XX Claim 8; Page 27; 63pp; English.

XX The present invention provides the sequences of a number of peptides found in ewe's colostrin. Colostrin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques.

XX Sequence 9 AA;

Query Match 100.0%; Score 7; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLYQE 7

Db 3 AFLLYQE 9

RESULT 10

AAU83297

ID AAU83297 standard; Peptide; 11 AA.

XX AC AAU83297;

DT 23-APR-2002 (first entry)

DE Antiviral composition peptide-A, fragment #15.

XX Virucide; Immunostimulant; interleukin-8; viral infection;

KW monocyte chemotactic protein 1; immune system.

XX Synthetic.

XX US2002004579-A1.

XX 10-JAN-2002.

XX 17-JAN-2001; 2001US-0764017.

XX peptide sequence. The composition comprises nucleotide-peptide comprising
PR a peptide linked through a serine residue and diphosphodiester to a
PR nucleotide; or peptides with about 31 amino acid residues capable of
PR stimulating production of interleukin-8 in cultured cells; or peptides
PR with about 31 amino acid residues capable of stimulating production of
PR monocyte chemotactic protein 1 in cultured cells. The peptides are useful
PR for treating viral infections and stimulating the immune system.
PA (ADVI-) ADVANCED VIRAL RES CORP.
PI Friedland B, Hirschman SZ, Taraporewala IB;
XX WPI; 2002-163727/21.
XX
XX
XX New peptides compositions, useful for treating viral infections and
PT stimulating the immune system -
XX
XX Disclosure; Page 7; 37pp; English.
XX
XX The invention relates to a new peptide composition comprising a specified
CC peptide sequence. The composition comprises nucleotide-peptide comprising
CC a peptide linked through a serine residue and diphosphodiester to a
CC nucleotide; or peptides with about 31 amino acid residues capable of
CC stimulating production of interleukin-8 in cultured cells; or peptides
CC with about 31 amino acid residues capable of stimulating production of
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC for treating viral infections and stimulating the immune system.
CC AAU83282-AAU83401 represent peptides used in the composition of the
CC invention.
XX
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 7; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.29; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AFLLYQE 7
Db 5 AFLLYQE 11
RESULT 11
AAU83299
ID AAU83299 standard; Peptide; 12 AA.
XX
AC AAU83299;
XX
XX 23-APR-2002 (first entry)
DT
DE Antiviral composition peptide-A, fragment #17.
XX
XX Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX
OS Synthetic.
XX
XX US2002004579-A1.
PN
XX 10-JAN-2002.
PD
XX 17-JAN-2001; 2001US-0764017.
PF
XX 22-OCT-1996; 96US-0735236.
PR
XX 25-JUN-1999; 99US-0344095.
PR
XX (ADVI-) ADVANCED VIRAL RES CORP.
PA
XX Friedland B, Hirschman SZ, Taraporewala IB;
PI WPI; 2002-163727/21.
XX
XX
XX New peptides compositions, useful for treating viral infections and
PT stimulating the immune system -
XX
XX Disclosure; Page 7; 37pp; English.
XX
XX The invention relates to a new peptide composition comprising a specified

CC peptide sequence. The composition comprises nucleotide-peptide comprising
CC a peptide linked through a serine residue and diphosphodiester to a
CC nucleotide; or peptides with about 31 amino acid residues capable of
CC stimulating production of interleukin-8 in cultured cells; or peptides
CC with about 31 amino acid residues capable of stimulating production of
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC for treating viral infections and stimulating the immune system.
CC AAU83282-AAU83401 represent peptides used in the composition of the
CC invention.
XX
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 7; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.31; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AFLLYQE 7
Db 4 AFLLYQE 10
RESULT 12
AAU83300
ID AAU83300 standard; Peptide; 12 AA.
XX
AC AAU83300;
XX
XX 23-APR-2002 (first entry)
DT
DE Antiviral composition peptide-A, fragment #18.
XX
XX Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX
OS Synthetic.
XX
XX US2002004579-A1.
PN
XX 10-JAN-2002.
PD
XX 17-JAN-2001; 2001US-0764017.
PF
XX 22-OCT-1996; 96US-0735236.
PR
XX 25-JUN-1999; 99US-0344095.
PR
XX (ADVI-) ADVANCED VIRAL RES CORP.
PA
XX Friedland B, Hirschman SZ, Taraporewala IB;
PI WPI; 2002-163727/21.
XX
XX
XX New peptides compositions, useful for treating viral infections and
PT stimulating the immune system -
XX
XX Disclosure; Page 7; 37pp; English.
XX
XX The invention relates to a new peptide composition comprising a specified
CC peptide sequence. The composition comprises nucleotide-peptide comprising
CC a peptide linked through a serine residue and diphosphodiester to a
CC nucleotide; or peptides with about 31 amino acid residues capable of
CC stimulating production of interleukin-8 in cultured cells; or peptides
CC with about 31 amino acid residues capable of stimulating production of
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC for treating viral infections and stimulating the immune system.
CC AAU83282-AAU83401 represent peptides used in the composition of the
CC invention.
XX
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 7; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.31; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AFLLYQE 7
Db 4 AFLLYQE 10
RESULT 12
AAU83300
ID AAU83300 standard; Peptide; 12 AA.
XX
AC AAU83300;
XX
XX 23-APR-2002 (first entry)
DT
DE Antiviral composition peptide-A, fragment #18.
XX
XX Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX
OS Synthetic.
XX
XX US2002004579-A1.
PN
XX 10-JAN-2002.
PD
XX 17-JAN-2001; 2001US-0764017.
PF
XX 22-OCT-1996; 96US-0735236.
PR
XX 25-JUN-1999; 99US-0344095.
PR
XX (ADVI-) ADVANCED VIRAL RES CORP.
PA
XX Friedland B, Hirschman SZ, Taraporewala IB;
PI WPI; 2002-163727/21.
XX
XX
XX New peptides compositions, useful for treating viral infections and
PT stimulating the immune system -
XX
XX Disclosure; Page 7; 37pp; English.
XX
XX The invention relates to a new peptide composition comprising a specified

QY 1 AFLLYQE 7
 Db 6 AFLLYQE 12

RESULT 13
 AAU83302
 ID AAU83302 standard; Peptide; 13 AA.
 XX
 AC AAU83302;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #20.
 XX
 KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX
 OS Synthetic.
 XX
 PN US2002004579-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX
 PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX
 DR WPI; 2002-163727/21.
 XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 PS Disclosure; Page 7; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 XX Sequence 13 AA;
 XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 PS Disclosure; Page 7; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 XX Sequence 13 AA;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #23.
 XX
 KW Virucide; Immunostimulant; interleukin-8; viral infection;

KW monocyte chemotactic protein 1; immune system.
 XX
 OS Synthetic.
 XX
 PN US2002004579-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX
 PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX
 DR WPI; 2002-163727/21.
 XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 PS Disclosure; Page 7; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 XX Sequence 13 AA;
 XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 PS Disclosure; Page 7; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 XX Sequence 13 AA;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #27.
 XX
 KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX
 OS Synthetic.
 XX
 PN US2002004579-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX
 PI Friedland B, Hirschman SZ, Taraporewala IB;

XX WPI; 2002-163727/21.
XX
XX New peptides compositions, useful for treating viral infections and
PT stimulating the immune system -
XX
XX Disclosure; Page 7; 37pp; English.
XX
XX The invention relates to a new peptide composition comprising a specified
CC peptide sequence. The composition comprises nucleotide-peptide comprising
CC a peptide linked through a serine residue and diphosphodiester to a
CC nucleotide; or peptides with about 31 amino acid residues capable of
CC stimulating production of interleukin-8 in cultured cells; or peptides
CC with about 31 amino acid residues capable of stimulating production of
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC for treating viral infections and stimulating the immune system.
CC AAU83282-AAU83401 represent peptides used in the composition of the
CC invention.
XX
XX Sequence 13 AA;
SQ
Query Match 100.0%; Score 7; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AFLLYQE 7
Db 6 AFLLYQE 12
|||||
RESULT 16
AAU83316
ID AAU83316 standard; Peptide; 14 AA.
XX
XX AC AAU83316;
XX
XX DT 23-APR-2002 (first entry)
XX
XX Antiviral composition peptide-A, fragment #34.
XX Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
KW
XX Synthetic.
OS
XX US2002004579-A1.
XX
XX PN 10-JAN-2002.
XX
XX PD 17-JAN-2001; 2001US-0764017.
XX
XX PF 22-OCT-1996; 96US-0735236.
XX
XX PR 25-JUN-1999; 99US-0344095.
XX
XX PS (ADVI-) ADVANCED VIRAL RES CORP.
XX
XX PI Friedland B, Hirschman SZ, Taraporewala IB;
XX WPI; 2002-163727/21.
XX
XX New peptides compositions, useful for treating viral infections and
PT stimulating the immune system -
XX
XX Disclosure; Page 8; 37pp; English.
XX
XX The invention relates to a new peptide composition comprising a specified
CC peptide sequence. The composition comprises nucleotide-peptide comprising
CC a peptide linked through a serine residue and diphosphodiester to a
CC nucleotide; or peptides with about 31 amino acid residues capable of
CC stimulating production of interleukin-8 in cultured cells; or peptides
CC with about 31 amino acid residues capable of stimulating production of
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC for treating viral infections and stimulating the immune system.

CC AAU83282-AAU83401 represent peptides used in the composition of the
CC invention.
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 7; DB 23; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AFLLYQE 7
Db 6 AFLLYQE 12
|||||
RESULT 17
AAU83325
ID AAU83325 standard; Peptide; 14 AA.
XX
XX AC AAU83325;
XX
XX DT 23-APR-2002 (first entry)
XX
XX DE Antiviral composition peptide-A, fragment #43.
XX Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
KW
XX Synthetic.
OS
XX US2002004579-A1.
XX
XX PN 10-JAN-2002.
XX
XX PD 17-JAN-2001; 2001US-0764017.
XX
XX PF 22-OCT-1996; 96US-0735236.
XX
XX PR 25-JUN-1999; 99US-0344095.
XX
XX PS (ADVI-) ADVANCED VIRAL RES CORP.
XX
XX PI Friedland B, Hirschman SZ, Taraporewala IB;
XX WPI; 2002-163727/21.
XX
XX New peptides compositions, useful for treating viral infections and
PT stimulating the immune system -
XX
XX Disclosure; Page 8; 37pp; English.
XX
XX The invention relates to a new peptide composition comprising a specified
CC peptide sequence. The composition comprises nucleotide-peptide comprising
CC a peptide linked through a serine residue and diphosphodiester to a
CC nucleotide; or peptides with about 31 amino acid residues capable of
CC stimulating production of interleukin-8 in cultured cells; or peptides
CC with about 31 amino acid residues capable of stimulating production of
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC for treating viral infections and stimulating the immune system.
CC AAU83282-AAU83401 represent peptides used in the composition of the
CC invention.
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 7; DB 23; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AFLLYQE 7
Db 8 AFLLYQE 14
|||||
RESULT 18
AAU83327

```

ID  AAU83327 standard; Peptide; 15 AA.
XX
AC  AAU83327;
XX
DT  23-APR-2002 (first entry)
XX
DE  Antiviral composition peptide-A, fragment #45.
XX
KW  Virucide; Immunostimulant; interleukin-8; viral infection;
KW  monocyte chemotactic protein 1; immune system.
XX
OS  Synthetic.
XX
PN  US2002004579-A1.
XX
PD  10-JAN-2002.
XX
PF  17-JAN-2001; 2001US-0764017.
XX
PR  22-OCT-1996; 96US-0735236.
PR  25-JUN-1999; 99US-0344095.
XX
PA  (ADVI-) ADVANCED VIRAL RES CORP.
XX
PI  Friedland B, Hirschman SZ, Taraporewala IB;
XX
DR  WPI; 2002-163727/21.
XX
PT  New peptides compositions, useful for treating viral infections and
PT  stimulating the immune system -
PS  Disclosure; Page 8; 37pp; English.
XX
CC  The invention relates to a new peptide composition comprising a specified
CC  peptide sequence. The composition comprises nucleotide-peptide comprising
CC  a peptide linked through a serine residue and diphosphodiester to a
CC  nucleotide; or peptides with about 31 amino acid residues capable of
CC  stimulating production of interleukin-8 in cultured cells; or peptides
CC  with about 31 amino acid residues capable of stimulating production of
CC  monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC  for treating viral infections and stimulating the immune system.
CC  AAU83282-AAU83401 represent peptides used in the composition of the
CC  invention.
XX
SQ  Sequence 15 AA;
    Query Match 100.0%; Score 7; DB 23; Length 15;
    Best Local Similarity 100.0%; Pred. No. 0.37;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 AFLLYQE 7
Db  6 AFLLYQE 12
    |||||
    6 AFLLYQE 12

RESULT 19
AAU83335
ID  AAU83335 standard; Peptide; 16 AA.
XX
AC  AAU83335;
XX
DT  23-APR-2002 (first entry)
XX
DE  Antiviral composition peptide-A, fragment #53.
XX
KW  Virucide; Immunostimulant; interleukin-8; viral infection;
KW  monocyte chemotactic protein 1; immune system.
XX
OS  Synthetic.
XX
PN  US2002004579-A1.
XX
PD  10-JAN-2002.
XX
PF  17-JAN-2001; 2001US-0764017.
XX
PR  22-OCT-1996; 96US-0735236.
PR  25-JUN-1999; 99US-0344095.
XX
PA  (ADVI-) ADVANCED VIRAL RES CORP.
XX
PI  Friedland B, Hirschman SZ, Taraporewala IB;
XX
DR  WPI; 2002-163727/21.
XX
PT  New peptides compositions, useful for treating viral infections and
PT  stimulating the immune system -
PS  Disclosure; Page 8; 37pp; English.
XX
CC  The invention relates to a new peptide composition comprising a specified
CC  peptide sequence. The composition comprises nucleotide-peptide comprising
CC  a peptide linked through a serine residue and diphosphodiester to a
CC  nucleotide; or peptides with about 31 amino acid residues capable of
CC  stimulating production of interleukin-8 in cultured cells; or peptides
CC  with about 31 amino acid residues capable of stimulating production of
CC  monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC  for treating viral infections and stimulating the immune system.
CC  AAU83282-AAU83401 represent peptides used in the composition of the
CC  invention.
XX
SQ  Sequence 16 AA;
    Query Match 100.0%; Score 7; DB 23; Length 16;
    Best Local Similarity 100.0%; Pred. No. 0.39;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 AFLLYQE 7
Db  7 AFLLYQE 13
    |||||
    7 AFLLYQE 13

RESULT 20
AAU83336
ID  AAU83336 standard; Peptide; 16 AA.
XX
AC  AAU83336;
XX
DT  23-APR-2002 (first entry)
XX
DE  Antiviral composition peptide-A, fragment #54.
XX
KW  Virucide; Immunostimulant; interleukin-8; viral infection;
KW  monocyte chemotactic protein 1; immune system.
XX
OS  Synthetic.
XX
PN  US2002004579-A1.
XX
PD  10-JAN-2002.
XX
PF  17-JAN-2001; 2001US-0764017.
XX
PR  22-OCT-1996; 96US-0735236.
PR  25-JUN-1999; 99US-0344095.
XX
PA  (ADVI-) ADVANCED VIRAL RES CORP.
XX
PI  Friedland B, Hirschman SZ, Taraporewala IB;
XX
DR  WPI; 2002-163727/21.
XX
PT  New peptides compositions, useful for treating viral infections and
PT  stimulating the immune system -
PS  Disclosure; Page 8; 37pp; English.
XX
CC  The invention relates to a new peptide composition comprising a specified
CC  peptide sequence. The composition comprises nucleotide-peptide comprising
CC  a peptide linked through a serine residue and diphosphodiester to a
CC  nucleotide; or peptides with about 31 amino acid residues capable of
CC  stimulating production of interleukin-8 in cultured cells; or peptides
CC  with about 31 amino acid residues capable of stimulating production of
CC  monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC  for treating viral infections and stimulating the immune system.
CC  AAU83282-AAU83401 represent peptides used in the composition of the
CC  invention.
XX
SQ  Sequence 16 AA;
    Query Match 100.0%; Score 7; DB 23; Length 16;
    Best Local Similarity 100.0%; Pred. No. 0.39;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 AFLLYQE 7
Db  7 AFLLYQE 13
    |||||
    7 AFLLYQE 13
```

XX The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.

XX Sequence 16 AA;

Query Match 100.0%; Score 7; DB 23; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.39;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLYQE 7

Db 9 AFLLYQE 15

RESULT 21

AAU83341
 ID AAU83341 standard; Peptide; 19 AA.

XX AC AAU83341;

DT 23-APR-2002 (first entry)

XX Antiviral composition peptide-A, fragment #59.

XX Virucide; Immunostimulant; interleukin-8; viral infection;

XX monocyte chemotactic protein 1; immune system.

XX Synthetic.

XX US2002004579-A1.

XX 10-JAN-2002.

XX 17-JAN-2001; 2001US-0764017.

XX 22-OCT-1996; 96US-0735236.

XX 25-JUN-1999; 99US-0344095.

XX (ADVI-) ADVANCED VIRAL RES CORP.

XX Friedland B, Hirschman SZ, Taraporewala IB;

XX WPI; 2002-163727/21.

XX New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -

XX Disclosure; Page 8; 37pp; English.

XX The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.

XX Sequence 19 AA;

Query Match 100.0%; Score 7; DB 23; Length 19;

Best Local Similarity 100.0%; Pred. No. 0.44;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLYQE 7

Db 13 AFLLYQE 19

RESULT 22

AAU83290
 ID AAU83290 standard; Peptide; 9 AA.

XX AC AAU83290;

XX 23-APR-2002 (first entry)

XX Antiviral composition peptide-A, fragment #8.

XX Virucide; Immunostimulant; interleukin-8; viral infection;

XX monocyte chemotactic protein 1; immune system.

XX Synthetic.

XX US2002004579-A1.

XX 10-JAN-2002.

XX 17-JAN-2001; 2001US-0764017.

XX 22-OCT-1996; 96US-0735236.

XX 25-JUN-1999; 99US-0344095.

XX (ADVI-) ADVANCED VIRAL RES CORP.

XX Friedland B, Hirschman SZ, Taraporewala IB;

XX WPI; 2002-163727/21.

XX New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -

XX Disclosure; Page 7; 37pp; English.

XX The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.

XX Sequence 9 AA;

Query Match 85.7%; Score 6; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLYQ 6

Db 4 AFLLYQ 9

RESULT 23

AAB72277
 ID AAB72277 standard; peptide; 13 AA.

XX AC AAB72277;

XX 14-MAY-2001 (first entry)

XX Colostrin derived cytokine inducing peptide SEQ ID 32.

SQ Sequence 13 AA;
 Query Match 85.7%; Score 6; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FLLYQE 7
 |||||
 Db 1 FLLYQE 6

RESULT 26
 AAB59338
 ID AAB59338 standard; Peptide; 13 AA.
 XX AC AAB59338;
 XX DT 21-MAR-2001 (first entry)
 XX DE Ewe colostrin peptide fragment C-13.
 XX KW Sheep; colostrin; proline rich polypeptide; colostrum; immune disorder;
 XX KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX OS Ovis sp.
 XX WN WO200075173-A2.
 XX PD 14-DEC-2000.
 XX PF 02-JUN-2000; 2000WO-GB02128.
 XX PR 02-JUN-1999; 99GB-0012852.
 XX PA (REGE-) REGEN THERAPEUTICS PLC.
 XX PI Georgiades JA;
 XX DR WPI; 2001-071059/08.
 XX PT Peptides having an N-terminal amino acid sequence isolated from
 PT colostrin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX PS Claim 7; Page 27; 63pp; English.
 XX CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrin. Colostrin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.

SQ Sequence 13 AA;
 Query Match 85.7%; Score 6; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FLLYQE 7
 |||||
 Db 1 FLLYQE 6

RESULT 27
 AAE20259
 ID AAE20259 standard; peptide; 13 AA.
 XX AC AAE20259;
 XX DT 30-MAY-2002 (first entry)
 XX

DT 18-JUN-2002 (first entry)
 XX Colostrin constituent peptide #31.
 XX KW Blood cell regulator; colostrin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnary.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 FT Modified-site 13
 FT /note= "Optionally C-terminal amide"
 XX WO200213850-A1.
 XX PD 21-FEB-2002.
 XX PF 17-AUG-2000; 2000WO-US22776.
 XX PR 17-AUG-2000; 2000WO-US22776.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Stanton GJ, Hughes TK, Boldogh I;
 XX WPI; 2002-269151/31.
 XX CC Composition useful for the modulation of blood cell proliferation in a
 CC patient comprises a blood cell regulator selected from colostrin, its
 CC constituent peptide and/or analog -
 CC PS Claim 6; Page 26; 51pp; English.
 XX CC The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/
 CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrin constituent peptide.

SQ Sequence 13 AA;
 Query Match 85.7%; Score 6; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FLLYQE 7
 |||||
 Db 1 FLLYQE 6

RESULT 28
 AAM51065
 ID AAM51065 standard; Peptide; 13 AA.
 XX AC AAM51065;
 XX DT 30-MAY-2002 (first entry)
 XX

DE Colostrinin constituent peptide (casein amino acids 203-214).
 XX Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; beta-casein; human.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Modified-site 13
 FT /note= "optional C-terminal amidation"
 XX WO200213849-A1.
 XX 21-FEB-2002.
 PD
 XX 17-AUG-2000; 2000WO-US22775.
 XX
 PF 17-AUG-2000; 2000WO-US22775.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX WPI; 2002-269150/31.
 DR
 XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -
 XX
 PS Claim 1; Page 34; 54pp; English.
 XX
 CC The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified
 CC as having a beta-casein homologue precursor, and corresponds to
 CC casein amino acids 203-214. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ
 CC or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the
 CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide.
 XX
 SQ Sequence 13 AA;
 Query Match 85.7%; Score 6; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FLLYQE 7
 Db 1 FLLYQE 6
 RESULT 29
 ID AAO14608
 AC AAO14608 standard; peptide; 13 AA.
 XX
 AC AAO14608;
 XX
 PD 27-MAY-2002 (first entry)
 XX

XX Neural cell regulatory colostrinin peptide 31.
 DE
 XX Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.
 XX
 OS Unidentified.
 FH Key Location/Qualifiers
 FT Modified-site 13
 FT /note= "Optional C-terminal amide"
 XX WO200213851-A1.
 XX 21-FEB-2002.
 PD
 XX 17-AUG-2000; 2000WO-US22777.
 XX
 PF 17-AUG-2000; 2000WO-US22777.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Boldogh I, Stanton JG, Hughes TK;
 PI WPI; 2002-269152/31.
 DR
 XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -
 XX
 PS Claim 7; Page 22; 37pp; English.
 XX
 CC The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention.
 XX
 SQ Sequence 13 AA;
 Query Match 85.7%; Score 6; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FLLYQE 7
 Db 1 FLLYQE 6
 RESULT 30
 ID AAU83314
 AC AAU83314 standard; Peptide; 13 AA.
 XX
 AC AAU83314;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #32.
 KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX
 OS Synthetic.
 XX
 PN US2002004579-A1.
 XX
 PD 10-JAN-2002.
 XX

PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX
 PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX
 DR WPI; 2002-163727/21.
 XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 PS Disclosure; Page 8; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 SQ Sequence 13 AA;
 Query Match 85.7%; Score 6; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AFLLYQ 6
 Db 8 AFLLYQ 13
 |||||
 |||||
 RESULT 31
 AAU83320
 ID AAU83320 standard; Peptide; 14 AA.
 XX
 AC AAU83320;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #38.
 XX
 KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX
 OS Synthetic.
 XX
 PN US2002004579-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX
 PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX
 DR WPI; 2002-163727/21.
 XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 PS Disclosure; Page 8; 37pp; English.
 XX

CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 SQ Sequence 14 AA;
 Query Match 85.7%; Score 6; DB 23; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AFLLYQ 6
 Db 9 AFLLYQ 14
 |||||
 |||||
 RESULT 32
 AAU83332
 ID AAU83332 standard; Peptide; 15 AA.
 XX
 AC AAU83332;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Antiviral composition peptide-A, fragment #50.
 XX
 KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX
 OS Synthetic.
 XX
 PN US2002004579-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 17-JAN-2001; 2001US-0764017.
 XX
 PR 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX
 PA (ADVI-) ADVANCED VIRAL RES CORP.
 XX
 PI Friedland B, Hirschman SZ, Taraporewala IB;
 XX
 DR WPI; 2002-163727/21.
 XX
 PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX
 PS Disclosure; Page 8; 37pp; English.
 XX
 CC The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.
 XX
 SQ Sequence 15 AA;
 Query Match 85.7%; Score 6; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX

QY 1 AFLLYQ 6
 DB 10 AFLLYQ 15

RESULT 33
 AAU83339
 ID AAU83339 standard; Peptide; 16 AA.
 AC AAU83339;
 DT 23-APR-2002 (first entry)
 XX Antiviral composition peptide-A, fragment #57.
 XX Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.
 XX Synthetic.
 OS US2002004579-A1.
 PN 10-JAN-2002.
 PD 17-JAN-2001; 2001US-0764017.
 PF 22-OCT-1996; 96US-0735236.
 PR 25-JUN-1999; 99US-0344095.
 XX (ADVI-) ADVANCED VIRAL RES CORP.
 PA Friedland B, Hirschman SZ, Taraporewala IB;
 PI WPI; 2002-163727/21.
 XX New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -
 XX Disclosure; Page 8; 37pp; English.
 XX The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC invention.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 XX SQ Sequence 16 AA;
 Query Match 85.7%; Score 6; DB 23; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLYQ 6
 DB 11 AFLLYQ 16

RESULT 34
 AAY17233
 ID AAY17233 standard; peptide; 19 AA.
 XX AAY17233;
 AC 09-AUG-1999 (first entry)
 DT Casein antimicrobial peptide.
 XX

KW Antimicrobial peptide; casein; dental caries; periodontal disease;
 KW antiplaque agent.
 XX Bos sp.
 OS WO9926971-A1.
 PN 03-JUN-1999.
 PD 24-NOV-1998; 98WO-AU00972.
 XX 24-NOV-1997; 97AU-0000514.
 PR (UYME) UNIV MELBOURNE.
 XX (VICT-) VICTORIAN DAIRY IND AUTHORITY.
 PA Dashper SG, Malkoski M, O'Brien-Simpson NM, Reynolds EC;
 PI Talbo GH;
 PI WPI; 1999-357812/30.
 DR Antimicrobial peptides, useful for prevention and treatment of
 XX periodontal disease
 XX Claim 1; Page 43; 57pp; English.
 XX Sequences AAY17229-245 represent non-glycosylated antimicrobial peptides
 CC that are derived from casein. The peptides are useful in antimicrobial
 CC compositions for treating or preventing dental caries or periodontal
 CC disease. The new peptides are clinically efficacious, safe and natural
 CC antiplaque agents, unlike prior art agents which have undesirable side-
 CC effects, negligible intra-oral activity, or an incompatibility with
 CC toothpaste formulations.
 XX SQ Sequence 19 AA;
 Query Match 85.7%; Score 6; DB 20; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLYQ 6
 DB 6 AFLLYQ 11

RESULT 35
 AAO18910
 ID AAO18910 standard; Peptide; 6 AA.
 XX AAO18910;
 AC 02-DEC-2002 (first entry)
 DT Human butyrylcholinesterase variant peptide fragment #5.
 XX Human; butyrylcholinesterase; enzyme; mutant; cocaine hydrolysis;
 KW cocaine addiction; antiaddictive; antidote.
 XX Homo sapiens.
 OS WO200264796-A2.
 PN 22-AUG-2002.
 PD 21-DEC-2001; 2001WO-US0450.
 PF 26-DEC-2000; 2000US-0748739.
 PR 20-DEC-2001; 2001US-0032233.
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
 PA (UYNE-) UNIV NEBRASKA MEDICAL CENT.
 XX Lockridge O, Watkins JD, Pancook JD;

XX WPI; 2002-636633/68.
 XX New human butyrylcholinesterase variant polypeptides, useful for
 PT treating cocaine-induced conditions -
 XX
 XX Disclosure; Fig 8; 150pp; English.
 XX
 CC The present invention relates to mutants of human butyrylcholinesterase.
 CC The enzymes have an increased cocaine hydrolysis activity and can be used
 CC for treating a cocaine-induced condition. The present sequence is a
 CC protein shown in the exemplification of the invention.
 XX
 XX Sequence 6'AA;
 SQ

Query Match 71.4%; Score 5; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APLLY 5
 Db 2 APLLY 6
 |||||

RESULT 36
 AAE07190
 ID AAE07190 standard; peptide; 7 AA.
 XX
 AC AAE07190;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Colostrinin peptide 6.
 XX
 KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral; cyclic.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl; this residue forms a cyclic
 FT linkage with Val found at the C-terminal end"
 FT
 XX WO200155199-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 26-JAN-2001; 2001WO-GB00329.
 XX
 PR 26-JAN-2000; 2000GB-0001825.
 XX
 PA (REG-) REGEN THERAPEUTICS PLC.
 XX
 PI Georgiades JA;
 XX
 DR WPI; 2001-488775/53.
 XX
 XX Peptide useful as an inter alia in the treatment of e.g. disorders of
 PT the immune system and the central nervous system comprises ten
 PT amino-terminal amino acid sequence derived from peptides present in
 PT colostrinin -
 XX
 PS Claim 1; Page 15; 40pp; English.
 XX
 CC The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g., psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,

CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is colostrinin peptide 6 related to the invention.
 CC Colostrinin peptide 6 corresponds to position 204-210 of beta-caesin.
 XX
 XX Sequence 7 AA;
 SQ

Query Match 71.4%; Score 5; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LLYQE 7
 Db 1 LLYQE 5
 |||||

RESULT 37
 AAE07200
 ID AAE07200 standard; peptide; 8 AA.
 XX
 AC AAE07200;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Modified colostrinin cyclic peptide #6.
 XX
 KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl; this residue forms a cyclic
 FT linkage with Val found at the C-terminal end"
 FT
 XX WO200155199-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 26-JAN-2001; 2001WO-GB00329.
 XX
 PR 26-JAN-2000; 2000GB-0001825.
 XX
 PA (REG-) REGEN THERAPEUTICS PLC.
 XX
 PI Georgiades JA;
 XX
 DR WPI; 2001-488775/53.
 XX
 XX Peptide useful as an inter alia in the treatment of e.g. disorders of
 PT the immune system and the central nervous system comprises ten
 PT amino-terminal amino acid sequence derived from peptides present in
 PT colostrinin -
 XX
 PS Example 2; Page 9; 40pp; English.
 XX
 CC The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,

CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is modified colostrinin cyclic peptide #6 related to
 CC the invention.

SQ Sequence 8 AA;

Query Match 71.4%; Score 5; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

Qy 3 LLYQE 7
 |||||
 Db 2 LLYQE 6

RESULT 38
 AAU83337
 ID AAU83337 standard; Peptide; 16 AA.

AC AAU83337;

DT 23-APR-2002 (first entry)

DE Antiviral composition peptide-A, fragment #55.

KW Virucide; Immunostimulant; interleukin-8; viral infection;
 KW monocyte chemotactic protein 1; immune system.

OS Synthetic.

PN US2002004579-A1.

PD 10-JAN-2002.

PF 17-JAN-2001; 2001US-0764017.

PR 22-OCT-1996; 96US-0735236.

PR 25-JUN-1999; 99US-0344095.

PA (ADVI-) ADVANCED VIRAL RES CORP.

PI Friedland B, Hirschman SZ, Taraporewala IB;

DR WPI; 2002-163727/21.

PT New peptides compositions, useful for treating viral infections and
 PT stimulating the immune system -

PS Disclosure; Page 8; 37pp; English.

XX The invention relates to a new peptide composition comprising a specified
 CC peptide sequence. The composition comprises nucleotide-peptide comprising
 CC a peptide linked through a serine residue and diphosphodiester to a
 CC nucleotide; or peptides with about 31 amino acid residues capable of
 CC stimulating production of interleukin-8 in cultured cells; or peptides
 CC with about 31 amino acid residues capable of stimulating production of
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
 CC for treating viral infections and stimulating the immune system.
 CC AAU83282-AAU83401 represent peptides used in the composition of the
 CC invention.

SQ Sequence 16 AA;

Query Match 71.4%; Score 5; DB 23; Length 16;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLLY 5
 |||||
 Db 12 AFLLY 16

RESULT 39

AAV16494

ID AAV16494 standard; peptide; 5 AA.

XX AC AAV16494;

DT 06-AUG-1999 (first entry)

DE Linear thrombin receptor peptide analogue.

XX Peptide analogue; N-terminal domain; cancer; angiogenesis; metastasis;
 KW human G protein linked thrombin receptor; cyclic; antagonist; agonist;
 KW cardiovascular disease; inflammatory disease; gastrointestinal disease;
 KW osteoporosis; tissue injury; tissue repair; nerve regeneration;
 KW thrombin-mimetic study; platelet function; myocardial infarction;
 KW arterial plaque formation.

OS Synthetic.

PN US5516889-A.

PD 14-MAY-1996.

PF 17-MAR-1995; 95US-0405933.

PR 21-JUN-1993; 93US-0080643.

PR 17-MAR-1995; 95US-0405933.

PA (UYTE-) UNIV TECHNOLOGIES INT INC.

PI Hollenberg MD, Matsoukas JM, Moore GJ;

DR WPI; 1996-251084/25.

PT New cyclic peptide(s) derived from the protein G linked thrombin
 PT receptor - are agonists or antagonists for treating diseases
 PT involving this receptor, e.g. myocardial infarction

PS Example 1; Column 53; 36pp; English.

XX AAV1645-98 represent peptide analogues of the N-terminal domain of
 CC the human G protein linked thrombin receptor sequence. The peptides,
 CC which may be cyclic, have the formula X1-Psi-X2-X3-Omega-X4 in which
 CC Psi = any (non-)natural aromatic amino acid (aa); Omega = any
 CC (non-)natural basic aa or derivatives; X1 is absent or is a natural
 CC aa, 1-3C acyl or 1-5C alkyl; X2 = any natural aa; X3 is absent or is
 CC any natural aa; and X4 is absent or is any natural aa. The peptides
 CC are antagonists and agonists for treating disorders involving
 CC thrombin receptors, e.g. cardiovascular, inflammatory or
 CC gastrointestinal diseases; osteoporosis; tissue injury and repair
 CC (including nerve regeneration); and cancer (by inhibiting angiogenesis
 CC and metastasis). They may also be used diagnostically and in
 CC thrombin-mimetic studies. The peptide analogues are particularly used to
 CC modulate platelet function (acting synergistically with aspirin-type
 CC compounds) and so are useful in cases of myocardial infarction, as well
 CC as to coat prostheses and to reduce arterial plaque formation.

XX Sequence 5 AA;

Query Match 57.1%; Score 4; DB 17; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;

QY 1 AFL 4
 DB 1 AFL 4

RESULT 40

AAU08616
 ID AAU08616 standard; Peptide; 6 AA.

AC AAU08616;

DT 18-DEC-2001 (first entry)

XX Human olfactory receptor PCR primer design motif #1.

XX Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
 food additive; cosmetic; fragrance; pharmaceutical additive.

XX Homo sapiens.

XX WO200168805-A2.

XX 20-SEP-2001.

XX 13-MAR-2001; 2001WO-US07771.

XX 13-MAR-2000; 2000US-0188914.

XX 24-MAR-2000; 2000US-0192033.

XX 12-APR-2000; 2000US-0198474.

XX 24-APR-2000; 2000US-0199335.

XX 26-MAY-2000; 2000US-0207702.

XX 23-JUN-2000; 2000US-0213849.

XX 16-AUG-2000; 2000US-0226534.

XX 07-SEP-2000; 2000US-0230732.

XX 07-FEB-2001; 2001US-0266862.

XX (SENO-) SENOMYX INC.

XX Zozulya S;

XX WPI; 2001-570867/64.

XX Nucleic acids encoding human olfactory G protein-coupled receptors,
 useful for screening for compounds involved in olfactory sensation,
 where the compounds can be used in the food, pharmaceutical and
 cosmetic industries to customise odours -
 Disclosure; Page 42; 319pp; English.

XX The invention relates to nucleic acids encoding human olfactory
 receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
 specifically recognise molecules, odourants, that elicit specific
 olfactory sensation. The human olfactory receptors and polynucleotides
 encoding them are useful for screening a library of chemical compounds
 for compounds that are involved in olfactory sensation. Modulators of
 their activity are useful for pharmacological and genetic modulation of
 olfactory signalling pathways. Therefore, they can be used in the food,
 pharmaceutical and cosmetic industries to customise odours and
 fragrances. The present sequence is a human olfactory receptor
 protein motif end used to design PCR primers against the first
 transmembrane domain.

XX Sequence 6 AA;
 Query Match 57.1%; Score 4; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLY 5
 DB 2 FLY 5

RESULT 41

AAG63026
 ID AAG63026 standard; peptide; 6 AA.

XX AC AAG63026;

XX 01-OCT-2001 (first entry)

XX Amino acid sequence of a Hepatitis A virus (HAV)-binding domain.

XX Hepatitis A virus; HAV; Quick Assay for Selecting Affinity Resins;

XX virus binding domain.

XX Unidentified.

XX WO200140265-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000WO-US42515.

XX 02-DEC-1999; 99US-0453115.

XX (VITE-) VI TECHNOLOGIES INC.

XX Hammond DJ;

XX WPI; 2001-475677/51.

XX Identifying ligands that interact with a target by Quick Assay for
 Selecting Affinity Resins, involves differentiating specific or
 non-specific false positive interactions from target-specific
 interactions -

XX Claim 4; Page 27; 39pp; English.

XX The present sequence represents a Hepatitis A virus (HAV)-binding
 domain. It was identified using the method of the invention. The method
 identifies ligands that interact with a target by Quick Assay for
 Selecting Affinity Resins. The method comprise differentiating false
 positive interactions (either specific or non-specific) from
 target-specific interaction, by distinguishing non-specific binding of
 ligands to agents in the screening solution from specific binding
 between a ligand and target. The method is useful for identifying
 CC ligands that interact with the target, and for multiple screenings of
 the same surface-immobilized library for a number of different ligands.

XX Sequence 6 AA;

XX Query Match 57.1%; Score 4; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLY 5
 DB 1 FLY 4

RESULT 42

AAG63034
 ID AAG63034 standard; peptide; 6 AA.

XX AC AAG63034;

XX 01-OCT-2001 (first entry)

XX Amino acid sequence of a Hepatitis A virus (HAV)-binding domain.

XX Hepatitis A virus; HAV; Quick Assay for Selecting Affinity Resins;

XX virus binding domain.

XX Unidentified.

CC positive interactions (either specific or non-specific) from
CC target-specific interaction, by distinguishing non-specific binding of
CC ligands to agents in the screening solution from specific binding
CC between a ligand and target. The method is useful for identifying
CC ligands that interact with the target, and for multiple screenings of
CC the same surface-immobilized library for a number of different ligands.
XX
XX SQ Sequence 6 AA;

Query Match 57.1%; Score 4; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLY 5
DB 1 FLLY 4
|||||

RESULT 45
AAG63106
ID AAG63106 standard; peptide; 6 AA.
XX AC AAG63106;
XX DT 01-OCT-2001 (first entry)
XX DE Amino acid sequence of a Poliovirus-binding domain.
XX KW Poliovirus; Quick Assay for Selecting Affinity Resins;
XX KW virus binding domain.
XX OS Unidentified.
XX PN WO200140265-A2.
XX PD 07-JUN-2001.
XX PF 01-DEC-2000; 2000WO-US42515.
XX PR 02-DEC-1999; 99US-0453115.
XX PA (VITE-) VI TECHNOLOGIES INC.
XX PI Hammond DJ;
XX WPI; 2001-475677/51.
XX PT Identifying ligands that interact with a target by Quick Assay for
XX PT Selecting Affinity Resins, involves differentiating specific or
XX PT non-specific false positive interactions from target-specific
XX PT interactions -
XX PS Claim 30; Page 30; 39pp; English.
XX CC The present sequence represents a Poliovirus-binding domain. It was
XX CC identified using the method of the invention. The method identifies
XX CC ligands that interact with a target by Quick Assay for Selecting Affinity
XX CC Resins. The method comprise differentiating false positive interactions
XX CC (either specific or non-specific) from target-specific interaction, by
XX CC distinguishing non-specific binding of ligands to agents in the
XX CC screening solution from specific binding between a ligand and target.
XX CC The method is useful for identifying ligands that interact with the
XX CC target, and for multiple screenings of the same surface-immobilized
XX CC library for a number of different ligands.
XX SQ Sequence 6 AA;

Query Match 57.1%; Score 4; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLY 5
DB 1 FLLY 4
|||||

RESULT 46
AAG63108
ID AAG63108 standard; peptide; 6 AA.
XX AC AAG63108;
XX DT 01-OCT-2001 (first entry)
XX DE Amino acid sequence of a Poliovirus-binding domain.
XX KW Poliovirus; Quick Assay for Selecting Affinity Resins;
XX KW virus binding domain.
XX OS Unidentified.
XX PN WO200140265-A2.
XX PD 07-JUN-2001.
XX PF 01-DEC-2000; 2000WO-US42515.
XX PR 02-DEC-1999; 99US-0453115.
XX PA (VITE-) VI TECHNOLOGIES INC.
XX PI Hammond DJ;
XX WPI; 2001-475677/51.
XX PT Identifying ligands that interact with a target by Quick Assay for
XX PT Selecting Affinity Resins, involves differentiating specific or
XX PT non-specific false positive interactions from target-specific
XX PT interactions -
XX PS Claim 30; Page 30; 39pp; English.
XX CC The present sequence represents a Poliovirus-binding domain. It was
XX CC identified using the method of the invention. The method identifies
XX CC ligands that interact with a target by Quick Assay for Selecting Affinity
XX CC Resins. The method comprise differentiating false positive interactions
XX CC (either specific or non-specific) from target-specific interaction, by
XX CC distinguishing non-specific binding of ligands to agents in the
XX CC screening solution from specific binding between a ligand and target.
XX CC The method is useful for identifying ligands that interact with the
XX CC target, and for multiple screenings of the same surface-immobilized
XX CC library for a number of different ligands.
XX SQ Sequence 6 AA;

Query Match 57.1%; Score 4; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLY 5
DB 1 FLLY 4
|||||

RESULT 47
ABU67261
ID ABU67261 standard; Peptide; 6 AA.
XX AC ABU67261;
XX DT 28-MAY-2003 (first entry)
XX DE Olfactory receptor ligand binding region I peptide.
XX KW Olfactory receptor; odourant; ligand-binding region;
XX KW olfactory neuron; olfactory epithelium; 7 transmembrane receptor;

KW olfactory response.
 OS Mammalia.
 XX
 PN US6492143-B1.
 XX
 PD 10-DEC-2002.
 XX
 PF 17-DEC-1999; 99US-0465901.
 XX
 PR 17-DEC-1998; 98US-112605P.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Reed RR, Yau K, Krautwurst D;
 XX
 XX WPI; 2003-327314/31.
 XX
 PT Novel amplification primer sequence pair for amplifying nucleic acid
 PT encoding an olfactory receptor ligand-binding region -
 XX
 XX Disclosure; Column 14; 46pp; English.
 XX
 CC The invention relates to an amplification primer sequence pair for
 CC amplifying a nucleic acid encoding an olfactory receptor ligand-binding
 CC region, comprising a primers appearing as ACA04888 and ACA04889.
 CC Also included is a kit for amplifying olfactory receptor sequences
 CC comprising the primers. The primers are useful for generating a nucleic
 CC acid sequence that encodes a ligand-binding region of an olfactory
 CC receptor. The amplified nucleic acid is genomic DNA, mRNA or cDNA derived
 CC from olfactory neurons or the olfactory epithelium. The olfactory
 CC receptors are 7 transmembrane receptors, manipulation of which can
 CC modulate an animals olfactory response and can be used to generate novel
 CC odourants. The present sequence is a olfactory receptor peptide consensus
 CC sequence used design degenerate PCR primer used to amplify an olfactory
 CC receptor ligand-binding region.
 XX
 SQ Sequence 6 AA;
 Query Match 57.1%; Score 4; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FLLY 5
 DB ||||
 2 FLLY 5
 RESULT 48
 ABUS8261
 ID ABUS8261 standard; Peptide; 6 AA.
 XX
 AC ABUS8261;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Peptide binding to hepatitis A virus in the presence of fibrinogen #7.
 XX
 KW Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;
 KW surface-immobilised library; blood composition.
 XX
 OS Synthetic.
 XX
 PN US2002155106-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 01-DEC-2000; 2000US-0727963.
 XX
 PR 01-DEC-2000; 2000US-0727963.
 XX
 PT New peptide comprising a porcine parvovirus-binding, hepatitis A
 PT virus-binding or prion-binding domain, useful for screening a library

(HAMM/) HAMMOND D J.
 Hamond DJ;
 WPI; 2003-198483/19.
 New peptide comprising a porcine parvovirus-binding, hepatitis A
 virus-binding or prion-binding domain, useful for screening a library
 of surface-immobilized ligands that bind to target molecules -
 Claim 4; Page 31; 35pp; English.
 The invention relates to a peptide, having a sequence of less than 20
 amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis
 A virus (HAV)-binding, or prion-binding domain. Also included are
 a composition comprising the peptide, removing a target from a biological
 fluid, identifying a ligand for a target or targets and identifying a
 peptide that binds to a virus present in a blood composition. The peptide
 is useful for identifying a ligand for a target or targets (Hepatitis A
 virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine
 viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,
 prion protein and alpha-1-proteinase inhibitor, API) or identifying a
 peptide that binds to a virus present in a blood composition. It is used
 to screen a library of surface-immobilised ligands that bind to target
 molecules. The peptide allows for multiple screenings of the same
 surface-immobilised library for a number of different ligands.
 The present sequence is a peptide of the invention, targeting one
 of the above listed targets.
 Sequence 6 AA;
 Query Match 57.1%; Score 4; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FLLY 5
 DB ||||
 1 FLLY 4
 RESULT 49
 ABUS8271
 ID ABUS8271 standard; Peptide; 6 AA.
 XX
 AC ABUS8271;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Peptide binding to hepatitis A virus in the presence of fibrinogen #12.
 XX
 KW Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;
 KW surface-immobilised library; blood composition.
 XX
 OS Synthetic.
 XX
 PN US2002155106-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 01-DEC-2000; 2000US-0727963.
 XX
 PR 01-DEC-2000; 2000US-0727963.
 XX
 PA (HAMM/) HAMMOND D J.
 XX
 PI Hamond DJ;
 XX
 XX WPI; 2003-198483/19.
 XX
 PT New peptide comprising a porcine parvovirus-binding, hepatitis A
 PT virus-binding or prion-binding domain, useful for screening a library

PT of surface-immobilized ligands that bind to target molecules -

XX Claim 4; Page 31; 35pp; English.

XX The invention relates to a peptide, having a sequence of less than 20

CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis

CC A virus (HAV)-binding, or prion-binding domain. Also included are

CC a composition comprising the peptide, removing a target from a biological

CC fluid, identifying a ligand for a target or targets and identifying a

CC peptide that binds to a virus present in a blood composition. The peptide

CC is useful for identifying a ligand for a target or targets (Hepatitis A

CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine

CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,

CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a

CC peptide that binds to a virus present in a blood composition. It is used

CC to screen a library of surface-immobilised ligands that bind to target

CC molecules. The peptide allows for multiple screenings of the same

CC surface-immobilised library for a number of different ligands.

CC The present sequence is a peptide of the invention, targeting one

CC of the above listed targets.

XX

SQ Sequence 6 AA;

Query Match 57.1%; Score 4; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLYY 5

DB 1 FLYY 4

RESULT 50

ABUS8273

ID ABUS8273 standard; Peptide; 6 AA.

AC ABUS8273;

XX

DT 14-APR-2003 (first entry)

XX

DE Peptide binding to hepatitis A virus in the presence of fibrinogen #14.

XX

XX Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;

KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;

KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;

KW surface-immobilised library; blood composition.

XX Synthetic.

OS

XX US2002155106-A1.

PN

XX 24-OCT-2002.

PD

XX 01-DEC-2000; 2000US-0727963.

PF

XX 01-DEC-2000; 2000US-0727963.

PR

XX (HAMM/) HAMMOND D J.

PA

XX Hammond DJ;

PI

XX WPI; 2003-198483/19.

DR

XX

XX New peptide comprising a porcine parvovirus-binding, hepatitis A

PT virus-binding or prion-binding domain, useful for screening a library

PT of surface-immobilized ligands that bind to target molecules -

XX

XX Claim 10; Page 31; 35pp; English.

PS

XX The invention relates to a peptide, having a sequence of less than 20

CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis

CC A virus (HAV)-binding, or prion-binding domain. Also included are

CC a composition comprising the peptide, removing a target from a biological

CC fluid, identifying a ligand for a target or targets and identifying a

CC peptide that binds to a virus present in a blood composition. The peptide

CC is useful for identifying a ligand for a target or targets (Hepatitis A

CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine

CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,

CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a

CC peptide that binds to a virus present in a blood composition. It is used

CC to screen a library of surface-immobilised ligands that bind to target

CC molecules. The peptide allows for multiple screenings of the same

CC surface-immobilised library for a number of different ligands.

CC The present sequence is a peptide of the invention, targeting one

CC of the above listed targets.

XX

SQ Sequence 6 AA;

Query Match 57.1%; Score 4; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLYY 5

DB 1 FLYY 4

RESULT 51

ABUS8291

ID ABUS8291 standard; Peptide; 6 AA.

AC ABUS8291;

XX

DT 14-APR-2003 (first entry)

XX

DE Poliovirus-binding peptide #6.

XX

XX Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;

KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;

KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;

KW surface-immobilised library; blood composition.

XX Synthetic.

XX US2002155106-A1.

XX 24-OCT-2002.

XX 01-DEC-2000; 2000US-0727963.

XX 01-DEC-2000; 2000US-0727963.

XX (HAMM/) HAMMOND D J.

XX Hammond DJ;

XX WPI; 2003-198483/19.

XX New peptide comprising a porcine parvovirus-binding, hepatitis A

PT virus-binding or prion-binding domain, useful for screening a library

PT of surface-immobilized ligands that bind to target molecules -

XX

XX Claim 30; Page 32; 35pp; English.

PS

XX The invention relates to a peptide, having a sequence of less than 20

CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis

CC A virus (HAV)-binding, or prion-binding domain. Also included are

CC a composition comprising the peptide, removing a target from a biological

CC fluid, identifying a ligand for a target or targets and identifying a

CC peptide that binds to a virus present in a blood composition. The peptide

CC is useful for identifying a ligand for a target or targets (Hepatitis A

CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine

CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,

CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a

CC peptide that binds to a virus present in a blood composition. It is used

CC to screen a library of surface-immobilised ligands that bind to target

CC molecules. The peptide allows for multiple screenings of the same
 CC surface-immobilised library for a number of different ligands.
 CC The present sequence is a peptide of the invention, targeting one
 CC of the above listed targets.

XX SQ Sequence 6 AA;

Query Match 57.1%; Score 4; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLY 5
 ||||
 Db 1 FLLY 4

RESULT 52
 ABUS8293
 ID ABUS8293 standard; Peptide; 6 AA.

XX AC ABUS8293;
 XX DT 14-APR-2003 (first entry)
 XX DE Poliovirus-binding peptide #8.
 XX DE Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;
 KW surface-immobilised library; blood composition.

XX OS Synthetic.
 XX US2002155106-A1.

XX PN 24-OCT-2002.

XX PF 01-DEC-2000; 2000US-0727963.

XX PR 01-DEC-2000; 2000US-0727963.

XX PA (HAMM/) HAMMOND D J.

XX PI Hammond DJ;

XX DR WPI; 2003-198483/19.

XX PT New peptide comprising a porcine parvovirus-binding, hepatitis A
 PT virus-binding or prion-binding domain, useful for screening a library
 PT of surface-immobilized ligands that bind to target molecules -

XX PS Claim 30; Page 32; 35pp; English.

XX CC The invention relates to a peptide, having a sequence of less than 20
 CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis
 CC A virus (HAV)-binding, or prion-binding domain. Also included are
 CC a composition comprising the peptide, removing a target from a biological
 CC fluid, identifying a ligand for a target or targets and identifying a
 CC peptide that binds to a virus present in a blood composition. The peptide
 CC is useful for identifying a ligand for a target or targets (Hepatitis A
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, EMCV, SV40,
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a
 CC peptide that binds to a virus present in a blood composition. It is used
 CC to screen a library of surface-immobilised ligands that bind to target
 CC molecules. The peptide allows for multiple screenings of the same
 CC surface-immobilised library for a number of different ligands.
 CC The present sequence is a peptide of the invention, targeting one
 CC of the above listed targets.

XX SQ Sequence 6 AA;

Query Match 57.1%; Score 4; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLY 5
 ||||
 Db 1 FLLY 4

RESULT 53
 ABUS8312
 ID ABUS8312 standard; Peptide; 6 AA.

XX AC ABUS8312;
 XX DT 14-APR-2003 (first entry)

XX DE Peptide binding to hepatitis A virus in the presence of fibrinogen #23.
 XX DE Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;
 KW surface-immobilised library; blood composition.

XX OS Synthetic.

XX US2002155106-A1.

XX PD 24-OCT-2002.

XX PF 01-DEC-2000; 2000US-0727963.

XX PR 01-DEC-2000; 2000US-0727963.

XX PA (HAMM/) HAMMOND D J.

XX PI Hammond DJ;

XX DR WPI; 2003-198483/19.

XX PT New peptide comprising a porcine parvovirus-binding, hepatitis A
 PT virus-binding or prion-binding domain, useful for screening a library
 PT of surface-immobilized ligands that bind to target molecules -

XX PS Claim 4; Page 31; 35pp; English.

XX CC The invention relates to a peptide, having a sequence of less than 20
 CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis
 CC A virus (HAV)-binding, or prion-binding domain. Also included are
 CC a composition comprising the peptide, removing a target from a biological
 CC fluid, identifying a ligand for a target or targets and identifying a
 CC peptide that binds to a virus present in a blood composition. The peptide
 CC is useful for identifying a ligand for a target or targets (Hepatitis A
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, EMCV, SV40,
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a
 CC peptide that binds to a virus present in a blood composition. It is used
 CC to screen a library of surface-immobilised ligands that bind to target
 CC molecules. The peptide allows for multiple screenings of the same
 CC surface-immobilised library for a number of different ligands.
 CC The present sequence is a peptide of the invention, targeting one
 CC of the above listed targets.

XX SQ Sequence 6 AA;

Query Match 57.1%; Score 4; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLY 5
 ||||
 Db 1 FLLY 4

```

RESULT 54
AAW04280
ID AAW04280 standard; peptide; 7 AA.
XX
AC AAW04280;
XX
DT 06-JUN-1997 (first entry)
XX
DE Milk derived non-anti-hypertensive peptide.
XX
XX Non-anti-hypertensive; fermentation; animal milk; Lactobacillus;
KW microorganism; digestion; protease; reduction; blood pressure.
XX
OS Mammalian spp.
XX
PN EF737690-A2.
XX
PD 16-OCT-1996.
XX
PF 10-APR-1996; 96EP-0302522.
XX
PR 10-APR-1995; 95JP-0084247.
XX
PA (CALV ) CALPIS FOOD IND CO LTD.
XX
PI Maeno M;
XX
XX WPI; 1996-457284/46.
XX
DR Antihypertensive compans. derived from milk - by fermentation or
PT protease digestion
XX
XX Example 1; Page 6; 10pp; English.
XX
CC The present non-anti-hypertensive (NAH) peptide was prepared by
CC fermenting an animal milk starting material with a Lactobacillus
CC microorganism, especially L. helveticus, L. delbrueckii subspecies
CC bulgaricus or L. acidophilus, or digesting it with a protease at
CC 20-50 degrees C for 3-30 hours, obtaining an eluent by
CC ultrafiltration and then fractionating the eluent by reverse phase
CC HPLC. The change in the systolic blood pressure of spontaneously
CC hypertensive rats treated intragastrically with 1 mg/kg of body
CC weight of the present NAH peptide was plus 1.2 +/- 9.8 mmHg.
XX
SQ Sequence 7 AA;
Query Match 57.1%; Score 4; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
Db 1 LLYQ 4

RESULT 55
AAV38067
ID AAV38067 standard; Peptide; 9 AA.
XX
AC AAV38067;
XX
DT 29-SEP-1999 (first entry)
XX
DE Hepatitis B virus-derived HLA-binding peptide.
XX
XX Immunogen; HLA; human leukocyte antigen; binding motif; antiviral;
KW MHC; major histocompatibility complex; viral infection; anticancer;
KW prostate cancer; lymphoma; hepatitis; AIDS; diagnostic; diagnosis.
XX
OS Hepatitis B virus.
XX
PN WO9403205-A1.
XX

PD 17-FEB-1994.
XX
PF 06-AUG-1993; 93WO-US07421.
XX
PR 05-MAR-1993; 93US-0027746.
PR 07-AUG-1992; 92US-0926666.
XX
PA (CYTE-) CYTEL CORP.
XX
XX Cellis E, Grey HM, Kubo RT, Sette A;
XX WPI; 1994-065403/08.
XX
PT Peptide which specifically binds selected MHC allele - used to
PT induce an immune response for treatment or prevention of viral
PT infection or cancer, or for diagnosis
XX
XX Disclosure; Page 106; 150pp; English.
XX
CC The sequence is a specific example of a group of new immunogenic
CC peptides having an HLA-A3.2, HLA-A1, HLA-A11 or HLA-A24.1 binding
CC motif. For example, the peptides having an HLA-A3.2 binding motif
CC each have 9-10 residues and contain, from the N-terminus to the
CC C-terminus, (a) a first conserved residue selected from L, M, I,
CC V, S, A, T, F, C, G, D and E and (b) a second conserved residue of
CC K, R, Y, H or F, where the first and second conserved residues are
CC separated by 6-7 residues. The peptides are capable of binding
CC selected MHC molecules and inducing an immune response. They can be
CC used to treat and/or prevent viral infection and cancer, e.g. prostate
CC cancer, lymphoma, hepatitis or AIDS. They can also be used to produce
CC antibodies for use as diagnostic or therapeutic agents. The peptides
CC can also be used as diagnostic agents.
XX
SQ Sequence 9 AA;
Query Match 57.1%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
Db 1 LLYQ 4

RESULT 56
AAV45635
ID AAV45635 standard; Peptide; 9 AA.
XX
AC AAV45635;
XX
DT 01-DEC-1999 (first entry)
XX
DE Immunogenic peptide having a human leukocyte antigen binding motif #246.
XX
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9945954-A1.
XX
XX 16-SEP-1999.
XX
PF 13-MAR-1998; 98WO-US05039.
XX
PR 13-MAR-1998; 98WO-US05039.
XX
PA (EPIM-) EPIMMUNE INC.
XX

```

```

PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX
XX New immunogenic peptides with HLA binding motif, useful in treatment
XX and diagnosis of cancers and viral diseases -
PT
PT
PT
PS Claim 1; Page 38; 150pp; English.
XX
XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX having a human major histocompatibility complex (MHC) Class I (also
XX known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX response against the antigen from which the peptide is derived.
XX Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX normally induced by an antigen in the form of a peptide fragment bound
XX to a HLA molecule, rather than the intact foreign antigen itself, and
XX are particularly important in tumour rejection and in fighting viral
XX infections. The peptides are therefore useful therapeutically to treat
XX or prevent viral infections and cancers in mammals (especially humans)
XX e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX They can be administered as vaccines to elicit an immune response in
XX individuals susceptible or otherwise at risk of viral infection or
XX cancer, or used to treat chronic or acute conditions. They are also
XX useful diagnostically, and can be used to induce a cytotoxic T cell
XX response, by contacting a cytotoxic T cell with the peptide e.g. to
XX produce CTLs ex vivo for infusion back into a patient. The
XX polynucleotides encoding the immunogenic peptides are also useful
XX therapeutically and for immunisation as above.
XX
SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
Db 1 LLYQ 4

RESULT 57
AAY46637
ID AAY46637 standard; Peptide; 9 AA.
XX
XX AAY46637;
AC
XX
XX 01-DEC-1999 (first entry)
DT
XX
XX Immunogenic peptide having a human leukocyte antigen binding motif #1248.
DE
XX
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX immune response; T cell activation; major histocompatibility complex;
XX cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX vaccine; immunisation.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX WO945954-A1.
PN
XX
XX 16-SEP-1999.
PD
XX
XX 13-MAR-1998; 98WO-US05039.
PF
XX
XX 13-MAR-1998; 98WO-US05039.
PR
XX
XX (EPIM-) EPIMMUNE INC.
PA
XX
XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
PI
XX WPI; 1999-551214/46.
XX

```

```

DR WPI; 1999-551214/46.
XX
XX New immunogenic peptides with HLA binding motif, useful in treatment
XX and diagnosis of cancers and viral diseases -
PT
PT
PS Claim 1; Page 79; 150pp; English.
XX
XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX having a human major histocompatibility complex (MHC) Class I (also
XX known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX response against the antigen from which the peptide is derived.
XX Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX normally induced by an antigen in the form of a peptide fragment bound
XX to a HLA molecule, rather than the intact foreign antigen itself, and
XX are particularly important in tumour rejection and in fighting viral
XX infections. The peptides are therefore useful therapeutically to treat
XX or prevent viral infections and cancers in mammals (especially humans)
XX e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX They can be administered as vaccines to elicit an immune response in
XX individuals susceptible or otherwise at risk of viral infection or
XX cancer, or used to treat chronic or acute conditions. They are also
XX useful diagnostically, and can be used to induce a cytotoxic T cell
XX response, by contacting a cytotoxic T cell with the peptide e.g. to
XX produce CTLs ex vivo for infusion back into a patient. The
XX polynucleotides encoding the immunogenic peptides are also useful
XX therapeutically and for immunisation as above.
XX
SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLY 5
Db 6 FLLY 9

RESULT 58
AAY46638
ID AAY46638 standard; Peptide; 9 AA.
XX
XX AAY46638;
AC
XX
XX 01-DEC-1999 (first entry)
DT
XX
XX Immunogenic peptide having a human leukocyte antigen binding motif #1249.
DE
XX
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX immune response; T cell activation; major histocompatibility complex;
XX cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX vaccine; immunisation.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX WO945954-A1.
PN
XX
XX 16-SEP-1999.
PD
XX
XX 13-MAR-1998; 98WO-US05039.
PF
XX
XX 13-MAR-1998; 98WO-US05039.
PR
XX
XX (EPIM-) EPIMMUNE INC.
PA
XX
XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
PI
XX WPI; 1999-551214/46.
XX

```

PT New immunogenic peptides with HLA binding motif, useful in treatment
 PT and diagnosis of cancers and viral diseases -
 XX
 PS Claim 1; Page 79; 150pp; English.
 XX
 CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
 CC response against the antigen from which the peptide is derived.
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
 CC normally induced by an antigen in the form of a peptide fragment bound
 CC to a HLA molecule, rather than the intact foreign antigen itself, and
 CC are particularly important in tumour rejection and in fighting viral
 CC infections. The peptides are therefore useful therapeutically to treat
 CC or prevent viral infections and cancers in mammals (especially humans)
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
 CC They can be administered as vaccines to elicit an immune response in
 CC individuals susceptible or otherwise at risk of viral infection or
 CC cancer, or used to treat chronic or acute conditions. They are also
 CC useful diagnostically, and can be used to induce a cytotoxic T cell
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to
 CC produce CTLs ex vivo for infusion back into a patient. The
 CC polynucleotides encoding the immunogenic peptides are also useful
 CC therapeutically and for immunisation as above.
 XX
 SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLYY 5
 ||||
 Db 6 FLYY 9

RESULT 59
 AAB09810
 ID AAB09810 standard; Peptide; 9 AA.
 AC AAB09810;
 XX
 XX 06-SEP-2000 (first entry)
 XX
 XX Antiviral antibody scFv 3a-2 epitope SEQ ID NO:146.
 XX
 XX Molecular pathogenicity; plant disease; resistance; antibody; scFv;
 KW gene construct; pathogen; toxin; fusion protein; antimicrobial;
 KW deoxyribonuclease; RNase; ribosome inactivator; immunomodulator.
 XX
 XX Tobacco mosaic virus.
 OS
 OS Synthetic.
 XX
 XX WO200023593-A2.
 XX
 XX 27-APR-2000.
 XX
 XX 15-OCT-1999; 99WO-EP07844.
 XX
 XX 16-OCT-1998; 98EP-0119630.
 PR 16-OCT-1998; 98IN-0000666.
 XX
 XX (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
 XX
 XX Fischer R, Schillberg S, Naehring J, Sack M, Monecke M, Liao Y;
 PI Spiegel H, Zimmerman S, Emans N, Holzner A;
 XX
 XX WFI; 2000-339692/29.
 DR
 XX New fusion proteins and gene constructs for expressing agents
 PT (antibodies, enzymes, vectors or molecular pathogenicities), useful for

PT protecting plants against pathogens and increasing resistance to
 PT disease -
 XX
 PS Example 6; Fig 25; 193pp; English.
 XX
 CC The present invention describes a fusion protein (I) comprising at least
 CC one binding domain specifically recognising an epitope of a plant
 CC pathogen and at least one further domain comprising a protein or peptide
 CC sequence which is toxic to the pathogen or detrimental to its
 CC replication, transmission or life cycle. Also described is a
 CC pathogenicide (II) comprising (I) and a cellular targeting sequence
 CC and/or membrane localisation sequence and/or motif that leads to
 CC membrane anchoring; or at least one binding domain that specifically
 CC recognises a viral movement and/or replicase protein. The fusion
 CC protein, pathogenicide, polynucleotide, vectors, and compositions from
 CC the present invention are useful for the protection of a plant against
 CC the action of a pathogen. The kit from the present invention is useful
 CC for carrying out the methods and may be employed in different
 CC applications, for example in the diagnostic field or as research tools.
 CC The kit or its components, such as the fusion protein, pathogenicide,
 CC polynucleotides, vectors or compositions are useful in plant cell and
 CC plant tissue culture, in agriculture. They are extremely useful for
 CC breeding new varieties of plants that display improved properties such as
 CC resistance to pathogens. AAY56587 to AAY56702 and AAB09774 to B097820
 CC represent sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQE 7
 ||||
 Db 6 LYQE 9

RESULT 60
 AAY96340
 ID AAY96340 standard; peptide; 9 AA.
 AC AAY96340;
 XX
 XX 29-AUG-2000 (first entry)
 XX
 XX HLA-A*0201 binding peptide hTERT W1072.
 XX
 XX hTERT; telomerase complex; reverse transcriptase; MHC; HLA; CTL; cancer;
 KW human leukocyte antigen; tumour-associated antigen; cytostatic; vaccine;
 KW major histocompatibility complex; cytotoxic T lymphocyte; immunotherapy.
 XX
 XX Homo sapiens.
 OS
 XX WO200025813-A1.
 PN
 XX 11-MAY-2000.
 XX
 XX 29-OCT-1999; 99WO-US25438.
 XX
 XX 29-OCT-1998; 98US-0106106.
 PR
 XX (DAND) DANA FARBER CANCER INST INC.
 XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA
 XX Nadler LM, Hahn WC, Schultze JL, Vonderheide RH;
 XX
 XX WFI; 2000-365402/31.
 DR
 XX Universal tumor-associated antigens such as telomerase catalytic
 PT subunit capable of binding major histocompatibility complex molecule
 PT useful for diagnosis, prevention and treatment of cancer
 XX

PS Disclosure; Page 73; 136pp; English.

XX Human telomerase complex reverse transcriptase (hTERT) is expressed in more than 85 percent of human cancers. hTERT is useful as a universal tumour-associated antigen (TAA) that binds to a major histocompatibility complex molecule (MHC). hTERT peptides were analyzed for the ability to bind to HLA (human leukocyte antigen) class I molecules. Cytotoxic T lymphocytes (CTL) were then generated that kill a cell expressing hTERT or a hTERT-TAA, in a hTERT or TAA specific MHC-restricted fashion. CC Antigen presenting cells (APC) were also generated ex vivo for presentation of a TAA peptide or hTERT. The APC can be used to activate CTL to kill cells expressing the TAA. The TAA, hTERT peptides, APC and CTL are useful for cancer immunotherapy. Measuring the level of CTL in a sample is useful for assessing the level of immunity of a patient to a TAA or a peptide, where the sample is obtained before or after a cancer treatment is given to the patient. TAA peptides (e.g. hTERT) are also useful for diagnosis and prophylactic treatment of cancer.

XX Sequence 9 AA;

Query Match 57.1%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLL 4
Db |||||
6 APLL 9

RESULT 61
AAV86649
ID AAY86649 standard; Peptide; 9 AA.
AC AAY86649;
XX
XX 05-MAY-2000 (first entry)
DT
XX
DE Telomerase peptide #64.
XX
KW Telomerase; antigenic peptide; cancer; therapy; human; tumour cell;
KW malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;
KW telomerase T lymphocyte.
XX
XX Homo sapiens.
XX
XX WO200002581-A1.
XX
XX 20-JAN-2000.
XX
XX 30-JUN-1999; 99WO-NO00220.
XX
XX 08-JUL-1998; 98NO-0003141.
XX
XX (NHVD) NORSK HYDRO AS.
XX
XX Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;
XX Saeboe-Larsen S;
XX WPI; 2000-145727/13.
XX
XX Protein or peptide fragments useful in the treatment and prophylaxis of cancer in mammals -
XX
XX Claim 12; Page 35; 53pp; English.

XX This sequence represents a telomerase peptide of the invention, and can be used in a method for the treatment or prophylaxis of cancer. The sequences are useful in the treatment or prophylaxis of cancer especially, breast, lung, ovarian, cervical, colorectal, prostate or pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary tract carcinomas. They are useful for generating telomerase T lymphocytes capable of recognising and destroying tumour cells in a mammal, the comprising T lymphocytes obtained from the mammal with the

CC peptides. Telomerase protein is expressed only by tumour cells, hence, CC other body cells are not targeted or destroyed by telomerase specific T cells.

CC Note: This sequence was indexed from WO200002581, which is the first CC major country equivalent to NO9803141.

XX Sequence 9 AA;

Query Match 57.1%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLL 4
Db |||||
6 APLL 9

RESULT 62
AAU23931
ID AAU23931 standard; Peptide; 9 AA.
XX
XX AC AAU23931;
XX
XX 17-DEC-2001 (first entry)
DT
XX
XX Human MHC class I molecule HLA-A2 binding 103P2D6 peptide #16.
XX
KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
KW single chain monoclonal antibody; cervix; human.
XX
XX Homo sapiens.
XX
XX WO200162925-A2.
XX
XX 30-AUG-2001.
XX
XX 26-FEB-2001; 2001WO-US05996.
XX
XX 24-FEB-2000; 2000US-0184558.
XX
XX 13-JUL-2000; 2000US-0218856.
XX
XX (UROG-) UROGENESYS INC.
XX
XX Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
XX Challita-eid PM, Faris M, Jakobovits A;
XX WPI; 2001-557705/62.
XX
XX New polynucleotide for treating and diagnosing prostate cancer is the 103P2D6 gene which encodes for 103P2D6-related proteins -
XX
XX Example 15; Page 83; 132pp; English.

XX Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and peptide fragments of the polypeptide. 103P2D6 is not expressed in normal adult tissue but is aberrantly expressed in some foetal tissues and many cancers including tumours of the prostate, testis, bladder, bone, cervix, ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its related protein and also peptide fragments of the protein are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 103P2D6-related protein, and a ribozyme capable of cleaving a polynucleotide having the 103P2D6 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 103P2D6. The sequences can be used in diagnostic methods to monitor the level of 103P2D6 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

XX Sequence 9 AA;

Query Match 57.1%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
DB 1 LLYQ 4

RESULT 63
AAU23957
ID AAU23957 standard; Peptide; 9 AA.
XX
XX AAU23957;
XX
DT 17-DEC-2001 (first entry)
XX
DE Human MHC class I molecule HLA-A2 binding 103P2D6 peptide #42.
XX
KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
KW single chain monoclonal antibody; cervix; human.
XX
OS Homo sapiens.
XX
XX WO200162925-A2.
XX
PD 30-AUG-2001.
XX
PF 26-FEB-2001; 2001WO-US05996.
XX
PR 24-FEB-2000; 2000US-0184558.
PR 13-JUL-2000; 2000US-0218856.
XX
XX (UROG-) UROGENESYS INC.
XX
XX Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
PI Challita-eid PM, Faris M, Jakobovits A;
XX
XX WPI; 2001-557705/62.
XX
PT New polynucleotide for treating and diagnosing prostate cancer is the
PT 103P2D6 gene which encodes for 103P2D6-related proteins -
XX
XX Example 15; Page 84; 132pp; English.
XX
CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
CC adult tissue but is aberrantly expressed in some foetal tissues and many
CC cancers including tumours of the prostate, testis, bladder, bone, cervix,
CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
CC related protein and also peptide fragments of the protein are therefore
CC useful for diagnosing and treating cancer. A vector comprising a
CC polynucleotide which encodes a single chain monoclonal antibody, that
CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme
CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
CC are both useful in the preparation of a composition for treating a
CC patient with a cancer that expresses 103P2D6. The sequences can be used
CC in diagnostic methods to monitor the level of 103P2D6 gene products in
CC serum, blood, urine and tissue and to thereby detect the presence of
CC cancerous cells.
SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
DB 2 LLYQ 5

RESULT 64
AAU24052
ID AAU24052 standard; Peptide; 9 AA.
XX
XX AAU24052;
XX
DT 17-DEC-2001 (first entry)
XX
DE Human MHC class I molecule HLA-A3 binding 103P2D6 peptide #37.
XX
KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
KW single chain monoclonal antibody; cervix; human.
XX
OS Homo sapiens.
XX
XX WO200162925-A2.
XX
PD 30-AUG-2001.
XX
PF 26-FEB-2001; 2001WO-US05996.
XX
PR 24-FEB-2000; 2000US-0184558.
PR 13-JUL-2000; 2000US-0218856.
XX
XX (UROG-) UROGENESYS INC.
XX
XX Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
PI Challita-eid PM, Faris M, Jakobovits A;
XX
XX WPI; 2001-557705/62.
XX
PT New polynucleotide for treating and diagnosing prostate cancer is the
PT 103P2D6 gene which encodes for 103P2D6-related proteins -
XX
XX Example 15; Page 87; 132pp; English.
XX
CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
CC adult tissue but is aberrantly expressed in some foetal tissues and many
CC cancers including tumours of the prostate, testis, bladder, bone, cervix,
CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
CC related protein and also peptide fragments of the protein are therefore
CC useful for diagnosing and treating cancer. A vector comprising a
CC polynucleotide which encodes a single chain monoclonal antibody, that
CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme
CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
CC are both useful in the preparation of a composition for treating a
CC patient with a cancer that expresses 103P2D6. The sequences can be used
CC in diagnostic methods to monitor the level of 103P2D6 gene products in
CC serum, blood, urine and tissue and to thereby detect the presence of
CC cancerous cells.
SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
DB 1 LLYQ 4

RESULT 65
AAU24158
ID AAU24158 standard; Peptide; 9 AA.
XX
XX AAU24158;
XX
DT 17-DEC-2001 (first entry)

XX DE Human MHC molecule HLA-A11 binding 103P2D6 peptide #43.
 XX KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
 KW single chain monoclonal antibody; cervix; human.
 XX OS Homo sapiens.
 XX PN WO200162925-A2.
 XX PD 30-AUG-2001.
 XX PF 26-FEB-2001; 2001WO-US05996.
 XX PR 24-FEB-2000; 2000US-0184558.
 XX PR 13-JUL-2000; 2000US-0218856.
 XX PA (UROC-) UROGENESYS INC.
 XX PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
 PI Challita-eid PM, Faris M, Jakobovits A;
 XX WPI; 2001-557705/62.
 XX PT New polynucleotide for treating and diagnosing prostate cancer is the
 PT 103P2D6 gene which encodes for 103P2D6-related proteins -
 XX Example 15; Page 90; 132pp; English.
 XX CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
 CC adult tissue but is aberrantly expressed in some foetal tissues and many
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
 CC related protein and also peptide fragments of the protein are therefore
 CC useful for diagnosing and treating cancer. A vector comprising a
 CC polynucleotide which encodes a single chain monoclonal antibody, that
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
 CC are both useful in the preparation of a composition for treating a
 CC patient with a cancer that expresses 103P2D6. The sequences can be used
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in
 CC serum, blood, urine and tissue and to thereby detect the presence of
 CC cancerous cells.
 XX SQ Sequence 9 AA;
 Query Match 57.1%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LLYQ 6
 ||||
 Db 3 LLYQ 6
 ||||
 RESULT 66
 AAU24257
 ID AAU24257 standard; Peptide; 9 AA.
 AC AAU24257;
 XX 17-DEC-2001 (first entry)
 XX Human MHC class I molecule HLA-A24 binding 103P2D6 peptide #42.
 XX KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
 KW single chain monoclonal antibody; cervix; human.
 XX OS Homo sapiens.
 XX PN WO200162925-A2.
 XX PD 30-AUG-2001.
 XX PF 26-FEB-2001; 2001WO-US05996.
 XX PR 24-FEB-2000; 2000US-0184558.
 XX PR 13-JUL-2000; 2000US-0218856.
 XX PA (UROC-) UROGENESYS INC.
 XX PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
 PI Challita-eid PM, Faris M, Jakobovits A;
 XX WPI; 2001-557705/62.
 XX PT New polynucleotide for treating and diagnosing prostate cancer is the
 PT 103P2D6 gene which encodes for 103P2D6-related proteins -
 XX Example 15; Page 90; 132pp; English.
 XX CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
 CC adult tissue but is aberrantly expressed in some foetal tissues and many
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
 CC related protein and also peptide fragments of the protein are therefore
 CC useful for diagnosing and treating cancer. A vector comprising a
 CC polynucleotide which encodes a single chain monoclonal antibody, that
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
 CC are both useful in the preparation of a composition for treating a
 CC patient with a cancer that expresses 103P2D6. The sequences can be used
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in
 CC serum, blood, urine and tissue and to thereby detect the presence of
 CC cancerous cells.
 XX SQ Sequence 9 AA;
 Query Match 57.1%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LLYQ 6
 ||||
 Db 3 LLYQ 6
 ||||
 RESULT 67
 AAU24261
 ID AAU24261 standard; Peptide; 9 AA.
 XX AAU24261;
 XX 17-DEC-2001 (first entry)
 XX Human MHC class I molecule HLA-A24 binding 103P2D6 peptide #46.
 XX KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
 KW single chain monoclonal antibody; cervix; human.
 XX OS Homo sapiens.
 XX PN WO200162925-A2.
 XX PD 30-AUG-2001.
 XX PF 26-FEB-2001; 2001WO-US05996.
 XX

OS Homo sapiens.
 XX WO200162925-A2.
 XX 30-AUG-2001.
 XX 26-FEB-2001; 2001WO-US05996.
 XX 24-FEB-2000; 2000US-0184558.
 XX 13-JUL-2000; 2000US-0218856.
 XX (UROC-) UROGENESYS INC.
 XX Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
 PI Challita-eid PM, Faris M, Jakobovits A;
 WPI; 2001-557705/62.
 PT New polynucleotide for treating and diagnosing prostate cancer is the
 PT 103P2D6 gene which encodes for 103P2D6-related proteins -
 XX Example 15; Page 93; 132pp; English.
 XX Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
 CC adult tissue but is aberrantly expressed in some foetal tissues and many
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
 CC related protein and also peptide fragments of the protein are therefore
 CC useful for diagnosing and treating cancer. A vector comprising a
 CC polynucleotide which encodes a single chain monoclonal antibody, that
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
 CC are both useful in the preparation of a composition for treating a
 CC patient with a cancer that expresses 103P2D6. The sequences can be used
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in
 CC serum, blood, urine and tissue and to thereby detect the presence of
 CC cancerous cells.
 XX SQ Sequence 9 AA;
 Query Match 57.1%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LLYQ 6
 ||||
 Db 1 LLYQ 4
 ||||
 RESULT 67
 AAU24261
 ID AAU24261 standard; Peptide; 9 AA.
 XX AAU24261;
 XX 17-DEC-2001 (first entry)
 XX Human MHC class I molecule HLA-A24 binding 103P2D6 peptide #46.
 XX KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
 KW single chain monoclonal antibody; cervix; human.
 XX OS Homo sapiens.
 XX PN WO200162925-A2.
 XX 30-AUG-2001.
 XX 26-FEB-2001; 2001WO-US05996.
 XX

PR 24-FEB-2000; 2000US-0184558.
 PR 13-JUL-2000; 2000US-0218856.
 XX (UROG-) UROGENESYS INC.
 XX
 PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
 PI Challita-eid PM, Faris M, Jakobovits A;
 XX
 DR WPI; 2001-557705/62.
 XX
 PT New polynucleotide for treating and diagnosing prostate cancer is the
 PT 103P2D6 gene which encodes for 103P2D6-related proteins -
 XX
 PS Example 15; Page 93; 132pp; English.
 XX
 CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
 CC adult tissue but is aberrantly expressed in some foetal tissues and many
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
 CC related protein and also peptide fragments of the protein are therefore
 CC useful for diagnosing and treating cancer. A vector comprising a
 CC polynucleotide which encodes a single chain monoclonal antibody, that
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
 CC are both useful in the preparation of a composition for treating a
 CC patient with a cancer that expresses 103P2D6. The sequences can be used
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in
 CC serum, blood, urine and tissue and to thereby detect the presence of
 CC cancerous cells.
 XX
 SQ Sequence 9 AA;
 CC
 Query Match 57.1%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LLYQ 6
 ||||
 Db 5 LLYQ 8
 CC
 RESULT 68
 AAU24330
 ID AAU24330 standard; Peptide; 9 AA.
 XX
 AC AAU24330;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Human MHC class I molecule HLA-B7 binding 103P2D6 peptide #15.
 XX
 KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
 KW Gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
 KW single chain monoclonal antibody; cervix; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200162925-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 26-FEB-2001; 2001WO-US05996.
 XX
 PR 24-FEB-2000; 2000US-0184558.
 PR 13-JUL-2000; 2000US-0218856.
 XX
 PA (UROG-) UROGENESYS INC.
 XX
 PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
 PI Challita-eid PM, Faris M, Jakobovits A;
 XX

DR WPI; 2001-557705/62.
 XX
 PT New polynucleotide for treating and diagnosing prostate cancer is the
 PT 103P2D6 gene which encodes for 103P2D6-related proteins -
 XX
 PS Example 15; Page 95; 132pp; English.
 XX
 CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
 CC adult tissue but is aberrantly expressed in some foetal tissues and many
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
 CC related protein and also peptide fragments of the protein are therefore
 CC useful for diagnosing and treating cancer. A vector comprising a
 CC polynucleotide which encodes a single chain monoclonal antibody, that
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
 CC are both useful in the preparation of a composition for treating a
 CC patient with a cancer that expresses 103P2D6. The sequences can be used
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in
 CC serum, blood, urine and tissue and to thereby detect the presence of
 CC cancerous cells.
 XX
 SQ Sequence 9 AA;
 CC
 Query Match 57.1%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LLYQ 6
 ||||
 Db 5 LLYQ 8
 CC
 RESULT 69
 AAU24341
 ID AAU24341 standard; Peptide; 9 AA.
 XX
 AC AAU24341;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Human MHC class I molecule HLA-B7 binding 103P2D6 peptide #26.
 XX
 KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
 KW Gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
 KW single chain monoclonal antibody; cervix; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200162925-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 26-FEB-2001; 2001WO-US05996.
 XX
 PR 24-FEB-2000; 2000US-0184558.
 PR 13-JUL-2000; 2000US-0218856.
 XX
 PA (UROG-) UROGENESYS INC.
 XX
 PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
 PI Challita-eid PM, Faris M, Jakobovits A;
 XX
 DR WPI; 2001-557705/62.
 XX
 PT New polynucleotide for treating and diagnosing prostate cancer is the
 PT 103P2D6 gene which encodes for 103P2D6-related proteins -
 XX
 PS Example 15; Page 95; 132pp; English.
 XX
 CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and

CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
 CC adult tissue but is aberrantly expressed in some foetal tissues and many
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
 CC related protein and also peptide fragments of the protein are therefore
 CC useful for diagnosing and treating cancer. A vector comprising a
 CC polynucleotide which encodes a single chain monoclonal antibody, that
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
 CC are both useful in the preparation of a composition for treating a
 CC patient with a cancer that expresses 103P2D6. The sequences can be used
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in
 CC serum, blood, urine and tissue and to thereby detect the presence of
 CC cancerous cells.

XX
 SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
 Db 1 LLYQ 4

RESULT 70

AAU24442
 ID AAU24442 standard; Peptide; 9 AA.

AC AAU24442;

DT 17-DEC-2001 (first entry)

DE Human MHC molecule HLA-B35 binding 103P2D6 peptide #27.

XX 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
 KW single chain monoclonal antibody; cervix; human.

OS Homo sapiens.

XX WO200162925-A2.

XX 30-AUG-2001.

XX 26-FEB-2001; 2001WO-US05996.

PR 24-FEB-2000; 2000US-0184558.

PR 13-JUL-2000; 2000US-0218856.

XX (UROC-) UROGENESYS INC.

XX Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;

PI Challita-eid FM, Paris M, Jakobovits A;

XX WPI; 2001-557705/62.

XX New polynucleotide for treating and diagnosing prostate cancer is the
 PT 103P2D6 gene which encodes for 103P2D6-related proteins -

PS Example 15; Page 98; 132pp; English.

XX Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
 CC adult tissue but is aberrantly expressed in some foetal tissues and many
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
 CC related protein and also peptide fragments of the protein are therefore
 CC useful for diagnosing and treating cancer. A vector comprising a
 CC polynucleotide which encodes a single chain monoclonal antibody, that
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme

CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
 CC are both useful in the preparation of a composition for treating a
 CC patient with a cancer that expresses 103P2D6. The sequences can be used
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in
 CC serum, blood, urine and tissue and to thereby detect the presence of
 CC cancerous cells.

XX
 SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
 Db 5 LLYQ 8

RESULT 71

AAU22143
 ID AAU22143 standard; Peptide; 9 AA.

AC AAU22143;

XX 22-OCT-2001 (first entry)

DE HIV peptide SEQ ID NO 28.

XX Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
 KW human immunodeficiency virus; vaccine.

XX Human immunodeficiency virus.

OS Synthetic.

XX WO200155177-A2.

XX 02-AUG-2001.

XX 29-JAN-2001; 2001WO-DK00059.

XX 28-JAN-2000; 2000EP-0610017.

XX 31-JAN-2000; 2000US-0179333.

XX (STAT-) STATENS SERUM INST.

XX Fomsgaard A, Brunak S, Buus S, Corbet S, Laemoller SL, Hansen J;

XX WPI; 2001-476184/51.

XX The generation of cytotoxic T cell lymphocytes epitopes for use in
 PT anti-HIV vaccines -

PS Claim 13; Page 49; 383pp; English.

XX The invention relates to identification of cytotoxic T cell lymphocyte
 CC (CTL) epitopes (AAU22116-AAU23484) that generate anti-HIV activity. CTL
 CC are a major protective mechanism against viral diseases. Antibodies may
 CC neutralise extracellular human immunodeficiency virus (HIV) and limit or
 CC prevent infection of cells in the host, but CTL will limit viral
 CC production by killing the cell. The CTL epitopes are useful in medicine,
 CC in the manufacture of vaccines or diagnostic agents.

XX Sequence 9 AA;

Query Match 57.1%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
 Db 2 LLYQ 5

```

RESULT 72
ABJ15353
ID ABJ15353 standard; Peptide; 9 AA.
XX
AC ABJ15353;
XX
DT 16-JAN-2003 (first entry)
XX
DE Zinc transporter protein 108P5H8 related HLA peptide SEQ ID No 7.
XX
XX Cytostatic; gene therapy; vaccine; zinc transporter protein 108P5H8;
KW cancer; breast; colon; ovarian; lung; humoral; cellular immune response;
KW passive immunisation.
XX
OS Unidentified.
XX
PN WO200260953-A2.
XX
PD 08-AUG-2002.
XX
PF Cytostatic; gene therapy; vaccine; zinc transporter protein 108P5H8;
KW cancer; breast; colon; ovarian; lung; humoral; cellular immune response;
KW passive immunisation.
XX
OS Unidentified.
XX
PN WO200260953-A2.
XX
PD 08-AUG-2002.
XX
PF 17-DEC-2001; 2001WO-US49133.
XX
PR 15-DEC-2000; 2000US-256210P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Challita-eid PM, Faris M, Afar DEH, Hubert RS, Mitchell SC;
PI Levin E, Morrison KJM, Raitano AB, Jakobovits A;
XX
WPI; 2002-627469/67.
XX
Composition comprising a substance that modulates the status of a zinc
transporter protein (108P5H8), useful in diagnosing and treating
patients with cancer that express 108P5H8, such as breast, colon,
ovarian or lung cancer -
XX
Claim 21; Page 172; 309pp; English.
XX
The invention relates to a new composition comprising a substance that
modulates the status of a zinc transporter protein, designated as
108P5H8, or a molecule that is modulated by 108P5H8. The composition is
useful in diagnosing, preventing, prognosticating or treating patients
with cancer that expresses 108P5H8, such as breast, colon, ovarian or
lung cancer. The 108P5H8 gene or its fragment can be used to elicit a
humoral or cellular immune response. The antibodies are useful in active
or passive immunisation. The 108P5H8 polynucleotides are useful as probes
and primers for the amplification or detection of 108P5H8 genes, as
coding sequences for directing the expression of 108P5H8 polypeptides, or
as tools for modulating or inhibiting the expression of 108P5H8 genes.
The polynucleotides of the invention can be used to treat disorders by
gene therapy. This sequence represents a zinc transporter protein 108P5H8
related peptide of the invention.
XX
SQ Sequence 9 AA;
Query Match 57.1%; Score 4; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLY 5
Db |||||
1 FLLY 4

RESULT 74
ABJ15465
ID ABJ15465 standard; Peptide; 9 AA.
XX
AC ABJ15465;
XX
DT 16-JAN-2003 (first entry)
XX
DE Zinc transporter protein 108P5H8 related HLA peptide SEQ ID No 119.
XX
XX Cytostatic; gene therapy; vaccine; zinc transporter protein 108P5H8;
KW cancer; breast; colon; ovarian; lung; humoral; cellular immune response;
KW passive immunisation.
XX
OS Unidentified.
XX
PN WO200260953-A2.
XX

```

```

PD 08-AUG-2002.
XX
PF 17-DEC-2001; 2001WO-US49133.
XX
XX PR 15-DEC-2000; 2000US-256210P.
XX
XX PA (AGEN-) AGENSYS INC.
XX
XX Challita-eid PM, Faris M, Afar DEH, Hubert RS, Mitchell SC;
PI Levin E, Morrison KJM, Raitano AB, Jakobovits A;
XX
XX WPI; 2002-627469/67.
XX
XX Composition comprising a substance that modulates the status of a zinc
PT transporter protein (108P5H8), useful in diagnosing and treating
PT patients with cancer that express 108P5H8, such as breast, colon,
PT ovarian or lung cancer -
XX
XX Claim 21; Page 177; 309pp; English.
XX
XX The invention relates to a new composition comprising a substance that
CC modulates the status of a zinc transporter protein, designated as
CC 108P5H8, or a molecule that is modulated by 108P5H8. The composition is
CC useful in diagnosing, preventing, prognosticating or treating patients
CC with cancer that expresses 108P5H8, such as breast, colon, ovarian or
CC lung cancer. The 108P5H8 gene or its fragment can be used to elicit a
CC humoral or cellular immune response. The antibodies are useful in active
CC or passive immunisation. The 108P5H8 polynucleotides are useful as probes
CC and primers for the amplification or detection of 108P5H8 genes, as
CC coding sequences for directing the expression of 108P5H8 polypeptides, or
CC as tools for modulating or inhibiting the expression of 108P5H8 genes.
CC The polynucleotides of the invention can be used to treat disorders by
CC gene therapy. This sequence represents a zinc transporter protein 108P5H8
CC related peptide of the invention.
XX
XX Sequence 9 AA;
SQ
Query Match 57.1%; Score 4; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FLLY 5
Db 4 FLLY 7
RESULT 75
ABJ15482
ID ABJ15482 standard; Peptide; 9 AA.
XX
XX AC ABJ15482;
XX
XX 16-JAN-2003 (first entry)
XX
XX Zinc transporter protein 108P5H8 related HLA peptide SEQ ID No 136.
XX
XX Cytostatic; gene therapy; vaccine; zinc transporter protein 108P5H8;
KW cancer; breast; colon; ovarian; lung; humoral; cellular immune response;
KW passive immunisation.
XX
XX OS Unidentified.
XX
XX WO200260953-A2.
XX
XX PD 08-AUG-2002.
XX
XX PF 17-DEC-2001; 2001WO-US49133.
XX
XX PR 15-DEC-2000; 2000US-256210P.
XX
XX PA (AGEN-) AGENSYS INC.
XX
XX Challita-eid PM, Faris M, Afar DEH, Hubert RS, Mitchell SC;
PI Levin E, Morrison KJM, Raitano AB, Jakobovits A;
XX
XX WPI; 2002-627469/67.
XX
XX Composition comprising a substance that modulates the status of a zinc
PT transporter protein (108P5H8), useful in diagnosing and treating
PT patients with cancer that express 108P5H8, such as breast, colon,
PT ovarian or lung cancer -
XX
XX Claim 21; Page 177; 309pp; English.
XX
XX The invention relates to a new composition comprising a substance that
CC modulates the status of a zinc transporter protein, designated as
CC 108P5H8, or a molecule that is modulated by 108P5H8. The composition is
CC useful in diagnosing, preventing, prognosticating or treating patients
CC with cancer that expresses 108P5H8, such as breast, colon, ovarian or
CC lung cancer. The 108P5H8 gene or its fragment can be used to elicit a
CC humoral or cellular immune response. The antibodies are useful in active
CC or passive immunisation. The 108P5H8 polynucleotides are useful as probes
CC and primers for the amplification or detection of 108P5H8 genes, as
CC coding sequences for directing the expression of 108P5H8 polypeptides, or
CC as tools for modulating or inhibiting the expression of 108P5H8 genes.
CC The polynucleotides of the invention can be used to treat disorders by
CC gene therapy. This sequence represents a zinc transporter protein 108P5H8
CC related peptide of the invention.
XX
XX Sequence 9 AA;
SQ
Query Match 57.1%; Score 4; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FLLY 5
Db 4 FLLY 7
Search completed: November 25, 2003, 19:27:17
Job time : 19.8663 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 11.2326 Seconds
(without alignments)
114.943 Million cell updates/sec

Title: US-09-641-801-28

Perfect score: 7

Sequence: 1 AFLYQE 7

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:*

1:	/cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/1/pubaa/PCR_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/1/pubaa/PCRUS_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
10:	/cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
13:	/cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
14:	/cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
15:	/cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
17:	/cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

1	7	100.0	7	15	US-10-281-652-28
2	6	85.7	13	15	US-10-281-652-32
3	6	85.7	19	12	US-10-280-833-7
4	4	57.1	6	10	US-09-727-963A-15
5	4	57.1	6	10	US-09-727-963A-25
6	4	57.1	6	10	US-09-727-963A-27
7	4	57.1	6	10	US-09-727-963A-45
8	4	57.1	6	10	US-09-727-963A-47
9	4	57.1	6	11	US-09-804-291-519
10	4	57.1	6	12	US-10-259-423-49
11	4	57.1	6	15	US-10-259-430-49
12	4	57.1	7	16	US-10-305-346-12
13	4	57.1	9	12	US-09-793-451-130
14	4	57.1	9	12	US-09-793-451-156
15	4	57.1	9	12	US-09-793-451-251

Sequence 28,	App				Sequence 28, App
Sequence 32,	App				Sequence 32, App
Sequence 7,	App				Sequence 7, App
Sequence 15,	App				Sequence 15, App
Sequence 25,	App				Sequence 25, App
Sequence 27,	App				Sequence 27, App
Sequence 45,	App				Sequence 45, App
Sequence 47,	App				Sequence 47, App
Sequence 519,	App				Sequence 519, App
Sequence 49,	App				Sequence 49, App
Sequence 12,	App				Sequence 12, App
Sequence 130,	App				Sequence 130, App
Sequence 156,	App				Sequence 156, App
Sequence 251,	App				Sequence 251, App

9	12	US-09-793-451-357	Sequence 357, App
9	12	US-09-793-451-456	Sequence 456, App
9	12	US-09-793-451-460	Sequence 460, App
9	12	US-09-793-451-529	Sequence 529, App
9	12	US-09-793-451-540	Sequence 540, App
9	12	US-09-793-451-641	Sequence 641, App
9	12	US-09-935-384-127	Sequence 127, App
9	12	US-09-935-384-145	Sequence 145, App
9	12	US-09-935-384-318	Sequence 318, App
9	12	US-09-935-384-402	Sequence 402, App
9	12	US-09-935-384-433	Sequence 433, App
9	12	US-09-935-384-510	Sequence 510, App
9	12	US-09-935-384-630	Sequence 630, App
9	12	US-10-283-722-130	Sequence 130, App
9	12	US-10-283-722-156	Sequence 156, App
9	12	US-10-283-722-251	Sequence 251, App
9	12	US-10-283-722-357	Sequence 357, App
9	12	US-10-283-722-456	Sequence 456, App
9	12	US-10-283-722-460	Sequence 460, App
9	12	US-10-283-722-529	Sequence 529, App
9	12	US-10-283-722-540	Sequence 540, App
9	12	US-10-283-722-641	Sequence 641, App
10	11	US-09-572-404B-1212	Sequence 1212, App
10	11	US-09-572-404B-2701	Sequence 2701, App
10	12	US-09-572-270A-350	Sequence 350, App
10	12	US-09-572-270A-585	Sequence 585, App
10	12	US-09-793-451-183	Sequence 183, App
10	12	US-09-793-451-206	Sequence 206, App
10	12	US-09-793-451-272	Sequence 272, App
10	12	US-09-793-451-303	Sequence 303, App
10	12	US-09-793-451-474	Sequence 474, App
10	12	US-09-793-451-502	Sequence 502, App
10	12	US-09-793-451-594	Sequence 594, App
10	12	US-09-793-451-596	Sequence 596, App
10	12	US-09-793-451-691	Sequence 691, App
10	12	US-09-935-384-159	Sequence 159, App
10	12	US-09-935-384-180	Sequence 180, App
10	12	US-09-935-384-278	Sequence 278, App
10	12	US-09-935-384-283	Sequence 283, App
10	12	US-09-935-384-358	Sequence 358, App
10	12	US-09-935-384-360	Sequence 360, App
10	12	US-09-935-384-459	Sequence 459, App
10	12	US-09-935-384-493	Sequence 493, App
10	12	US-09-935-384-574	Sequence 574, App
10	12	US-09-935-384-575	Sequence 575, App
10	12	US-09-935-384-691	Sequence 691, App
10	12	US-10-283-722-183	Sequence 183, App
10	12	US-10-283-722-206	Sequence 206, App
10	12	US-10-283-722-272	Sequence 272, App
10	12	US-10-283-722-303	Sequence 303, App
10	12	US-10-283-722-474	Sequence 474, App
10	12	US-10-283-722-502	Sequence 502, App
10	12	US-10-283-722-594	Sequence 594, App
10	12	US-10-283-722-596	Sequence 596, App
10	12	US-10-283-722-691	Sequence 691, App
10	12	US-09-573-822C-734	Sequence 734, App
10	15	US-10-001-546-18	Sequence 18, App
13	11	US-09-983-802-439	Sequence 439, App
15	12	US-10-350-405-197	Sequence 197, App
15	15	US-10-033-741-77	Sequence 77, App
15	15	US-10-033-662-71	Sequence 71, App
16	9	US-09-728-721-47	Sequence 47, App
16	9	US-09-837-867A-42	Sequence 42, App
16	11	US-09-962-969-42	Sequence 42, App
16	15	US-10-225-567A-1892	Sequence 1892, App
16	15	US-10-295-981-47	Sequence 47, App
18	9	US-09-735-995-99	Sequence 99, App
18	12	US-10-396-964-9	Sequence 9, App
19	11	US-09-759-130B-84	Sequence 84, App
19	11	US-09-776-724A-221	Sequence 221, App
19	14	US-10-013-770-4	Sequence 4, App
19	14	US-10-045-180A-4	Sequence 4, App

89 4 57.1 19 15 US-10-153-344-18 Sequence 18, Appl
90 4 57.1 20 9 US-09-759-143-500 Sequence 508, App
91 4 57.1 20 9 US-09-780-669-500 Sequence 500, App
92 4 57.1 20 9 US-09-822-827-500 Sequence 500, App
93 4 57.1 20 10 US-09-835-793-500 Sequence 500, App
94 4 57.1 20 10 US-09-835-814-500 Sequence 500, App
95 4 57.1 20 11 US-09-798-889-118 Sequence 118, App
96 4 57.1 20 12 US-10-144-678A-500 Sequence 500, App
97 4 57.1 20 12 US-10-196-394-61 Sequence 61, Appl
98 4 57.1 20 12 US-10-294-025-500 Sequence 500, App
99 4 57.1 20 14 US-10-012-896-500 Sequence 500, App
100 4 57.1 20 15 US-10-000-823-13 Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-10-281-652-28
; Sequence 28, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-28

Query Match 100.0%; Score 7; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLYQE 7
 |||||
DB 1 AFLYQE 7

RESULT 2
US-10-281-652-32
; Sequence 32, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 32
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-32

Query Match 85.7%; Score 6; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLYQE 7
 |||||
DB 1 FLLYQE 6

RESULT 3
US-10-280-833-7
; Sequence 7, Application US/10280833
; Publication No. US20030195150A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Charles Eric
; APPLICANT: Dashper, Stuart Geoffrey
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Talbo, Gert Hoy
; APPLICANT: Malkoski, Marina
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: BDWP-00100N
; CURRENT APPLICATION NUMBER: US/10/280,833
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/554,997
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: PP 0514
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 19
; TYPE: PRT
; ORGANISM: bovine
; OTHER INFORMATION: peptide
US-10-280-833-7

Query Match 85.7%; Score 6; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLYQ 6
 |||||
DB 6 AFLLYQ 11

RESULT 4
US-09-727-963A-15
; Sequence 15, Application US/09727963A
; Patent No. US20020155106A1
; GENERAL INFORMATION:
; APPLICANT: V.I. Technologies, Inc.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: U.S.N. 60/327,557
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence : peptide
; OTHER INFORMATION: ligand
US-09-727-963A-15

Query Match 57.1%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLYY 5
|||
Db 1 FLYY 4

RESULT 5

US-09-727-963A-25
; Sequence 25, Application US/09727963A
; Patent No. US20020155106A1
; GENERAL INFORMATION:
; APPLICANT: V.I. Technologies, Inc.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; CURRENT FILING DATE: 2000-12-01
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence : peptide
; OTHER INFORMATION: ligand
US-09-727-963A-25

Query Match 57.1%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLYY 5
|||
Db 1 FLYY 4

RESULT 6

US-09-727-963A-27
; Sequence 27, Application US/09727963A
; Patent No. US20020155106A1
; GENERAL INFORMATION:
; APPLICANT: V.I. Technologies, Inc.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; CURRENT FILING DATE: 2000-12-01
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence : peptide
; OTHER INFORMATION: ligand
US-09-727-963A-27

Query Match 57.1%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLYY 5
|||
Db 1 FLYY 4

RESULT 7

US-09-727-963A-45
; Sequence 45, Application US/09727963A
; Patent No. US20020155106A1
; GENERAL INFORMATION:
; APPLICANT: V.I. Technologies, Inc.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; CURRENT FILING DATE: 2000-12-01
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide Ligand
US-09-727-963A-45

Query Match 57.1%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLYY 5
|||
Db 1 FLYY 4

RESULT 8

US-09-727-963A-47
; Sequence 47, Application US/09727963A
; Patent No. US20020155106A1
; GENERAL INFORMATION:
; APPLICANT: V.I. Technologies, Inc.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; CURRENT FILING DATE: 2000-12-01
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide Ligand
US-09-727-963A-47

Query Match 57.1%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLYY 5
|||
Db 1 FLYY 4

RESULT 9

US-09-804-291-519
; Sequence 519, Application US/09804291

Query Match: 57.1%; Score 4; DB 12; Length 6;

Query Match	57.1%;	Score 4;	DB 16;	Length 7;
Best Local Similarity	100.0%;	Pred. No. 66+05;		
Matches	4;	Conservative	0;	Mismatches 0; Indels
Qy	4	LYQE	7	
Db	1	LYQE	4	

Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	3	LLYQ	6						
Db	2	LLYQ	5						
RESULT 15									
US-09-793-451-251									
; Sequence 251, Application US/09793451									
; Publication No. US20030157597A1									
; GENERAL INFORMATION:									
; APPLICANT: Arthur B. Raitano									
; APPLICANT: Daniel E.H. Afar									
; APPLICANT: Gazelle S. Rastegar									
; APPLICANT: Steve Chappell Mitchell									
; APPLICANT: Rene S. Hubert									
; APPLICANT: Pia M. Challita-Eid									
; APPLICANT: Mary Paris									
; APPLICANT: Aya Jakobovits									
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY									
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS									
; FILE REFERENCE: 129.2USU2									
; CURRENT APPLICATION NUMBER: US/09/793,451									
; CURRENT FILING DATE: 2001-02-26									
; PRIOR APPLICATION NUMBER: 60/184,558									
; PRIOR FILING DATE: 2000-02-24									
; PRIOR APPLICATION NUMBER: 60/218,856									
; PRIOR FILING DATE: 2000-07-13									
; NUMBER OF SEQ ID NOS: 752									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 251									
; LENGTH: 9									
; TYPE: PRT									
; ORGANISM: homo sapiens									
US-09-793-451-251									
Query Match 57.1%; Score 4; DB 12; Length 9;									
Best Local Similarity 100.0%; Pred. No. 6e+05;									
Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	3	LLYQ	6						
Db	1	LLYQ	4						
RESULT 16									
US-09-793-451-357									
; Sequence 357, Application US/09793451									
; Publication No. US20030157597A1									
; GENERAL INFORMATION:									
; APPLICANT: Arthur B. Raitano									
; APPLICANT: Daniel E.H. Afar									
; APPLICANT: Gazelle S. Rastegar									
; APPLICANT: Steve Chappell Mitchell									
; APPLICANT: Rene S. Hubert									
; APPLICANT: Pia M. Challita-Eid									
; APPLICANT: Mary Paris									
; APPLICANT: Aya Jakobovits									
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY									
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS									
; FILE REFERENCE: 129.2USU2									
; CURRENT APPLICATION NUMBER: US/09/793,451									
; CURRENT FILING DATE: 2001-02-26									
; PRIOR APPLICATION NUMBER: 60/184,558									
; PRIOR FILING DATE: 2000-02-24									
; PRIOR APPLICATION NUMBER: 60/218,856									
; PRIOR FILING DATE: 2000-07-13									
; NUMBER OF SEQ ID NOS: 752									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 357									
; LENGTH: 9									
; TYPE: PRT									

```
; ORGANISM: homo sapiens
US-09-793-451-357

Query Match      57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
Db 3 LLYQ 6

RESULT 17
US-09-793-451-456
; Sequence 456, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 456
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-456

Query Match      57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
Db 1 LLYQ 4

RESULT 18
US-09-793-451-460
; Sequence 460, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13

; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 457
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-457

Query Match      57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
Db 5 LLYQ 8

RESULT 19
US-09-793-451-529
; Sequence 529, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 529
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-529

Query Match      57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
Db 5 LLYQ 8

RESULT 20
US-09-793-451-540
; Sequence 540, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
```

; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 540
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-540

Query Match 57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
Db 1 LLYQ 4

RESULT 21
US-09-793-451-641
; Sequence 641, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazele S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 641
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-641

Query Match 57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
Db 5 LLYQ 8

RESULT 22
US-09-935-384-127
; Sequence 127, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 127
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-127

Query Match 57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
Db 3 AFLL 6

RESULT 23
US-09-935-384-145
; Sequence 145, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 145
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-145

Query Match 57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
Db 2 AFLL 5

RESULT 24
US-09-935-384-318
; Sequence 318, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL

```
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 318
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-318

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4
Db 1 AFLL 4

RESULT 25
US-09-935-384-402
; Sequence 402, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 402
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-402

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4
Db 6 AFLL 9

RESULT 26
US-09-935-384-433
; Sequence 433, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
```

```
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 433
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-433

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4
Db 2 AFLL 5

RESULT 27
US-09-935-384-510
; Sequence 510, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 510
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-510

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4
Db 2 AFLL 5

RESULT 28
US-09-935-384-630
; Sequence 630, Application US/09935384
```

```

; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 630
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-630

Query Match      57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AFLL 4
        |||
Db       2 AFLL 5

RESULT 29
US-10-283-722-130
; Sequence 130, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-130

Query Match      57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LLYQ 6
        |||
Db       2 LLYQ 5

RESULT 31
US-10-283-722-251
; Sequence 251, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 251
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-156
; Sequence 156, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-156

Query Match      57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LLYQ 6
        |||
Db       2 LLYQ 5

RESULT 31
US-10-283-722-251
; Sequence 251, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 251
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-130

Query Match      57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LLYQ 6
        |||

```

```
; ORGANISM: homo sapiens
US-10-283-722-251

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
   ||||
Db 1 LLYQ 4

RESULT 32
US-10-283-722-357
; Sequence 357, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 357
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-357

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
   ||||
Db 3 LLYQ 6

RESULT 33
US-10-283-722-456
; Sequence 456, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 357
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-357

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
   ||||
Db 3 LLYQ 6

RESULT 34
US-10-283-722-460
; Sequence 460, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 460
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-460

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
   ||||
Db 1 LLYQ 4

RESULT 35
US-10-283-722-529
; Sequence 529, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
```

; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 529
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-529

Query Match 57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
|
|
|
Db 5 LLYQ 8

RESULT 36
US-10-283-722-540
; Sequence 540, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 540
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-540

Query Match 57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
|
|
|
Db 1 LLYQ 4

RESULT 37
US-10-283-722-641

; Sequence 641, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 641
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-641

Query Match 57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
|
|
|
Db 5 LLYQ 8

RESULT 38
US-09-572-404B-1212
; Sequence 1212, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human Patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1212
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in SCN4A at 835-844 and may interact with Seq
; OTHER INFORMATION: in this patent.
US-09-572-404B-1212

Query Match 57.1%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 4
|
|
|
Db 4 AFL 7

RESULT 39
US-09-572-404B-2701
; Sequence 2701, Application US/09572404B
; Publication No. US20030078374A1


```
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2701
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in CRHR2 OR CRF2R OR CRH2R at 132-141 and may in
; OTHER INFORMATION: with Sequence 2702 in this patent.
US-09-572-404B-2701

Query Match          57.1%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AFLL 4
        ||||
Db      1 AFLL 4

RESULT 42
US-09-793-451-183
; Sequence 183, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-183

Query Match          57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LLYQ 6
        ||||
Db      2 LLYQ 5

RESULT 43
US-09-793-451-206
; Sequence 206, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
```

```
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2701
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in CRHR2 OR CRF2R OR CRH2R at 132-141 and may in
; OTHER INFORMATION: with Sequence 2702 in this patent.
US-09-572-404B-2701

Query Match          57.1%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AFLL 4
        ||||
Db      3 AFLL 6

RESULT 40
US-09-572-270A-350
; Sequence 350, Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572,270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 350
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in ATJ. at 649-658 and may interact with
US-09-572-270A-350

Query Match          57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AFLL 4
        ||||
Db      5 AFLL 8

RESULT 41
US-09-572-270A-585
; Sequence 585, Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572,270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 585
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in ATJ. at 653-662 and may interact with
US-09-572-270A-585
```

; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-206

Query Match 57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
|||
Db 6 LLYQ 9

RESULT 44

US-09-793-451-272
; Sequence 272, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:

; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 272
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-272

Query Match 57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
|||
Db 1 LLYQ 4

RESULT 45

US-09-793-451-303
; Sequence 303, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:

; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-303

Query Match 57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
|||
Db 2 LLYQ 5

RESULT 46

US-09-793-451-474
; Sequence 474, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-474

Query Match 57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
|||
Db 2 LLYQ 5

RESULT 47

US-09-793-451-502
; Sequence 502, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24

; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 502
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-594

Query Match 57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
Db 6 LLYQ 9

RESULT 48

US-09-793-451-594
; Sequence 594, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 594
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-594

Query Match 57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
Db 2 LLYQ 5

RESULT 49

US-09-793-451-596
; Sequence 596, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert

; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 596
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-596

Query Match 57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
Db 6 LLYQ 9

RESULT 50

US-09-793-451-691
; Sequence 691, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 691
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-691

Query Match 57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
Db 5 LLYQ 8

RESULT 51

US-09-935-384-159
; Sequence 159, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:

```

; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: PARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-159

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4
Db 7 AFLL 10

RESULT 52
US-09-935-384-180
; Sequence 180, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: PARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 180
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-180

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4
Db 3 AFLL 6

RESULT 53
US-09-935-384-278
; Sequence 278, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: PARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 278
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-278

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4
Db 7 AFLL 10

RESULT 54
US-09-935-384-283
; Sequence 283, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: PARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 283
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-283

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4
Db 7 AFLL 10
```

```

RESULT 55
US-09-935-384-358
; Sequence 358, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 358
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-358

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AFLL 4
Db      1 AFLL 4

RESULT 56
US-09-935-384-360
; Sequence 360, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 360
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-360

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AFLL 4
Db      1 AFLL 4

RESULT 57
US-09-935-384-459
; Sequence 459, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 459
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-459

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AFLL 4
Db      3 AFLL 6

RESULT 58
US-09-935-384-475
; Sequence 475, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 475
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-475

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 10;

Qy      1 AFLL 4
Db      1 AFLL 4

```

```
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4
Db 6 AFLL 9

RESULT 59
US-09-935-384-493
; Sequence 493, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 493
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-493

Query Match 57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4
Db 7 AFLL 10

RESULT 60
US-09-935-384-574
; Sequence 574, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 574
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-574
```

```
Query Match 57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4
Db 7 AFLL 10

RESULT 61
US-09-935-384-575
; Sequence 575, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 575
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-575

Query Match 57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4
Db 3 AFLL 6

RESULT 62
US-09-935-384-691
; Sequence 691, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 691
; LENGTH: 10
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-691

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 4
   ||||
Db 3 AFL 6

RESULT 63
US-10-283-722-183
; Sequence 183, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-07-13
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-183

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
   ||||
Db 2 LLYQ 5

RESULT 64
US-10-283-722-206
; Sequence 206, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
```

```
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-206

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
   ||||
Db 6 LLYQ 9

RESULT 65
US-10-283-722-272
; Sequence 272, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR APPLICATION NUMBER: 60/218,856
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 272
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-272

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
   ||||
Db 1 LLYQ 4

RESULT 66
US-10-283-722-303
; Sequence 303, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
```

APPLICANT: Pia M. Challita-Eid
APPLICANT: Mary Faris
APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-303

Query Match 57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
Db 2 LLYQ 5

RESULT 67
US-10-283-722-474
; Sequence 474, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-474

Query Match 57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
Db 2 LLYQ 5

RESULT 68

US-10-283-722-502
; Sequence 502, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 502
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-502

Query Match 57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
Db 6 LLYQ 9

RESULT 69
US-10-283-722-594
; Sequence 594, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 594
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-594

Query Match 57.1%; Score 4; DB 12; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy 3 LLYQ 6
|||
Db 2 LLYQ 5

RESULT 70

US-10-283-722-596
; Sequence 596, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 596
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-596

Query Match 57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
|||
Db 6 LLYQ 9

RESULT 71

US-10-283-722-691
; Sequence 691, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13

; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 691
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-691

Query Match 57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
|||
Db 5 LLYQ 8

RESULT 72

US-09-573-822C-734
; Sequence 734, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 734
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG468 at 1655-1664 and may interact with ;
; OTHER INFORMATION: 733 in this patent.
US-09-573-822C-734

Query Match 57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 4
|||
Db 5 AFL 8

RESULT 73

US-10-001-546-18
; Sequence 18, Application US/10001546
; Publication No. US20030027766A1
; GENERAL INFORMATION:
; APPLICANT: IOANNIDES, CONSTANTIN G.
; APPLICANT: FISK, BRYAN A.
; APPLICANT: IOANNIDES, MARIA G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
; FILE OF INVENTION: T-LYMPHOCYTES
; FILE REFERENCE: UTSC:390USC2
; CURRENT APPLICATION NUMBER: US/10/001,546
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 08/403,459
; PRIOR FILING DATE: 1995-03-14
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-001-546-18

Query Match 57.1%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
|||
Db 2 LLYQ 5

RESULT 74

US-09-983-802-439
; Sequence 439, Application US/09983802
; Publication No. US20030022185A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US/09/983,802
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 09/227,357
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: PCT/US98/13684
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,926
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,929
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,803
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,732
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,931
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,932
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,916
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,930
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,918
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,920
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,733
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,795
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,919
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,928
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/055,722
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,723
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,948
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,949
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,953
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,950
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,947
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,964
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056,360
; PRIOR FILING DATE: 1997-08-18

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 439
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-802-439

Query Match 57.1%; Score 4; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLY 5
|||
Db 7 FLY 10

RESULT 75

US-10-350-405-197
; Sequence 197, Application US/10350405
; Publication No. US20030215894A1
; GENERAL INFORMATION:
; APPLICANT: Niman, Henry L.
; TITLE OF INVENTION: Polypeptide-Induced Monoclonal Receptors
; FILE REFERENCE: TSRI 35.5 CON 7/LIG
; CURRENT APPLICATION NUMBER: US/10/350,405
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 09/427,576
; PRIOR FILING DATE: 1999-10-26
; PRIOR APPLICATION NUMBER: 08/461,583
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 08/294,879
; PRIOR FILING DATE: 1994-08-23
; PRIOR APPLICATION NUMBER: 08/054,864
; PRIOR FILING DATE: 1993-04-28
; PRIOR APPLICATION NUMBER: 07/900,502
; PRIOR FILING DATE: 1992-06-16
; PRIOR APPLICATION NUMBER: 07/780,415
; PRIOR FILING DATE: 1991-10-22
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 197
; LENGTH: 15
; TYPE: PRT
; ORGANISM: retrovirus
US-10-350-405-197

Query Match 57.1%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQE 7
|||
Db 8 LYQE 11

Search completed: November 25, 2003, 20:37:05
Job time : 12.2326 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 5.65698 Seconds
(without alignments)
52.356 Million cell updates/sec

Title: US-09-641-801-28
Perfect score: 7
Sequence: 1 AFLLYQE 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	4	US-09-641-803-28
2	6	85.7	13	4	Sequence 28, Appl
3	5	71.4	10	2	Sequence 32, Appl
4	5	71.4	14	2	Sequence 14, Appl
5	4	57.1	5	1	Sequence 16, Appl
6	4	57.1	6	4	Sequence 41, Appl
7	4	57.1	7	4	Sequence 49, Appl
8	4	57.1	9	3	Sequence 12, Appl
9	4	57.1	10	3	Sequence 366, Appl
10	4	57.1	11	4	Sequence 375, Appl
11	4	57.1	11	1	Sequence 18, Appl
12	4	57.1	11	1	Sequence 1, Appl
13	4	57.1	11	1	Sequence 19, Appl
14	4	57.1	11	1	Sequence 20, Appl
15	4	57.1	11	5	Sequence 21, Appl
16	4	57.1	11	5	Sequence 1, Appl
17	4	57.1	11	5	Sequence 19, Appl
18	4	57.1	11	5	Sequence 20, Appl
19	4	57.1	12	1	Sequence 139, Appl
20	4	57.1	12	1	Sequence 139, Appl
21	4	57.1	12	1	Sequence 139, Appl
22	4	57.1	12	2	Sequence 139, Appl
23	4	57.1	12	2	Sequence 139, Appl
24	4	57.1	12	2	Sequence 139, Appl
25	4	57.1	12	2	Sequence 139, Appl
26	4	57.1	12	3	Sequence 139, Appl
27	4	57.1	12	3	Sequence 139, Appl

28	4	57.1	12	3	US-08-018-760-139	Sequence 139, Appl
29	4	57.1	13	1	US-08-064-400B-16	Sequence 16, Appl
30	4	57.1	13	1	US-08-291-601-1	Sequence 1, Appl
31	4	57.1	13	1	US-08-291-601-2	Sequence 2, Appl
32	4	57.1	13	1	US-08-291-601-3	Sequence 3, Appl
33	4	57.1	13	4	US-09-227-357-439	Sequence 439, Appl
34	4	57.1	15	2	US-08-637-759B-246	Sequence 246, Appl
35	4	57.1	15	3	US-08-871-355A-246	Sequence 246, Appl
36	4	57.1	15	4	US-09-201-945-246	Sequence 246, Appl
37	4	57.1	16	3	US-08-205-697A-42	Sequence 42, Appl
38	4	57.1	16	3	US-08-702-525-42	Sequence 42, Appl
39	4	57.1	16	4	US-09-340-620A-47	Sequence 47, Appl
40	4	57.1	16	5	PCT-US95-02576-42	Sequence 42, Appl
41	4	57.1	18	1	US-08-401-512-64	Sequence 64, Appl
42	4	57.1	18	1	US-08-244-116B-9	Sequence 9, Appl
43	4	57.1	18	3	US-09-226-012-99	Sequence 99, Appl
44	4	57.1	19	1	US-08-507-124-5	Sequence 5, Appl
45	4	57.1	19	1	US-08-451-472-12	Sequence 12, Appl
46	4	57.1	19	1	US-08-451-472-46	Sequence 46, Appl
47	4	57.1	19	3	US-08-928-213B-35	Sequence 35, Appl
48	4	57.1	19	4	US-09-486-580A-4	Sequence 4, Appl
49	4	57.1	20	2	US-08-617-929-1	Sequence 1, Appl
50	4	57.1	20	3	US-08-460-576-15	Sequence 15, Appl
51	4	57.1	20	4	US-09-439-313-500	Sequence 500, Appl
52	3	42.9	4	1	US-07-657-769B-14	Sequence 14, Appl
53	3	42.9	4	1	US-07-657-769B-54	Sequence 54, Appl
54	3	42.9	4	1	US-08-405-933-4	Sequence 4, Appl
55	3	42.9	4	1	US-08-405-933-6	Sequence 6, Appl
56	3	42.9	4	1	US-08-405-933-14	Sequence 14, Appl
57	3	42.9	4	1	US-08-405-933-38	Sequence 38, Appl
58	3	42.9	4	1	US-08-405-933-39	Sequence 39, Appl
59	3	42.9	4	1	US-07-789-184-35	Sequence 35, Appl
60	3	42.9	4	1	US-07-789-184-109	Sequence 109, Appl
61	3	42.9	4	1	US-07-789-184-117	Sequence 117, Appl
62	3	42.9	4	1	US-08-549-008-29	Sequence 29, Appl
63	3	42.9	4	1	US-08-475-263-35	Sequence 35, Appl
64	3	42.9	4	1	US-08-475-263-109	Sequence 109, Appl
65	3	42.9	4	1	US-08-475-263-117	Sequence 117, Appl
66	3	42.9	4	1	US-08-205-511-1	Sequence 1, Appl
67	3	42.9	4	1	US-08-485-886-35	Sequence 35, Appl
68	3	42.9	4	1	US-08-485-886-109	Sequence 109, Appl
69	3	42.9	4	1	US-08-485-886-117	Sequence 117, Appl
70	3	42.9	4	2	US-08-477-362-35	Sequence 35, Appl
71	3	42.9	4	2	US-08-477-362-109	Sequence 109, Appl
72	3	42.9	4	2	US-08-477-362-117	Sequence 117, Appl
73	3	42.9	4	2	US-08-188-583-37	Sequence 37, Appl
74	3	42.9	4	2	US-08-477-134-35	Sequence 35, Appl
75	3	42.9	4	2	US-08-477-134-109	Sequence 109, Appl
76	3	42.9	4	2	US-08-477-134-117	Sequence 117, Appl
77	3	42.9	4	2	US-08-685-589A-7	Sequence 7, Appl
78	3	42.9	4	3	US-08-473-489A-35	Sequence 35, Appl
79	3	42.9	4	3	US-08-473-489A-117	Sequence 117, Appl
80	3	42.9	4	3	US-08-473-489A-109	Sequence 109, Appl
81	3	42.9	4	3	US-08-485-695-35	Sequence 35, Appl
82	3	42.9	4	3	US-08-485-695-109	Sequence 109, Appl
83	3	42.9	4	3	US-08-485-695-117	Sequence 117, Appl
84	3	42.9	4	3	US-08-018-760-35	Sequence 35, Appl
85	3	42.9	4	3	US-08-018-760-109	Sequence 109, Appl
86	3	42.9	4	3	US-08-018-760-117	Sequence 117, Appl
87	3	42.9	4	4	US-08-956-653A-22	Sequence 22, Appl
88	3	42.9	4	4	US-09-431-705-23	Sequence 23, Appl
89	3	42.9	5	1	US-07-690-284A-10	Sequence 10, Appl
90	3	42.9	5	1	US-07-657-769B-13	Sequence 13, Appl
91	3	42.9	5	1	US-07-657-769B-53	Sequence 53, Appl
92	3	42.9	5	1	US-07-805-727-6	Sequence 6, Appl
93	3	42.9	5	1	US-08-087-423-3	Sequence 3, Appl
94	3	42.9	5	1	US-08-390-272-6	Sequence 6, Appl
95	3	42.9	5	1	US-08-405-933-2	Sequence 2, Appl
96	3	42.9	5	1	US-08-405-933-5	Sequence 5, Appl
97	3	42.9	5	1	US-08-405-933-8	Sequence 8, Appl
98	3	42.9	5	1	US-08-405-933-32	Sequence 32, Appl
99	3	42.9	5	1	US-08-405-933-36	Sequence 36, Appl
100	3	42.9	5	1	US-08-405-933-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
 US-09-641-803-28
 ; Sequence 28, Application US/09641803
 ; Patent No. 6500798
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDOGH, Istvan
 ; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
 ; FILE REFERENCE: 265.00220101
 ; CURRENT FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: US/09/641,803
 ; PRIOR FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 28
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: peptide
 US-09-641-803-28

Query Match 100.0%; Score 7; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLYQE 7
 Db 1 AFLLYQE 7

RESULT 2
 US-09-641-803-32
 ; Sequence 32, Application US/09641803
 ; Patent No. 6500798
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDOGH, Istvan
 ; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
 ; FILE REFERENCE: 265.00220101
 ; CURRENT APPLICATION NUMBER: US/09/641,803
 ; CURRENT FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: 60/149,310
 ; PRIOR FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 32
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: peptide
 US-09-641-803-32

Query Match 85.7%; Score 6; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.81;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLYQE 7
 Db 1 FLLYQE 6

RESULT 3
 US-08-617-929-14
 ; Sequence 14, Application US/08617929
 ; Patent No. 5885771
 ; GENERAL INFORMATION:
 ; APPLICANT: KUMAZAWA, Toshiaki
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDE COMPOUND AND
 ; TITLE OF INVENTION: IMMUNOASSAY
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/617,929
 ; FILING DATE: 24-APR-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/JP94/01823
 ; FILING DATE: 28-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6/207695
 ; FILING DATE: 31-AUG-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 5/272864
 ; FILING DATE: 29-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SAXE, Bernhard D.
 ; REGISTRATION NUMBER: 28,665
 ; REFERENCE/DOCKET NUMBER: 77384/109
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-08-617-929-14

Query Match 71.4%; Score 5; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQE 7
 Db 3 LLYQE 7

RESULT 4
 US-08-617-929-16
 ; Sequence 16, Application US/08617929
 ; Patent No. 5885771
 ; GENERAL INFORMATION:
 ; APPLICANT: KUMAZAWA, Toshiaki
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDE COMPOUND AND
 ; TITLE OF INVENTION: IMMUNOASSAY
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500

```

; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,929
; FILING DATE: 24-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JF94/01823
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6/207695
; FILING DATE: 31-AUG-1994
; APPLICATION NUMBER: JP 5/272864
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 77384/109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-617-929-16

Query Match 71.4%; Score 5; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQE 7
Db 10 LLYQE 14

RESULT 5
US-08-405-933-41
; Sequence 41, Application US/08405933
; Patent No. 5516889
; GENERAL INFORMATION:
; APPLICANT: Hollenberg, Morley D.
; APPLICANT: Matsoukas, John M.
; APPLICANT: Moore, Graham J.
; TITLE OF INVENTION: Synthetic Thrombin Receptor Peptides
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: Washington & Prince Streets, P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,933
; FILING DATE:
; CLASSIFICATION: 514

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,643
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dillahunty, Mary Ann
; REGISTRATION NUMBER: 34,576
; REFERENCE/DOCKET NUMBER: 028722-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-7400
; TELEFAX: (415)854-8275
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-405-933-41

Query Match 57.1%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 4
Db 1 AFL 4

RESULT 6
US-09-465-901-49
; Sequence 49, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-Wai
; APPLICANT: Krautwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expression Libraries
; TITLE OF INVENTION: ad Methods of Making and Using Them
; FILE REFERENCE: 001107.00105
; CURRENT APPLICATION NUMBER: US/09/465,901
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/112,605
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: PCR primer
; US-09-465-901-49

Query Match 57.1%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLY 5
Db 2 FLY 5

RESULT 7
US-09-492-766-12
; Sequence 12, Application US/09492766
; Patent No. 6506732
; GENERAL INFORMATION:
; APPLICANT: AMIOT, Jean
; TITLE OF INVENTION: ENZYMIC HYDROLYSATE OF MILK PROTEINS
; FILE REFERENCE: 6013-57"US"
; CURRENT APPLICATION NUMBER: US/09/492,766
; CURRENT FILING DATE: 2000-01-27
; EARLIER APPLICATION NUMBER: 60/117,661
; EARLIER FILING DATE: 1999-01-28

```

; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk
; OTHER INFORMATION: proteins
US-09-492-766-12

Query Match 57.1%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LLYQ 7
Db 1 LLYQ 4

RESULT 8
US-08-159-339A-366
; Sequence 366, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 366:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-366

Query Match 57.1%; Score 4; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
Db 1 LLYQ 4

RESULT 9
US-08-159-339A-375
; Sequence 375, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 375:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-375

Query Match 57.1%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
Db 2 LLYQ 5

RESULT 10
US-08-403-459-18
; Sequence 18, Application US/08403459
; Patent No. 6514942

GENERAL INFORMATION:
APPLICANT: Ioannides, Constantin G.
APPLICANT: Fisk, Bryan A.
APPLICANT: Ioannides, Maria G.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
TITLE OF INVENTION: T-LYMPHOCYTES
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,459
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSC:390/KIT
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-403-459-18

Query Match 57.1%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
Db 2 LLYQ 5

RESULT 11
US-08-443-568B-1
Sequence 1, Application US/08443568B
Patent No. 5759807
GENERAL INFORMATION:
APPLICANT: Breece, Tim
APPLICANT: Hayenga, Kirk
APPLICANT: Rindersknecht, Ernst
APPLICANT: Vandlien, Richard
APPLICANT: Daniel, Yansura
TITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,568B
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/080,354
FILING DATE: 21-JUNE-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B.
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 7842-037
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-443-568B-1

Query Match 57.1%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4
Db 6 AFLL 9

RESULT 12
US-08-443-568B-19
Sequence 19, Application US/08443568B
Patent No. 5759807
GENERAL INFORMATION:
APPLICANT: Breece, Tim
APPLICANT: Hayenga, Kirk
APPLICANT: Rindersknecht, Ernst
APPLICANT: Vandlien, Richard
APPLICANT: Daniel, Yansura
TITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,568B
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/080,354
FILING DATE: 21-JUNE-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B.
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 7842-037
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556


```

;       TELEX: 66141 PENNIE
;       INFORMATION FOR SEQ ID NO: 19:
;       SEQUENCE CHARACTERISTICS:
;       LENGTH: 11 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: unknown
;       TOPOLOGY: unknown
;       MOLECULE TYPE: peptide
US-08-443-568B-19

Query Match      57.1%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AFLL 4
Db      6 AFLL 9

RESULT 13
US-08-443-568B-20
; Sequence 20, Application US/08443568B
; Patent No. 5759807
; GENERAL INFORMATION:
; APPLICANT: Breece, Tim
; APPLICANT: Hayenga, Kirk
; APPLICANT: Rindersknecht, Ernst
; APPLICANT: Vandlen, Richard
; APPLICANT: Daniel, Yansura
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,568B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/080,354
; FILING DATE: 21-JUNE-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B.
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 7842-037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-443-568B-20

Query Match      57.1%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AFLL 4
Db      6 AFLL 9

RESULT 14
US-08-443-568B-21
; Sequence 21, Application US/08443568B
; Patent No. 5759807
; GENERAL INFORMATION:
; APPLICANT: Breece, Tim
; APPLICANT: Hayenga, Kirk
; APPLICANT: Rindersknecht, Ernst
; APPLICANT: Vandlen, Richard
; APPLICANT: Daniel, Yansura
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,568B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/080,354
; FILING DATE: 21-JUNE-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B.
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 7842-037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-443-568B-21

Query Match      57.1%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AFLL 4
Db      6 AFLL 9

RESULT 15
PCT-US94-06997-1
; Sequence 1, Application PC/TUS9406997
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: 460 Point San Bruno Boulevard
; APPLICANT: South San Francisco, California
; APPLICANT: United States of America
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Boulevard
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94080
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-443-568B-20

Query Match      57.1%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AFLL 4
Db      6 AFLL 9
```

```

;       TELEX: 66141 PENNIE
;       INFORMATION FOR SEQ ID NO: 19:
;       SEQUENCE CHARACTERISTICS:
;       LENGTH: 11 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: unknown
;       TOPOLOGY: unknown
;       MOLECULE TYPE: peptide
US-08-443-568B-19

Query Match      57.1%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AFLL 4
Db      6 AFLL 9

RESULT 13
US-08-443-568B-20
; Sequence 20, Application US/08443568B
; Patent No. 5759807
; GENERAL INFORMATION:
; APPLICANT: Breece, Tim
; APPLICANT: Hayenga, Kirk
; APPLICANT: Rindersknecht, Ernst
; APPLICANT: Vandlen, Richard
; APPLICANT: Daniel, Yansura
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,568B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/080,354
; FILING DATE: 21-JUNE-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B.
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 7842-037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-443-568B-20

Query Match      57.1%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AFLL 4
Db      6 AFLL 9

RESULT 14
US-08-443-568B-21
; Sequence 21, Application US/08443568B
; Patent No. 5759807
; GENERAL INFORMATION:
; APPLICANT: Breece, Tim
; APPLICANT: Hayenga, Kirk
; APPLICANT: Rindersknecht, Ernst
; APPLICANT: Vandlen, Richard
; APPLICANT: Daniel, Yansura
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,568B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/080,354
; FILING DATE: 21-JUNE-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B.
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 7842-037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-443-568B-21

Query Match      57.1%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AFLL 4
Db      6 AFLL 9

RESULT 15
PCT-US94-06997-1
; Sequence 1, Application PC/TUS9406997
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: 460 Point San Bruno Boulevard
; APPLICANT: South San Francisco, California
; APPLICANT: United States of America
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Boulevard
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94080
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-443-568B-20

Query Match      57.1%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AFLL 4
Db      6 AFLL 9
```

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06997
FILING DATE: 20-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7842-025-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US94-06997-1

Query Match 57.1%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
|||
Db 6 AFLL 9

RESULT 16
PCT-US94-06997-19
Sequence 19, Application PC/TUS9406997
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: 460 Point San Bruno Boulevard
APPLICANT: South San Francisco, California
APPLICANT: United States of America
TITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06997
FILING DATE: 20-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7842-025-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660

TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US94-06997-19

Query Match 57.1%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
|||
Db 6 AFLL 9

RESULT 17
PCT-US94-06997-20
Sequence 20, Application PC/TUS9406997
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: 460 Point San Bruno Boulevard
APPLICANT: South San Francisco, California
APPLICANT: United States of America
TITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06997
FILING DATE: 20-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7842-025-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US94-06997-20

Query Match 57.1%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
|||
Db 6 AFLL 9

RESULT 18

PCT-US94-06997-21
 ; Sequence 21, Application PC/TUS9406997
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: 460 Point San Bruno Boulevard
 ; APPLICANT: South San Francisco, California
 ; APPLICANT: United States of America
 ; TITLE OF INVENTION: Process for Producing Relaxin
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/06997
 ; FILING DATE: 20-JUN-1994
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Halluin, Albert P.
 ; REGISTRATION NUMBER: 25,227
 ; REFERENCE/DOCKET NUMBER: 7842-025-228
 ; TELEPHONE: 415-854-3660
 ; TELEFAX: 415-854-3694
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: DNA
 PCT-US94-06997-21

Query Match 57.1%; Score 4; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLL 4
 Db 6 APLL 9

RESULT 19
 US-07-789-184-139
 ; Sequence 139, Application US/07789184
 ; Patent No. 5688768
 ; GENERAL INFORMATION:
 ; APPLICANT: COUGHLIN, SHAUN R.
 ; APPLICANT: SCARBOROUGH, ROBERT M.
 ; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
 ; TITLE OF INVENTION: RELATED PHARMACEUTICALS
 ; NUMBER OF SEQUENCES: 223
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/789,184
 ; FILING DATE: 19911107
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 22000-20502.20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 34-0154
 ; INFORMATION FOR SEQ ID NO: 139:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12 amino acids
 ; TYPE: AMINO ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-07-789-184-139

Query Match 57.1%; Score 4; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLL 4
 Db 1 APLL 4

RESULT 20
 US-08-475-263-139
 ; Sequence 139, Application US/08475263
 ; Patent No. 5759994
 ; GENERAL INFORMATION:
 ; APPLICANT: COUGHLIN, SHAUN R.
 ; APPLICANT: SCARBOROUGH, ROBERT M.
 ; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
 ; TITLE OF INVENTION: RELATED PHARMACEUTICALS
 ; NUMBER OF SEQUENCES: 223
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 2000 Pennsylvania Ave., NW
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20006-1812
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/475,263
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 22000-20502.03
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 887-1500
 ; TELEFAX: (202) 887-0763
 ; TELEX: 90-4030
 ; INFORMATION FOR SEQ ID NO: 139:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-475-263-139

Query Match 57.1%; Score 4; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4
 ||||
 Db 1 AFLL 4

RESULT 21
 US-08-485-886-139
 ; Sequence 139, Application US/08485886
 ; Patent No. 5798248
 ; GENERAL INFORMATION:
 ; APPLICANT: COUGHLIN, SHAUN R.
 ; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
 ; RELATED PHARMACEUTICALS
 ; NUMBER OF SEQUENCES: 223
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/485,886
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/789,184
 ; FILING DATE: 07-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 22000-20502.20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 34-0154
 ; INFORMATION FOR SEQ ID NO: 139:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-485-886-139

Query Match 57.1%; Score 4; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 AFLL 4
 ||||
 Db 1 AFLL 4

RESULT 22
 US-08-477-362-139
 ; Sequence 139, Application US/08477362
 ; Patent No. 5849507
 ; GENERAL INFORMATION:
 ; APPLICANT: COUGHLIN, SHAUN R.
 ; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
 ; RELATED PHARMACEUTICALS
 ; NUMBER OF SEQUENCES: 223
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/477,362
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/789,184
 ; FILING DATE: 07-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 22000-20502.20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 34-0154
 ; INFORMATION FOR SEQ ID NO: 139:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-477-362-139

Query Match 57.1%; Score 4; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4
 ||||
 Db 1 AFLL 4

RESULT 23
 US-08-477-134-139
 ; Sequence 139, Application US/08477134
 ; Patent No. 5856448
 ; GENERAL INFORMATION:
 ; APPLICANT: COUGHLIN, SHAUN R.
 ; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
 ; RELATED PHARMACEUTICALS
 ; NUMBER OF SEQUENCES: 223
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/477,134
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/789,184
 ; FILING DATE: 07-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.

; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-477-134-139

Query Match 57.1%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 AFLL 4
Db 1 AFLL 4

RESULT 24
US-08-750-856A-9
; Sequence 9, Application US/08750856A
; Patent No. 5858672
; GENERAL INFORMATION:
; APPLICANT: SONIGO, PIERRE
; APPLICANT: PANCINO, GIANFRANCO
; APPLICANT: PETERHANS, ERNST
; APPLICANT: BERTONI, GUISEPPE
; TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS AND CORRESPONDING
; TITLE OF INVENTION: PEPTIDE FRAGMENTS FROM THE CAPRINE ARTHRITIS-ENCEPHALITIS
; TITLE OF INVENTION: VIRUS (CEAV) GENOME, AND USES THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBOLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,856A
; FILING DATE: 30-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/07933
; FILING DATE: 28-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBOLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 917-052-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-750-856A-9

Query Match. 57.1%; Score 4; DB 2; Length 12;

Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 4 LYQE 7
Db 9 LYQE 12

RESULT 25
US-08-617-929-17
; Sequence 17, Application US/08617929
; Patent No. 585771
; GENERAL INFORMATION:
; APPLICANT: KUMAZAWA, Toshiaki
; TITLE OF INVENTION: ANTIGENIC PEPTIDE COMPOUND AND
; TITLE OF INVENTION: IMMUNOASSAY
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,929
; FILING DATE: 24-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01823
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6/207695
; FILING DATE: 31-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5/272864
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 77384/109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-617-929-17

Query Match 57.1%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 3 LLYQ 6
Db 9 LLYQ 12

RESULT 26
US-08-473-489A-139
; Sequence 139, Application US/08473489A
; Patent No. 6024936
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.

APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
TITLE OF INVENTION: RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,489A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/789,184
FILING DATE: 1991-11-07
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-473-489A-139

Query Match 57.1%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 AFLL 4
Db 1 AFLL 4

RESULT 27
US-08-485-695-139
Sequence 139, Application US/08485695
Patent No. 6124101
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
TITLE OF INVENTION: RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,695
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-695-139

Query Match 57.1%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 AFLL 4
Db 1 AFLL 4

RESULT 28
US-08-018-760-139
Sequence 139, Application US/08018760
Patent No. 6197541
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
TITLE OF INVENTION: RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/018,760
FILING DATE: 17-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-018-760-139

Query Match 57.1%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AFLL 4
Db 1 AFLL 4

RESULT 29
US-08-064-400B-16
; Sequence 16, Application US/08064400B
; Patent No. 5559028
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E.
; TITLE OF INVENTION: Regulation of Antigen Presentation
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/064,400B
FILING DATE: May 19, 1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH93-01
TELEPHONE: 207-363-0558
TELEFAX: 207-363-0528
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-064-400B-16

Query Match 57.1%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LYOE 7
Db 1 LYOE 4

RESULT 30
US-08-291-601-1
; Sequence 1, Application US/08291601
; Patent No. 5679527
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE STRUCTURE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: US

ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,601
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9401M
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-291-601-1

Query Match 57.1%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYOE 7
Db 1 LYOE 4

RESULT 31
US-08-291-601-2
; Sequence 2, Application US/08291601
; Patent No. 5679527
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE STRUCTURE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: US
; ZIP: 03911

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,601
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9401M
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-291-601-2

Query Match 57.1%; Score 4; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQE 7
 ||||
 Db 1 LYQE 4

RESULT 32
 US-08-291-601-3
 ; Sequence 3, Application US/08291601
 ; Patent No. 5679527
 ; GENERAL INFORMATION:
 ; APPLICANT: Humphreys, Robert E.
 ; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE STRUCTURE
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kevin M. Farrell, P.C.
 ; STREET: P.O. Box 999
 ; CITY: York Harbor
 ; STATE: Maine
 ; COUNTRY: US
 ; ZIP: 03911
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/291,601
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Farrell, Kevin M.
 ; REGISTRATION NUMBER: 35,505
 ; REFERENCE/DOCKET NUMBER: REH-9401M
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (207) 363-0558
 ; TELEFAX: (207) 363-0528
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-291-601-3

Query Match 57.1%; Score 4; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQE 7
 ||||
 Db 1 LYQE 4

RESULT 33
 US-09-227-357-439
 ; Sequence 439, Application US/09227357
 ; Patent No. 6342581
 ; GENERAL INFORMATION:
 ; APPLICANT: Fischer et al.
 ; TITLE OF INVENTION: 123 Human Secreted Proteins
 ; FILE REFERENCE: PZ010P1
 ; CURRENT APPLICATION NUMBER: US/09/227,357
 ; CURRENT FILING DATE: 1999-01-08
 ; EARLIER APPLICATION NUMBER: PCT/US98/13684
 ; EARLIER FILING DATE: 1998-07-07
 ; EARLIER APPLICATION NUMBER: 60/051,926
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,793
 ; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,925
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,929
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,803
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,732
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,931
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,932
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,916
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,930
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,918
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,920
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,733
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,795
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,919
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,928
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/055,722
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,723
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,948
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,949
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,953
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,950
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,947
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,964
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/056,360
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,684
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,984
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/055,954
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/058,785
 ; EARLIER FILING DATE: 1997-09-12
 ; EARLIER APPLICATION NUMBER: 60/058,664
 ; EARLIER FILING DATE: 1997-09-12
 ; EARLIER APPLICATION NUMBER: 60/058,660
 ; EARLIER FILING DATE: 1997-09-12
 ; EARLIER APPLICATION NUMBER: 60/058,661
 ; EARLIER FILING DATE: 1997-09-12
 ; NUMBER OF SEQ ID NOS: 672
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 439
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-227-357-439

Query Match 57.1%; Score 4; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLYY 5


```

Db      |||||
        7 FLLY 10

RESULT 34
US-08-637-759B-246
; Sequence 246, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,759B
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RIMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-637-759B-246

Query Match      57.1%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AFLL 4
Db      |||||
        3 AFLL 6

RESULT 35
US-08-637-759B-246
; Sequence 246, Application US/08637759B
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia

Query Match      57.1%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AFLL 4
Db      |||||
        3 AFLL 6

RESULT 36
US-09-201-945-246
; Sequence 246, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,945
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/637,759
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284

```

; PRIOR FILING DATE: 1998-02-06

```
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-340-620A-47

Query Match          57.1%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AFLL 4
        ||||
Db      13 AFLL 16

RESULT 40
PCT-US95-02576-42
; Sequence 42, Application PC/TUS9502576
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02576
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120CPPC
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-02576-42

Query Match          57.1%; Score 4; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AFLL 4
        ||||
Db      11 AFLL 14

RESULT 41
US-08-401-512-64
; Sequence 64, Application US/08401512
; Patent No. 5599673
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
```

```
; APPLICANT: Curran, Mark E.
; APPLICANT: Wang, Qing
; TITLE OF INVENTION: Long QT Syndrome Genes
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3917
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/401,512
; FILING DATE: 09-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 19780-113879
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4848
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-401-512-64

Query Match          57.1%; Score 4; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AFLL 4
        ||||
Db      13 AFLL 16

RESULT 42
US-08-244-116B-9
; Sequence 9, Application US/08244116B
; Patent No. 5763159
; GENERAL INFORMATION:
; APPLICANT: Simmonds, Peter
; APPLICANT: Chan, Shiu-Wan
; APPLICANT: Yap, Peng L.
; TITLE OF INVENTION: Hepatitis-C Virus Testing
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson, P.A.
; STREET: 1211 East Morehead Street
; CITY: Charlotte
; STATE: No. 5763159th Carolina
; COUNTRY: United States
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,116B
; FILING DATE: 15-JUL-1994
; CLASSIFICATION: 435
```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02143
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 1749-125
TELEPHONE: 704-377-1561
TELEFAX: 704-334-2014
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Hepatitis-C virus
US-08-244-116B-9

Query Match 57.1%; Score 4; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 4 LYQE 7
|
|
|
|
Db 11 LYQE 14

RESULT 43
US-09-226-012-99
Sequence 99, Application US/09226012
Patent No. 6207383
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Spilawski, Igor
TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
FILE REFERENCE: 2323-136
CURRENT APPLICATION NUMBER: US/09/226,012
CURRENT FILING DATE: 1999-01-06
EARLIER APPLICATION NUMBER: 09/122,847
EARLIER FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 99
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-09-226-012-99

Query Match 57.1%; Score 4; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 AFLL 4
|
|
|
|
Db 13 AFLL 16

RESULT 44
US-08-507-124-5
Sequence 5, Application US/08507124
Patent No. 5670618
GENERAL INFORMATION:
APPLICANT: McKenzie, Maureen A.
TITLE OF INVENTION: Insulin-Like Peptide
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch

STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/507,124
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/956,342
FILING DATE: 05-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1828-102P
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Geodia cydonium
FEATURE:
NAME/KEY: Peptide
LOCATION: 1-19
OTHER INFORMATION: /label= peptide
OTHER INFORMATION: /note= "Amino-terminal sequence of insulin-like
peptide from Geodia cydonium."
US-08-507-124-5

Query Match 57.1%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 4 LYQE 7
|
|
|
|
Db 12 LYQE 15

RESULT 45
US-08-451-472-12
Sequence 12, Application US/08451472
Patent No. 5770192
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: BIOLOGICAL CONTROL AGENTS
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 5770192th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

;/ CURRENT APPLICATION DATA: US/08/451,472
;/ FILING DATE:
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/117,125
;/ FILING DATE: 24-NOV-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Mary J Wilson
;/ REGISTRATION NUMBER: 32,955
;/ REFERENCE/DOCKET NUMBER: 117-187
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (703) 816 4000
;/ TELEFAX: (703) 816 4100
;/ TELEX: 200797 NIXN UR
;/ INFORMATION FOR SEQ ID NO: 12:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 19 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-451-472-12

Query Match 57.1%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
Db 9 AFLL 12

RESULT 46
US-08-451-472-46
;/ Sequence 46, Application US/08451472
;/ Patent No. 5770192
;/ GENERAL INFORMATION:
;/ APPLICANT:
;/ TITLE OF INVENTION: BIOLOGICAL CONTROL AGENTS
;/ NUMBER OF SEQUENCES: 73
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Nixon & Vanderhye PC
;/ STREET: 8th Floor, 1100 No. 5770192th Glebe Road
;/ CITY: Arlington
;/ STATE: Virginia
;/ COUNTRY: USA
;/ ZIP: 22201-4714
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ FILING DATE: US/08/451,472
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/117,125
;/ FILING DATE: 24-NOV-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Mary J Wilson
;/ REGISTRATION NUMBER: 32,955
;/ REFERENCE/DOCKET NUMBER: 117-187
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (703) 816 4000
;/ TELEFAX: (703) 816 4100
;/ TELEX: 200797 NIXN UR
;/ INFORMATION FOR SEQ ID NO: 46:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 19 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide

US-08-451-472-46

Query Match 57.1%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
Db 9 AFLL 12

RESULT 47
US-08-928-213B-35
;/ Sequence 35, Application US/08928213B
;/ Patent No. 6238905
;/ GENERAL INFORMATION:
;/ APPLICANT: McHenry, Charles S.
;/ Cull, Millard G.
;/ TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III
;/ HOLOENZYME
;/ NUMBER OF SEQUENCES: 195
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: MEDLEN & CARROLL, LLP
;/ STREET: 220 Montgomery Street, Suite 2200
;/ CITY: San Francisco
;/ STATE: CA
;/ COUNTRY: USA
;/ ZIP: 94104
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/928,213B
;/ FILING DATE: 12-Sep-1997
;/ CLASSIFICATION: <Unknown>
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: MacKnight, Kamrin T.
;/ REGISTRATION NUMBER: 38,230
;/ REFERENCE/DOCKET NUMBER: ENZYCO-02550
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 415-705-8410
;/ TELEFAX: 415-397-8338
;/ INFORMATION FOR SEQ ID NO: 35:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 19 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: not relevant
;/ TOPOLOGY: not relevant
;/ MOLECULE TYPE: protein
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 35:
;/ US-08-928-213B-35

Query Match 57.1%; Score 4; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQE 7
Db 10 LYQE 13

RESULT 48
US-09-486-580A-4
;/ Sequence 4, Application US/09486580A
;/ Patent No. 6329340
;/ GENERAL INFORMATION:
;/ APPLICANT: GENSET SA
;/ TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DNAC
;/ TITLE OF INVENTION: COMPOSITION CONTAINING SAME AND DIAGNOSTIC AND
;/ THERAPEUTIC APPLICATIONS

;/ NUMBER OF SEQUENCES: 6
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Knobbe, Martens, Olson & Bear
;/ STREET: 550 West C Street
;/ CITY: San Diego
;/ STATE: California
;/ COUNTRY: USA
;/ ZIP: 92101
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/486,580A
;/ FILING DATE: FEBRUARY 25, 2000
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Hart, Daniel
;/ REGISTRATION NUMBER: 40,637
;/ REFERENCE/DOCKET NUMBER: GENSET.064C1
;/ INFORMATION FOR SEQ ID NO: 4:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 19 AMINO ACIDS
;/ TYPE: AMINO ACID
;/ STRANDEDNESS: SINGLE
;/ TOPOLOGY: LINEAR
;/ MOLECULE TYPE: SIGNAL PEPTIDE
;/ ORIGINAL SOURCE:
;/ ORGANISM: Homo sapiens
;/ US-09-486-580A-4

Query Match 57.1%; Score 4; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLL 4
Db 9 APLL 12

RESULT 49
US-08-617-929-1
;/ Sequence 1, Application US/08617929
;/ Patent No. 5885771
;/ GENERAL INFORMATION:
;/ APPLICANT: KUMAZAWA, Toshiaki
;/ TITLE OF INVENTION: ANTIGENIC PEPTIDE COMPOUND AND
;/ INFORMATION: IMMUNOASSAY
;/ NUMBER OF SEQUENCES: 42
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Foley & Lardner
;/ STREET: 3000 K Street, N.W., Suite 500
;/ CITY: Washington
;/ STATE: D.C.
;/ COUNTRY: USA
;/ ZIP: 20007-5109
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/617,929
;/ FILING DATE: 24-APR-1996
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: WO PCT/JP94/01823
;/ FILING DATE: 28-OCT-1994
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: JP 6/207695
;/ FILING DATE: 31-AUG-1994
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: JP 5/272864

;/ FILING DATE: 29-OCT-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Saxe, Bernhard D.
;/ REGISTRATION NUMBER: 28,665
;/ REFERENCE/DOCKET NUMBER: 77384/109
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (202)672-5300
;/ TELEFAX: (202)672-5399
;/ TELEX: 904136
;/ INFORMATION FOR SEQ ID NO: 1:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 20 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ US-08-617-929-1

Query Match 57.1%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQE 7
Db 14 LYQE 17

RESULT 50
US-08-460-576-15
;/ Sequence 15, Application US/08460576
;/ Patent No. 6033903
;/ GENERAL INFORMATION:
;/ APPLICANT: SISK, William P.
;/ TITLE OF INVENTION: A METHOD OF EXPRESSING AND SECRETING
;/ INFORMATION: SOLUBLE EXTRACELLULAR DOMAINS OF HUMAN GONADOTROPIN
;/ NUMBER OF SEQUENCES: 18
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: BROWDY AND NEIMARK
;/ STREET: 419 Seventh Street, N.W., Suite 300
;/ CITY: Washington
;/ STATE: D.C.
;/ COUNTRY: USA
;/ ZIP: 20004
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/460,576
;/ FILING DATE:
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: YUN, Allen C.
;/ REGISTRATION NUMBER: 37,971
;/ REFERENCE/DOCKET NUMBER: SISK-1
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 202-628-5197
;/ TELEFAX: 202-737-3528
;/ TELEX: 248633
;/ INFORMATION FOR SEQ ID NO: 15:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 20 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-460-576-15

Query Match 57.1%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4
|
|
|
Db 5 AFLL 8

RESULT 51

US-09-439-313-500
; Sequence 500, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 500
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-439-313-500

Query Match 57.1%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4
|
|
|
Db 4 AFLL 7

RESULT 52

US-07-657-769B-14
; Sequence 14, Application US/07657769B
; Patent No. 5256766
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAIN R.
; TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IRELL & MANELLA
; STREET: 545 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/657,769B
; FILING DATE: 19910219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 2000-0502.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-657-769B-14

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
|
|
|
Db 2 FLL 4

RESULT 53

US-07-657-769B-54
; Sequence 54, Application US/07657769B
; Patent No. 5256766
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAIN R.
; TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IRELL & MANELLA
; STREET: 545 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/657,769B
; FILING DATE: 19910219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0502.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-657-769B-54

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
|
|
|
Db 2 FLL 4

RESULT 54

```

US-08-405-933-4
; Sequence 4, Application US/08405933
; Patent No. 5516889
; GENERAL INFORMATION:
; APPLICANT: Hollenberg, Morley D.
; APPLICANT: Matsoukas, John M.
; APPLICANT: Moore, Graham J.
; TITLE OF INVENTION: Synthetic Thrombin Receptor Peptides
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: Washington & Prince Streets, P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,933
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,643
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dillahunty, Mary Ann
; REGISTRATION NUMBER: 34,576
; REFERENCE/DOCKET NUMBER: 028722-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-8275
; TELEFAX: (415)854-8275
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
US-08-405-933-4

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db 1 FLL 3

RESULT 55
US-08-405-933-6
; Sequence 6, Application US/08405933
; Patent No. 5516889
; GENERAL INFORMATION:
; APPLICANT: Hollenberg, Morley D.
; APPLICANT: Matsoukas, John M.
; APPLICANT: Moore, Graham J.
; TITLE OF INVENTION: Synthetic Thrombin Receptor Peptides
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: Washington & Prince Streets, P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,933
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,643
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dillahunty, Mary Ann
; REGISTRATION NUMBER: 34,576
; REFERENCE/DOCKET NUMBER: 028722-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-8275
; TELEFAX: (415)854-8275

```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,933
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,643
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dillahunty, Mary Ann
; REGISTRATION NUMBER: 34,576
; REFERENCE/DOCKET NUMBER: 028722-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-7400
; TELEFAX: (415)854-8275
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= Arg
; OTHER INFORMATION: /note= "Arg is acetylated"
US-08-405-933-6

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db 1 FLL 3

RESULT 56
US-08-405-933-14
; Sequence 14, Application US/08405933
; Patent No. 5516889
; GENERAL INFORMATION:
; APPLICANT: Hollenberg, Morley D.
; APPLICANT: Matsoukas, John M.
; APPLICANT: Moore, Graham J.
; TITLE OF INVENTION: Synthetic Thrombin Receptor Peptides
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: Washington & Prince Streets, P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,933
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,643
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dillahunty, Mary Ann
; REGISTRATION NUMBER: 34,576
; REFERENCE/DOCKET NUMBER: 028722-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-7400
; TELEFAX: (415)854-8275

```


; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-405-933-14

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db 2 FLL 4

RESULT 57
US-08-405-933-38
; Sequence 38, Application US/08405933
; Patent No. 5516889
; GENERAL INFORMATION:
; APPLICANT: Hollenberg, Morley D.
; APPLICANT: Matsoukas, John M.
; APPLICANT: Moore, Graham J.
; TITLE OF INVENTION: Synthetic Thrombin Receptor Peptides
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: Washington & Prince Streets, P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,933
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,643
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dillahunty, Mary Ann
; REGISTRATION NUMBER: 34,576
; REFERENCE/DOCKET NUMBER: 028722-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-7400
; TELEFAX: (415)854-8275
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Phe
; OTHER INFORMATION: /note= "Phe is n-propionyl Phe"

US-08-405-933-38
Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db 1 FLL 3

RESULT 58
US-08-405-933-39
; Sequence 39, Application US/08405933
; Patent No. 5516889
; GENERAL INFORMATION:
; APPLICANT: Hollenberg, Morley D.
; APPLICANT: Matsoukas, John M.
; APPLICANT: Moore, Graham J.
; TITLE OF INVENTION: Synthetic Thrombin Receptor Peptides
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: Washington & Prince Streets, P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,933
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,643
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dillahunty, Mary Ann
; REGISTRATION NUMBER: 34,576
; REFERENCE/DOCKET NUMBER: 028722-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-7400
; TELEFAX: (415)854-8275
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= Arg
; OTHER INFORMATION: /note= "Arg is Arg-NH3"

US-08-405-933-39
Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db 1 FLL 3

RESULT 59
US-07-789-184-35
; Sequence 35, Application US/07789184
; Patent No. 5688768
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND

US-08-405-933-39
Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db 1 FLL 3

```

; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,184
; FILING DATE: 19911107
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr,
; OTHER INFORMATION: S-Me Mpr or Mba."
; US-07-789-184-35

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4
Db 2 FLL 4

RESULT 60
US-07-789-184-109
; Sequence 109, Application US/07789184
; Patent No. 5688768
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,184
; FILING DATE: 19911107
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is L-NH2."
; US-07-789-184-117

Query Match 42.9%; Score 3; DB 1; Length 4;

```

```

; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-789-184-109

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4
Db 2 FLL 4

RESULT 61
US-07-789-184-117
; Sequence 117, Application US/07789184
; Patent No. 5688768
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,184
; FILING DATE: 19911107
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is L-NH2."
; US-07-789-184-117

Query Match 42.9%; Score 3; DB 1; Length 4;

```

```
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4
Db 2 FLL 4

RESULT 62
US-08-549-008-29
; Sequence 29, Application US/08549008
; Patent No. 5714342
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Protease in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/549,008
; FILING DATE: 27-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,383
; FILING DATE: 28-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 016865-000110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-549-008-29

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3
Db 2 AFL 4

RESULT 63
US-08-475-263-35
; Sequence 35, Application US/08475263
; Patent No. 5759994
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,263
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
```

```
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,263
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr,
; OTHER INFORMATION: S-Me Mpr or Mba."
; US-08-475-263-35

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4
Db 2 FLL 4

RESULT 64
US-08-475-263-109
; Sequence 109, Application US/08475263
; Patent No. 5759994
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,263
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
```

```
/
/ REGISTRATION NUMBER: 29,959
/ REFERENCE/DOCKET NUMBER: 22000-20502.03
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 887-1500
/ TELEFAX: (202) 887-0763
/ TELEX: 90-4030
/ INFORMATION FOR SEQ ID NO: 109:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-475-263-109

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db |||
2 FLL 4

RESULT 65
US-08-475-263-117
/ Sequence 117, Application US/08475263
/ Patent No. 5759994
/ GENERAL INFORMATION:
/ APPLICANT: COUGHLIN, SHAUN R.
/ TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
/ TITLE OF INVENTION: RELATED PHARMACEUTICALS
/ NUMBER OF SEQUENCES: 223
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORRISON & FOERSTER
/ STREET: 2000 Pennsylvania Ave., NW
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20006-1812
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/475,263
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MURASHIGE, KATE H.
/ REGISTRATION NUMBER: 29,959
/ REFERENCE/DOCKET NUMBER: 22000-20502.03
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 887-1500
/ TELEFAX: (202) 887-0763
/ TELEX: 90-4030
/ INFORMATION FOR SEQ ID NO: 117:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 4
/ OTHER INFORMATION: /note= "This position is L-NH2."
/ US-08-475-263-117

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 FLL 4
Db |||
2 FLL 4

RESULT 66
US-08-205-511-1
/ Sequence 1, Application US/08205511
/ Patent No. 5792451
/ GENERAL INFORMATION:
/ APPLICANT: Sarubbi, Donald J.
/ APPLICANT: Leone-Bay, Andrea
/ APPLICANT: Paton, Duncan R.
/ TITLE OF INVENTION: ORAL DRUG DELIVERY COMPOSITIONS AND
/ TITLE OF INVENTION: METHODS
/ NUMBER OF SEQUENCES: 1
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Darby & Darby, P.C.
/ STREET: 805 Third Avenue
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10022
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/205,511
/ FILING DATE: 02-MAR-1994
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Robinson, Joseph R.
/ REGISTRATION NUMBER: 33,448
/ REFERENCE/DOCKET NUMBER: 1946/09323
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-527-7700
/ TELEFAX: 212-753-6237
/ TELEX: 236687
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 1
/ OTHER INFORMATION: /product= "ACETYL-PHENYLALANINE"
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 4
/ OTHER INFORMATION: /product= "ARGININE ALDEHYDE"
/ US-08-205-511-1

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db |||
1 FLL 3

RESULT 67
US-08-485-886-35
/ Sequence 35, Application US/08485886
/ Patent No. 5798248
/ GENERAL INFORMATION:
/ APPLICANT: COUGHLIN, SHAUN R.
/ APPLICANT: SCARBOROUGH, ROBERT M.
```

```

; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,886
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr,
; OTHER INFORMATION: S-Me Mpr or Mba."
; US-08-485-886-35

```

```

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2 FLL 4
Db 2 FLL 4

```

```

RESULT 68
US-08-485-886-109
; Sequence 109, Application US/08485886
; Patent No. 5798248
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,886
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-485-886-109

```

```

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2 FLL 4
Db 2 FLL 4

```

```

RESULT 69
US-08-485-886-117
; Sequence 117, Application US/08485886
; Patent No. 5798248
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,886
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids

```

```

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is L-NH2."
; US-08-485-886-117

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db 2 FLL 4

RESULT 70
US-08-477-362-35
; Sequence 35, Application US/08477362
; Patent No. 5849507
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr,
; OTHER INFORMATION: S-Me Mpr or Mba."
; US-08-477-362-35

Query Match 42.9%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4

```

```

Db 2 FLL 4

RESULT 71
US-08-477-362-109
; Sequence 109, Application US/08477362
; Patent No. 5849507
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-477-362-109

Query Match 42.9%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db 2 FLL 4

RESULT 72
US-08-477-362-117
; Sequence 117, Application US/08477362
; Patent No. 5849507
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California

```

```

; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,362
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is L-NH2."
; US-08-477-362-117

Query Match 42.9%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4
Db 2 FLL 4

RESULT 73
US-08-188-583-37
; Sequence 37, Application US/08188583
; Patent No. 5851813
; GENERAL INFORMATION:
; APPLICANT: Destroiers, Ronald C.
; TITLE OF INVENTION: PRIMATE LENTIVIRUS VACCINES
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,583
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/727,494
; FILING DATE: July 9, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/551,945
; FILING DATE: July 12, 1990

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: Reg. No. 5851813 29,066
; REFERENCE/DOCKET NUMBER: 00246/079002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-188-583-37

Query Match 42.9%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6
Db 1 LYQ 3

RESULT 74
US-08-477-134-35
; Sequence 35, Application US/08477134
; Patent No. 5856448
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,134
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr,
; OTHER INFORMATION: S-Me Mpr or Mba."

```

US-08-477-134-35

Query Match 42.9%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
|||
Db 2 FLL 4

RESULT 75

US-08-477-134-109
; Sequence 109, Application US/08477134
; Patent No. 5856448
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSES: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,134
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-477-134-109

Query Match 42.9%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
|||
Db 2 FLL 4

Search completed: November 25, 2003, 20:30:04
Job time : 6.65698 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 5.48837 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-29

Perfect score: 8

Sequence: 1 RGPPFLV 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	75.0	15	2	P80452
2	4	50.0	15	2	A56970
3	3	37.5	6	2	A61049
4	3	37.5	8	2	A61328
5	3	37.5	9	2	S15850
6	3	37.5	9	2	S66419
7	3	37.5	10	2	S26506
8	3	37.5	11	2	S33782
9	3	37.5	11	2	PA0028
10	3	37.5	11	2	P00029
11	3	37.5	11	2	P33098
12	3	37.5	11	4	P03290
13	3	37.5	11	4	PC2391
14	3	37.5	11	4	PC2392
15	3	37.5	11	4	PC2393
16	3	37.5	12	2	S11238
17	3	37.5	12	2	S67528
18	3	37.5	12	2	P00696
19	3	37.5	12	2	S43957
20	3	37.5	12	2	P00046
21	3	37.5	12	4	JK0315
22	3	37.5	13	2	P00700
23	3	37.5	13	2	A61544
24	3	37.5	13	2	S33273
25	3	37.5	13	2	C53275
26	3	37.5	14	2	B61309
27	3	37.5	14	2	S09721
28	3	37.5	14	2	B28018
29	3	37.5	14	2	S36678
30	3	37.5	15	2	LFTWL
31	3	37.5	15	2	A28497
32	3	37.5	15	2	PW0004
33	3	37.5	15	2	S20410
34	3	37.5	15	2	PA0024
35	3	37.5	15	2	P80455
36	3	37.5	16	2	A42411
37	3	37.5	16	2	PH1790
38	3	37.5	16	2	I46275
39	3	37.5	16	2	S78415
40	3	37.5	17	2	I78870
41	3	37.5	17	2	G85956
42	3	37.5	18	2	S09722
43	3	37.5	18	2	S09723
44	3	37.5	18	2	S13974
45	3	37.5	18	2	S40502
46	3	37.5	19	1	EWSMCN
47	3	37.5	19	2	T30825
48	3	37.5	20	2	S65339
49	3	37.5	20	2	S61278
50	3	37.5	20	2	S09720
51	3	37.5	20	2	B30208
52	3	37.5	20	2	S58382
53	3	37.5	20	2	B53283
54	3	37.5	20	2	A60801
55	2	25.0	3	3	PQ0010
56	2	25.0	4	2	B43848
57	2	25.0	4	2	T46627
58	2	25.0	4	2	S53508
59	2	25.0	4	2	PT0675
60	2	25.0	4	2	S47552
61	2	25.0	5	2	C41225
62	2	25.0	5	2	E60274
63	2	25.0	5	2	B37988
64	2	25.0	5	2	JS0319
65	2	25.0	5	2	PT0267
66	2	25.0	5	2	PT0520
67	2	25.0	5	2	PT0525
68	2	25.0	5	2	PT0608
69	2	25.0	5	2	PT0669
70	2	25.0	5	2	PT0695
71	2	25.0	5	2	PT0700
72	2	25.0	6	2	A60986
73	2	25.0	6	2	PQ0008
74	2	25.0	6	2	I51317
75	2	25.0	6	2	I51434
76	2	25.0	6	2	A41346
77	2	25.0	7	2	S71867
78	2	25.0	7	2	S71870
79	2	25.0	7	2	PH1408
80	2	25.0	7	2	PQ0663
81	2	25.0	7	2	A44428
82	2	25.0	7	2	A25269
83	2	25.0	7	2	A30812
84	2	25.0	7	2	PN0150
85	2	25.0	7	2	PQ0728
86	2	25.0	7	2	A33098
87	2	25.0	7	2	PT0246
88	2	25.0	7	2	S42620
89	2	25.0	7	2	E39332
90	2	25.0	7	2	PT0515
91	2	25.0	7	2	PT0620
92	2	25.0	7	2	PT0556
93	2	25.0	7	2	PT0542
94	2	25.0	7	2	PT0676
95	2	25.0	7	2	PT0671
96	2	25.0	7	2	FX0008
97	2	25.0	7	2	B48394
98	2	25.0	7	4	I55382
99	2	25.0	7	4	S15597
100	2	25.0	8	2	PH1407

leu leader peptide
neurotensin-relate
chlorophyll a/b-bi
protein kinase IEC
protein QA300050 -
superoxide dismuta
myosin light chain
T cell receptor al
hemoglobin beta-x
ribosomal protein
gene RB1 protein -
hypothetical prote
2S albumin small c
2S albumin small c
chlorophyll a/b-bi
20-alpha-hydroxyst
cinnamycin - Strep
RNA polymerase bet
immunodeficiency v
nikkomycin synthes
2S albumin small c
hypothetical prote
major cat allergen
acrosome stabilizi
angiotensin-conver
cell surface adhes
hypothetical prote
starvation-induced
T-cell receptor be
ubiquitin - rat
copper resistance
major protein anti
acid proteinase li
subesophageal gang
Ig heavy chain CRD
Ig kappa chain V-I
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be
N-formyl oligopept
angiotensin-conver
bHtH transcription
H4 histone - Afric
T-cell receptor ga
glutathione transf
glutathione transf
Ig heavy chain V r
membrane protein -
platelet aggregati
sex pheromone cAM3
sex pheromone cCF1
omega-gliadine 1,
unidentified 5.0/1
244K exantigen -
Ig heavy chain CRD
aggreccan - bovine
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be
glucuronosyltransf
major fat-globule
hypothetical pepti
orf 4 rara 5'-regi
Ig heavy chain V r

ALIGNMENTS

```

RESULT 1
PS0452
32K protein 3306 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C:Accession: PS0452
R:Tsugita, A.; Miyatake, N.
submitted to JIPID, April 1993
A:Reference number: PS0208
A:Accession: PS0452
A:Molecule type: protein
A:Residues: 1-15 <TSU>
A:Experimental source: bran, strain Nihonbare
C:Comment: molecular weight 32K, pI 5.3.

Query Match          75.0%; Score 6; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GPPFIL 7
      |||||
Db      5 GPPFIL 10

RESULT 2
A56970
GLYMA1 - soybean (fragment)
C:Species: Glycine max (soybean)
C:Date: 02-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 08-Sep-1995
C:Accession: A56970
R:Codina, M.R.
submitted to the Protein Sequence Database, September 1995
A:Reference number: A56970
A:Accession: A56970
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <COD>

Query Match          50.0%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGPF 4
      |||||
Db     11 RGPF 14

RESULT 3
A61049
halo-toxin - Pseudomonas syringae pv. mori
C:Species: Pseudomonas syringae pv. mori
A:Note: host mulberry tree
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Jan-1997
C:Accession: A61049
R:Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, M.;
Chem. Lett. 00, 679-680, 1989
A:Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas syri
A:Reference number: A61049
A:Accession: A61049
A:Molecule type: protein
A:Residues: 1-6 <KXJ>
A:Note: sequence confirmed by synthesis
C:Comment: This toxin is one of the etiological agents of halo bright disease in mulberry
C:Keywords: toxin

Query Match          37.5%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PFP 5

```

```

Db      |||
      1 PFP 3

```

```

RESULT 4
A61328
trypsin (EC 3.4.21.4) precursor - minke whale (fragment)
C:Species: Balenoptera acutorostrata (minke whale, lesser rorqual)
C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C:Accession: A61328
R:Bricteux-Gregoire, S.; Schvyns, R.; Florin, M.; Emmens, M.; Welling, G.W.; Beintema
Biochim. Biophys. Acta 386, 244-255, 1975
A:Title: N-terminal amino acid sequence of trypsinogen from the lesser rorqual, Balae
creas.
A:Reference number: A61328; MUID:75146765; PMID:1125273
A:Accession: A61328
A:Molecule type: protein
A:Residues: 1-8 <BRI>
C:Keywords: hydrolase; protein digestion; serine proteinase; zymogen
Fi-8/Domain: activation peptide #status experimental <APT>

Query Match          37.5%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPI 6
      |||
Db      1 PPI 3

RESULT 5
S15850
vitamin D3 26-monoxygenase (EC 1.14.14.-) cytochrome P450 27 - pig (fragment)
N:Alternate names: cytochrome P450(26); vitamin D3 26-hydroxylase
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 05-Mar-1999
C:Accession: S15850
R:Berghman, T.; Postlind, H.
Biochem. J. 276, 427-432, 1991
A:Title: Characterization of mitochondrial cytochromes P-450 from pig kidney and liver
A:Reference number: S15850; MUID:91264797; PMID:2049072
A:Accession: S15850
A:Molecule type: protein
A:Residues: 1-9 <BIO>
C:Genetics:
A:Gene: CYP27
C:Superfamily: unassigned cytochrome P450; cytochrome P450 homology
C:Keywords: heme; mitochondrion; monooxygenase; oxidoreductase; transmembrane protein

Query Match          37.5%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GPF 4
      |||
Db      6 GPF 8

RESULT 6
S66419
tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)
C:Species: Spinacia oleracea (spinach)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
C:Accession: S66419
R:Kuwabara, T.
FEBS Lett. 371, 195-198, 1995
A:Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric proteinase of
A:Reference number: S66419; MUID:95402209; PMID:7672127
A:Accession: S66419
A:Molecule type: protein
A:Residues: 1-9 <KUN>

Query Match          37.5%; Score 3; DB 2; Length 9;

```

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0;

QY 5 PTL 7
|||
Db 2 PTL 4

RESULT 7
S26506
collagen alpha 1(VI) chain - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Dec-1998
C/Accession: S26506
R/Jander, R.; Rautenberg, J.; Glanville, R.W.
Eur. J. Biochem. 133, 39-46, 1983
A/Title: Further characterization of the three polypeptide chains of bovine and human stromelysin
A/Reference number: S26506; MUID:83209648; PMID:6852033
A/Accession: S26506
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <JAN>
C/Keywords: hydroxyproline
F/9/Modified site: hydroxyproline (Pro) #status experimental

Query Match 37.5%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0;

QY 1 RGP 3
|||
Db 6 RGP 8

RESULT 8
S33782
acetolactate synthase (EC 4.1.3.18) small chain, valine-sensitive - Serratia marcescens
C/Species: Serratia marcescens
C/Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C/Accession: S33782
R/Jiang, J.H.; Kim, S.S.
Biochim. Biophys. Acta 1157, 178-184, 1993
A/Title: Purification and characterization of the valine sensitive acetolactate synthase
A/Reference number: S33781; MUID:93283409; PMID:8507653
A/Accession: S33782
A/Molecule type: protein
A/Residues: 1-11 <YAN>
A/Experimental source: ATCC 25419
C/Complex: heterotetramer; two small and two large chains
C/Function:
A/Description: catalyzes the condensation of pyruvate and alpha-ketobutyrate to form alpha-ketoglutarate
A/Pathway: valine, leucine, and isoleucine biosynthesis
A/Note: this isoenzyme exhibits homotropic allosterism with pyruvate
C/Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein; heme

Query Match 37.5%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0;

QY 6 ILV 8
|||
Db 2 ILV 4

RESULT 9
PA0028
protein OA300042 - Arabidopsis thaliana (fragment)
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C/Accession: PA0028
R/Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A/Description: Separation and characterization of Arabidopsis proteins by two-dimensional

A/Reference number: PA0001
A/Accession: PA0028
A/Molecule type: protein
A/Residues: 1-11 <KAM>
A/Experimental source: seed
C/Keywords: seed

Query Match 37.5%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0;

QY 3 PFP 5
|||
Db 6 PFP 8

RESULT 10
PU0029
33K protein 3218 - rice (strain Nohonbare) (fragment)
C/Species: Oryza sativa (rice)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C/Accession: PU0029
R/Tsugita, A.; Miyatake, N.
submitted to JIPID, April 1993
A/Reference number: FS0208
A/Accession: PU0029
A/Molecule type: protein
A/Residues: 1-11 <TSU>
A/Experimental source: bran
C/Comment: molecular weight 33K, pI 6.0.

Query Match 37.5%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0;

QY 2 GPF 4
|||
Db 5 GPF 7

RESULT 11
I33098
173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C/Species: Plasmodium falciparum
C/Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C/Accession: I33098
R/Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A/Reference number: A33098
A/Accession: I33098
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-11 <NIC>

Query Match 37.5%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0;

QY 4 FPI 6
|||
Db 9 FPI 11

RESULT 12
PC2390
Trichozoin I - fungus (Trichoderma harzianum)
C/Species: Trichoderma harzianum
C/Date: 17-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Oct-2000
C/Accession: PC2390
R/Iida, A.; Saneoka, M.; Wada, S.; Fujita, T.; Tanaka, H.; Enoki, A.; Fuse, G.; Kana
Chem. Pharm. Bull. 43, 392-397, 1995
A/Title: Fungal metabolites. XVIII. New membrane-modifying peptides, trichorozins I-I
A/Reference number: PC2390; MUID:95292356; PMID:7539721

A:Accession: PC2390
A:Status: unencoded polypeptide
A:Molecule type: protein
A:Residues: 1-11 <IID>
C:Comment: This peptide exhibits voltage-dependent ion channel-like activity in lipid bilayers
C:Keywords: antibiotic; unencoded polypeptide
F:1/Modified site: acetylated amino end #status experimental
F:1,5,9/Modified site: 2-amino-2-methylpropanoic acid #status experimental
F:11/Modified site: valinol #status experimental

Query Match 37.5%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7
|||
Db 6 PIL 8

RESULT 13
PC2391
trichorozin II - fungus (Trichoderma harzianum)
C:Species: Trichoderma harzianum
C:Date: 17-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Oct-2000
C:Accession: PC2391
R:Ida, A.; Sanekata, M.; Wada, S.; Fujita, T.; Tanaka, H.; Enoki, A.; Fuse, G.; Kanai, Chem. Pharm. Bull. 43, 392-397, 1995
A:Title: Fungal metabolites. XVIII. New membrane-modifying peptides, trichorozins I-IV, F:1,5,9/Modified site: 2-amino-2-methylpropanoic acid #status experimental
A:Reference number: PC2390; PMID:7539721
A:Accession: PC2391
A:Status: unencoded polypeptide
A:Molecule type: protein
A:Residues: 1-11 <IID>
C:Comment: This peptide exhibits voltage-dependent ion channel-like activity in lipid bilayers
C:Keywords: antibiotic; unencoded polypeptide
F:1/Modified site: acetylated amino end #status experimental
F:1,5,9/Modified site: 2-amino-2-methylpropanoic acid #status experimental
F:11/Modified site: valinol #status experimental

Query Match 37.5%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7
|||
Db 6 PIL 8

RESULT 14
PC2392
trichorozin III - fungus (Trichoderma harzianum)
C:Species: Trichoderma harzianum
C:Date: 17-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Oct-2000
C:Accession: PC2392
R:Ida, A.; Sanekata, M.; Wada, S.; Fujita, T.; Tanaka, H.; Enoki, A.; Fuse, G.; Kanai, Chem. Pharm. Bull. 43, 392-397, 1995
A:Title: Fungal metabolites. XVIII. New membrane-modifying peptides, trichorozins I-IV, F:1,5,9/Modified site: 2-amino-2-methylpropanoic acid #status experimental
A:Reference number: PC2390; PMID:7539721
A:Accession: PC2392
A:Status: unencoded polypeptide
A:Molecule type: protein
A:Residues: 1-11 <IID>
C:Comment: This peptide exhibits voltage-dependent ion channel-like activity in lipid bilayers
C:Keywords: antibiotic; unencoded polypeptide
F:1/Modified site: acetylated amino end #status experimental
F:1,5,9/Modified site: 2-amino-2-methylpropanoic acid #status experimental
F:11/Modified site: valinol #status experimental

Query Match 37.5%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7
|||
Db 6 PIL 8

Db |||
6 PIL 8

RESULT 15
PC2393
trichorozin IV - fungus (Trichoderma harzianum)
C:Species: Trichoderma harzianum
C:Date: 17-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Oct-2000
C:Accession: PC2393
R:Ida, A.; Sanekata, M.; Wada, S.; Fujita, T.; Tanaka, H.; Enoki, A.; Fuse, G.; Kanai, Chem. Pharm. Bull. 43, 392-397, 1995
A:Title: Fungal metabolites. XVIII. New membrane-modifying peptides, trichorozins I-IV, F:1,5,9/Modified site: 2-amino-2-methylpropanoic acid #status experimental
A:Reference number: PC2390; PMID:7539721
A:Accession: PC2393
A:Status: unencoded polypeptide
A:Molecule type: protein
A:Residues: 1-11 <IID>
C:Comment: This peptide exhibits voltage-dependent ion channel-like activity in lipid bilayers
C:Keywords: antibiotic; unencoded polypeptide
F:1/Modified site: acetylated amino end #status experimental
F:1,5,9/Modified site: 2-amino-2-methylpropanoic acid #status experimental
F:11/Modified site: leucinol #status experimental

Query Match 37.5%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7
|||
Db 6 PIL 8

RESULT 16
S11298
hemagglutinin precursor - influenza A virus (strain A/FPV/Rostock/34 [H7N1]) (fragment)
C:Species: influenza A virus
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 08-Apr-1994
C:Accession: S11298
R:Robertson, J.S.
Nucleic Acids Res. 6, 3745-3757, 1979
A:Title: 5' and 3' terminal nucleotide sequences of the RNA genome segments of influenza A virus
A:Reference number: S11286; PMID:80034428; PMID:493121
A:Accession: S11298
A:Molecule type: genomic RNA
A:Residues: 1-12 <ROB>
A:Cross-references: GB:J02111
C:Genetics:
A:Map position: segment 4
C:Superfamily: influenza virus hemagglutinin
C:Keywords: homotrimer

Query Match 37.5%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IIV 8
|||
Db 5 IIV 7

RESULT 17
S67528
napin - rape (fragments)
C:Species: Brassica napus (rape)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S67528
R:Muren, E.; Ek, B.; Rask, L.
Eur. J. Biochem. 227, 316-321, 1995
A:Title: Processing of the 2S storage protein napin in Brassica napus and in transgenic Arabidopsis thaliana
A:Reference number: S67528; PMID:95154306; PMID:7851402
A:Accession: S67528
A:Status: preliminary

A:Molecule type: protein
A:Residues: 1-6;7-12 <MUR>

Query Match 37.5%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
|||
Db 3 GPF 5

RESULT 18
PQ0696
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) [imported] - rice (fragment)
C:Species: Oryza sativa (rice)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PQ0696
R:Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A:Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A:Reference number: PQ0696
A:Accession: PQ0696
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <KOM>
C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 37.5%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
|||
Db 5 GPF 7

RESULT 19
S43957
Ig mu chain V region (clone 3) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C:Accession: S43957
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.; Nucleic Acids Res. 22, 1389-1393, 1994
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A:Reference number: S43956; MUID:94248036; PMID:8190629
A:Accession: S43957
A:Molecule type: DNA
A:Residues: 1-12 <WAG>
C:Keywords: immunoglobulin

Query Match 37.5%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
|||
Db 4 GPF 6

RESULT 20
PN0046
ATP synthase D chain, mitochondrial - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
C:Accession: PN0046
R:Kato, H.
Kawasaki Igakkaishi 22, 245-259, 1996
A:Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro
A:Reference number: PN0041
A:Accession: PN0046
A:Molecule type: protein

A:Residues: 1-12 <KAT>
A:Experimental source: neuroblastoma cell
C:Comment: The molecular mass is 24,400 and the pI is 5.37. The amino-terminus is blo
C:Keywords: brain; mitochondrion

Query Match 37.5%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7
|||
Db 8 PIL 10

RESULT 21
JX0315
aminotransferase chimera DY18 - synthetic (fragment)
C:Species: synthetic
C>Date: 28-May-1999 #sequence_revision 28-May-1999 #text_change 28-May-1999
C:Accession: JX0315
R:Myazawa, K.; Kawaguchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S.
J. Biochem. 115, 568-577, 1994
A:Title: Construction of aminotransferase chimeras and analysis of their substrate sp
A:Reference number: JX0315; MUID:94334304; PMID:8056774
A:Accession: JX0315
A:Molecule type: DNA
A:Residues: 1-12 <MIY>
C:Comment: This enzyme is a chimeric enzyme of Escherichia coli aspartate aminotransf
C:Comment: The parental enzymes catalyze the reversible amino group transfer reaction
C:Keywords: aminotransferase

Query Match 37.5%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7
|||
Db 5 PIL 7

RESULT 22
PQ0700
unidentified 6.3/40K protein [imported] - rice (fragment)
C:Species: Oryza sativa (rice)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PQ0700
R:Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A:Title: A rice protein library; a data-file of rice proteins separated by two-dimens
A:Reference number: PQ0696
A:Accession: PQ0700
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <KOM>

Query Match 37.5%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
|||
Db 11 ILV 13

RESULT 23
A61514
glutathione transferase (EC 2.5.1.18), 26k - fluke (Schistosoma japonicum) (fragment)
C:Species: Schistosoma japonicum
C>Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 07-May-1999
C:Accession: A61514
R:Mitchell, G.F.
Mol. Biochem. Parasitol. 27, 249-256, 1988
A:Title: Expression of an enzymatically active parasite molecule in Escherichia coli:

A:Reference number: A61514; MUID:88142994; PMID:3278228
 A:Accession: A61514
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13 <MIT>
 C:Keywords: transférase

Query Match 37.5%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7
 ||||
 Db 2 PIL 4

RESULT 24

S33273
 85K glycoprotein - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 07-May-1999
 C:Accession: S33273; S33274
 R:Cunningham, H.B.; Yazaki, P.J.; Domingo, R.C.; Oades, K.V.; Bohlen, H.; Sabbadini, R.A.
 Arch. Biochem. Biophys. 303, 32-43, 1993
 A>Title: The skeletal muscle transverse tubular Mg-ATPase: identity with Mg-ATPases of s
 A:Reference number: S33272; MUID:93256569; PMID:8489264
 A:Accession: S33273
 A:Molecule type: protein
 A:Residues: 1-13 <CUN>
 A:Experimental source: gizzard
 A:Accession: S33274
 A:Molecule type: protein
 A:Residues: 1-13 <CUN>
 A:Experimental source: brain
 C:Keywords: glycoprotein

Query Match 37.5%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7
 ||||
 Db 6 PIL 8

RESULT 25

C53275
 Ig kappa-1 chain J3 segment b95 allotype - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
 C:Accession: C53275
 R:Ayadi, H.; Marche, P.N.; Cazenave, P.A.
 Immunogenetics 34, 201-207, 1991
 A>Title: Evolution of the rabbit immunoglobulin kappa chain genes.

A:Reference number: A53275; MUID:91372868; PMID:1909995
 A:Accession: C53275
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-13 <AYA>

A>Note: sequence extracted from NCBI backbone (NCBI:56069, NCBI:P:56164)
 C:Comment: This J3 segment may not be functional because of substitutions in the 7 mer
 C:Keywords: heterotetramer; immunoglobulin

Query Match 37.5%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
 ||||
 Db 3 RGP 5

RESULT 26

B61309
 lutropin beta chain - hamster (fragment)
 N:Alternate names: lutinizing hormone beta chain
 C:Species: Cricetinae gen. sp. (hamster)
 C>Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
 C:Accession: B61309
 R:Glenn, S.D.; Nahm, H.S.; Greenwald, G.S.; Ward, D.N.
 Endocrinology 111, 1263-1269, 1982
 A>Title: Isolation and characterization of hamster lutinizing hormone.
 A:Reference number: A61309; MUID:83003498; PMID:6889489
 A:Accession: B61309
 A>Status: Preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <GLE>
 C:Superfamily: pituitary glycoprotein hormone beta chain
 C:Keywords: glycoprotein

Query Match 37.5%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
 ||||
 Db 2 RGP 4

RESULT 27

S09721
 2S albumin small chain nIII - rape (fragments)
 C:Species: Brassica napus (rape)
 C>Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
 C:Accession: S09721
 R:Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
 FEBS Lett. 263, 209-212, 1990
 A>Title: beta-Turns as structural motifs for the proteolytic processing of seed prot
 A:Reference number: S09720; MUID:90242374; PMID:2185951
 A:Accession: S09721
 A:Molecule type: protein
 A:Residues: 1-9;10-14 <MON>
 A:Experimental source: seed

Query Match 37.5%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
 ||||
 Db 3 GPF 5

RESULT 28

B28018
 very late antigen-2 alpha chain - human (fragment)
 N:Alternate names: VLA-2 alpha chain
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 12-May-1994
 C:Accession: B28018
 R:Takada, Y.; Strominger, J.L.; Hemler, M.E.
 Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987
 A>Title: The very late antigen family of heterodimers is part of a superfamily of mo
 A:Reference number: A94151; MUID:87204112; PMID:3033641
 A:Accession: B28018
 A:Molecule type: protein
 A:Residues: 1-14 <TAK>
 C:Keywords: duplication; heterodimer; membrane protein

Query Match 37.5%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
 ||||
 Db 12 RGP 14

RESULT 29

S36678 dodecenoyl-CoA Delta-isomerase (EC 5.3.3.8) / enoyl-CoA hydratase (EC 4.2.1.17) / 3-hydroxyacyl-CoA lyase (house mouse)

C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 24-Jul-1998

C;Accession: S36678

R;Chen, N.; Crane, D.I.

Biochem. J. 283, 605-610, 1992

A;Title: Induction of the major integral membrane protein of mouse liver peroxisomes by

A;Reference number: S21285; PMID:92246895; PMID:1575703

A;Accession: S36678

A;Molecule type: protein

A;Residues: 1-14 <CH>

A;Experimental source: liver

C;Function:

A;Pathway: fatty acid beta-oxidation

C;Keywords: carbon-oxygen lyase; fatty acid beta-oxidation; hydro-lyase; intramolecular

Query Match 37.5%; Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4

DB 6 GPF 8

RESULT 30

LFTWL leu leader peptide - Thermus aquaticus

C;Species: Thermus aquaticus

C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999

C;Accession: S00901

R;Croft, J.E.; Love, D.R.; Bergquist, P.L.

Mol. Gen. Genet. 210, 490-497, 1987

A;Title: Expression of leucine genes from an extremely thermophilic bacterium in Escheri

A;Reference number: S00901; PMID:88121725; PMID:3323845

A;Accession: S00901

A;Molecule type: DNA

A;Residues: 1-15 <CRO>

A;Cross-references: EMBL:X06604; NID:948244; PIDN:CAA29823.1; PID:948245

A;Note: the source is designated as Thermus thermophilus

C;Superfamily: Thermus aquaticus leu leader peptide

Query Match 37.5%; Score 3; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8

DB 6 ILV 8

RESULT 31

A28497 neurotensin-related protein - turkey (fragment)

C;Species: Melleagris gallopavo (common turkey)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 23-May-1997

C;Accession: A28497

R;Carraway, R.E.; Cochran, D.E.; Ruane, S.E.

J. Biol. Chem. 262, 15886-15889, 1987

A;Title: Isolation, structures, and biologic activity of neurotensin-related peptides ge

A;Reference number: A28497; PMID:88058942; PMID:2445741

A;Accession: A28497

A;Molecule type: protein

A;Residues: 1-15 <CAR>

C;Superfamily: collagen alpha 3(VI) chain; animal Kunitz-type proteinase inhibitor homol

C;Keywords: neuropeptide

Query Match 37.5%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2e+03;

QY 6 ILV 8

DB 6 ILV 8

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3

DB 10 RGP 12

RESULT 32

PW0004 chlorophyll a/b-binding protein 24.5K - green alga (Dunaliella tertiolecta) (fragment

N;Alternate names: photosystem II light-harvesting chlorophyll 24.5K protein

C;Species: Dunaliella tertiolecta

C;Date: 04-Sep-1998 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999

C;Accession: PW0004

R;Laroche, J.; Bennett, J.; Falkowski, P.G.

Gene 95, 165-171, 1990

A;Title: Characterization of a cDNA encoding for the 28.5-kDa LHCII apoprotein from t

A;Reference number: JW0040; PMID:91065528; PMID:2249775

A;Accession: PW0004

A;Molecule type: protein

A;Residues: 1-15 <LAR>

C;Superfamily: chlorophyll a/b-binding protein

C;Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane

Query Match 37.5%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4

DB 13 GPF 15

RESULT 33

S20410 protein kinase (EC 2.7.1.37) - spinach chloroplast (fragment)

N;Alternate names: LHCII protein kinase

C;Species: chloroplast Spinacia oleracea (spinach)

C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999

C;Accession: S20410

R;Gal, A.; Herxmann, R.G.; Lottspeich, F.; Ohad, I.

FEBS Lett. 298, 33-35, 1992

A;Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cy

A;Reference number: S20410; PMID:92183823; PMID:1544419

A;Accession: S20410

A;Molecule type: protein

A;Residues: 1-15 <GAL>

C;Genetics:

A;Genome: chloroplast

C;Function:

A;Description: is responsible for the regulation of energy distribution between photo

A;Note: does not exhibit redox-controlled activation

C;Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phosph

Query Match 37.5%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7

DB 2 PIL 4

RESULT 34

PA0024 protein OA300050 - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997

C;Accession: PA0024

R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A;Description: Separation and characterization of Arabidopsis proteins by two-dimensi.

A;Reference number: PA0001

A:Accession: PA0024
A:Molecule type: Protein
A:Residues: 1-15 <RAM>
A:Experimental source: seed

Query Match 37.5%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFP 5
|||
Db 6 PFP 8

RESULT 35
PS0455
superoxide dismutase (BC 1.15.1.1) (Mn) - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Mar-1999
C:Accession: PS0455

R:Tsugita, A.
submitted to JIPID, April 1993
A:Reference number: PS0206
A:Accession: PS0455
A:Molecule type: Protein
A:Residues: 1-15 <TSU>
A:Experimental source: germ
C:Function:
C:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Keywords: metalloprotein; oxidoreductase

Query Match 37.5%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7
|||
Db 7 PIL 9

RESULT 36
A42411
myosin light chain kinase - chicken
C:Species: Gallus gallus (chicken)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995
C:Accession: A42411
R:Leachman, S.A.; Gallagher, P.J.; Herring, B.P.; McPhaul, M.J.; Stull, J.T.
J. Biol. Chem. 267, 4930-4938, 1992
A:Title: Biochemical properties of chimeric skeletal and smooth muscle myosin light chain
A:Reference number: A42411; MUID:92165861; PMID:1371510
A:Accession: A42411
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-16 <LEA>
A:Experimental source: skeletal muscle
A>Note: sequence extracted from NCBI backbone (NCBIP:84332)

Query Match 37.5%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
|||
Db 1 RGP 3

RESULT 37
PH1790
T cell receptor alpha chain V region (clone 2BBL V alpha 24-6) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1790
R:Porcellini, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood lymphocytes (T cells)
A:Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1790
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <POR>

Query Match 37.5%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
|||
Db 6 RGP 8

RESULT 38
I46275
hemoglobin beta-x chain - goat (fragment)
C:Species: Capra aegagrus hircus (domestic goat)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
C:Accession: I46275
R:Haynes, J.R.; Rostock, P.R.; Schon, E.A.; Gallagher, P.M.; Burks, D.J.; Smith, K.; J. Biol. Chem. 255, 6355-6367, 1980
A:Title: The isolation of the beta-a-, beta-c-, and gamma-globin genes and a presumpt
A:Reference number: I46273; MUID:80227766; PMID:6248519
A:Accession: I46275
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <HAV>
A:Cross-references: GB:K00659; NID:G164151; PIDN:AAA30919.1; PID:G164156

Query Match 37.5%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
|||
Db 5 ILV 7

RESULT 39
S78415
ribosomal protein RL27, mitochondrial [validated] - rat (tentative sequence) (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C:Accession: S78415
R:Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A:Reference number: S78411
A:Accession: S78415
A:Molecule type: protein
A:Residues: 1-16 <GOL>
A>Note: 1-Val was also found
A>Note: the protein is designated as mitochondrial ribosomal protein L27
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 37.5%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
|||
Db 12 RGP 14

RESULT 40
I78870
gene RB1 protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999


```

C:Accession: I78870
P:Hogg, A.; Onadin, Z.; Baird, P.N.; Cowell, J.K.
Oncogene 7, 1445-1451, 1992
A:Title: Detection of heterozygous mutations in the RB1 gene in retinoblastoma patients
A:Reference number: I58362; MUID:92319557; PMID:1352398
A:Accession: I78870
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-17 <RES>
A:Cross-references: GB:L41911; NID:G794004; PIDN:AA859483.1; PID:G794005
C:Genetics:
A:Gene: GDB:RB1
A:Cross-references: GDB:118734; OMIM:180200
A:Map position: 13q14.3-13q14.3

Query Match      37.5%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 ILV 8
      |||
Db      1 ILV 3

RESULT 41
G85956
hypothetical protein Z4331 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: G85956
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 523-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85956
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-17 <STO>
A:Cross-references: GB:AB005174; NID:gl2517539; PIDN:AA858115.1; GSPDB:GN00145; UWGP:Z43
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z4331

Query Match      37.5%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PFP 5
      |||
Db      6 PFP 8

RESULT 42
S09722
2S albumin small chain 1 nIV - rape (fragments)
C:Species: Brassica napus (rape)
C:Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C:Accession: S09722
R:Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990
A:Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins
A:Reference number: S09720; MUID:90242974; PMID:2185951
A:Accession: S09722
A:Molecule type: protein
A:Residues: 1-9;10-18 <MON>
A:Experimental source: seed

Query Match      37.5%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GPF 4
      |||
Db      3 GPF 5

RESULT 43
S09723
2S albumin small chain 2 nIV - rape (fragments)
C:Species: Brassica napus (rape)
C:Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C:Accession: S09723
R:Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990
A:Title: beta-Turns as structural motifs for the proteolytic processing of seed prote
A:Reference number: S09720; MUID:90242974; PMID:2185951
A:Accession: S09723
A:Molecule type: protein
A:Residues: 1-9;10-18 <MON>
A:Experimental source: seed

Query Match      37.5%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GPF 4
      |||
Db      3 GPF 5

RESULT 44
S13974
chlorophyll a/b-binding protein type I - garden pea (fragment)
C:Species: Pisum sativum (garden pea)
C:Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C:Accession: S13974
R:Jahns, P.; Junge, W.
Eur. J. Biochem. 193, 731-736, 1990
A:Title: Dicyclohexylcarbodiimide-binding proteins related to the short circuit of th
A:Reference number: S13973; MUID:91065379; PMID:2174365
A:Accession: S13974
A:Molecule type: protein
A:Residues: 1-18 <JAH>
C:Genetics:
A:Genome: nuclear
C:Keywords: chlorophyll; chloroplast; light-harvesting complex; photosystem I; thylak

Query Match      37.5%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 ILV 8
      |||
Db      6 ILV 8

RESULT 45
S40502
20-alpha-hydroxysteroid dehydrogenase - Tetrahymena pyriformis
C:Species: Tetrahymena pyriformis
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-Dec-1999
C:Accession: S40502
R:Iinazu, A.; Sato, K.; Nakayama, T.; Deyashiki, Y.; Hara, A.; Nozawa, Y.
Biochem. J. 297, 195-200, 1994
A:Title: Purification and characterization of a novel dimeric 20-alpha-hydroxysteroid
A:Reference number: S40502; MUID:94107273; PMID:8280099
A:Accession: S40502
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <INA>
C:Genetics:
A:Genetic code: SGC5

Query Match      37.5%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GPF 4
      |||
Db      3 GPF 5

```

```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 FPI 6
   |||
Db 13 FPI 15

RESULT 46
EWSMCN
cinnamycin - Streptovorticillium cinnamoneum
N:Alternate names: lanthiopeptin; lantibiotic Ro 09-0198
C:Species: Streptovorticillium cinnamoneum
C>Date: 30-Sep-1993 #sequence_revision 12-May-1994 #text_change 07-May-1999
C:Accession: A45767
R:Naruse, N.; Tenmyo, O.; Tomita, K.; Konishi, M.; Miyaki, T.; Kawaguchi, H.; Fukase, K.
J. Antibiot. 42, 837-845, 1989
A:Title: Lanthiopeptin, a new peptide antibiotic. Production, isolation and properties of
A:Reference number: A45767; MUID:89291558; PMID:2544544
A:Accession: A45767
A:Molecule type: protein
A:Residues: 1-19 <NAR>
R:Wakamiya, T.; Fukase, K.; Naruse, N.; Konishi, M.; Shiba, T.
Tetrahedron Lett. 29, 4771-4772, 1988
A:Title: Lanthiopeptin, a new peptide effective against Herpes simplex virus: structural
A:Reference number: A53359
A:Contents: annotation; strain L337-2
C:Superfamily: cinnamycin precursor
C:Keywords: antibiotic; beta-hydroxyaspartic acid; lanthionine
F:1-18/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:4-11/Cross-link: sn-(2S,6R)-lanthionine (Ser-Cys) #status experimental
F:5-11/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:6-19/Cross-link: (2Xi,9S)-lysinoalanine (Ser-Lys) #status experimental
F:15/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

Query Match 37.5%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPF 4
   |||
Db 8 GPF 10

RESULT 47
T30825
RNA polymerase beta' chain - Neisseria meningitidis (fragment)
C:Species: Neisseria meningitidis
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: T30825
R:Nolte, O.J.
submitted to the EMBL Data Library, October 1995
A:Description: Cloning and sequencing of the rpoB gene of Neisseria meningitidis which i
A:Reference number: Z20888
A:Accession: T30825
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <NOL>
A:Cross-references: EMBL:Z54353; NID:gi325954; PID:e244319; PIDN:CAA91165.1
C:Genetics:
A>Note: rpoC

Query Match 37.5%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 FPI 6
   |||
Db 15 FPI 17

RESULT 48
S65399
immunodeficiency virus type 1, HIV-1 gp120 - human (fragments)

```

```

C:Species: Homo sapiens (man)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S65399
R:Niwa, Y.; Yano, M.; Futaki, S.; Okumura, Y.; Kido, H.
Eur. J. Biochem. 237, 64-70, 1996
A:Title: T-cell membrane-associated serine protease, tryptase TL(2), binds human immu
man immunodeficiency virus type 1 inhibit cleavage of gp120.
A:Reference number: S65399; MUID:96203909; PMID:8620895
A:Accession: S65399
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10;11-20 <NIW>
C:Superfamily: type E retrovirus env polyprotein

Query Match 37.5%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGP 3
   |||
Db 1 RGP 3

RESULT 49
S61278
nikkomycin synthesis protein P4 - Streptomyces tendae (fragment)
C:Species: Streptomyces tendae
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C:Accession: S61278
R:Moehrl, V.; Roos, U.; Borkmann, C.
Mol. Microbiol. 15, 561-571, 1995
A:Title: Identification of cellular proteins involved in nikkomycin production in St;
A:Reference number: S61278; MUID:95302967; PMID:7783626
A:Accession: S61278
A:Molecule type: protein
A:Residues: 1-20 <MOE>

Query Match 37.5%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPF 4
   |||
Db 6 GPF 8

RESULT 50
S09720
2S albumin small chain nII - rape (fragments)
C:Species: Brassica napus (rape)
C>Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C:Accession: S09720
R:Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990
A:Title: beta-Turns as structural motifs for the proteolytic processing of seed prot;
A:Reference number: S09720; MUID:90242974; PMID:2185951
A:Accession: S09720
A:Molecule type: protein
A:Residues: 1-9;10-20 <MON>
A:Experimental source: seed
A>Note: 1-Ser was also found

Query Match 37.5%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPF 4
   |||
Db 3 GPF 5

RESULT 51
B30208

```

hypothetical protein 1 (cpc-1 5' region) - Neurospora crassa
 C;Species: Neurospora crassa
 C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
 C;Accession: B30208
 R;Paluh, J.B.; Orbach, M.J.; Legerton, T.L.; Yanofsky, C.
 Proc. Natl. Acad. Sci. U.S.A. 85, 3728-3732, 1988
 A;Title: The cross-pathway control gene of Neurospora crassa, cpc-1, encodes a protein s
 A;Reference number: A30208; MUID:86234499; PMID:2967496
 A;Accession: B30208
 A;Molecule type: DNA
 A;Residues: 1-20 <PAL>
 A;Cross-references: GB:J03262

Query Match 37.5%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFP 5
 |||
 Db 6 PFP 8

RESULT 52
 S58382
 hypothetical protein 1 - human
 C;Species: Homo sapiens (man)
 C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 08-Oct-1999
 C;Accession: S58382
 R;Dirks, R.P.H.; Onnekink, C.; Jansen, H.J.; de Jong, A.; Bloemers, H.P.J.
 Nucleic Acids Res. 23, 2815-2822, 1995
 A;Title: A novel human c-sis mRNA species is transcribed from a promoter in c-sis intron
 A;Reference number: S58382; MUID:95388493; PMID:7659502
 A;Accession: S58382
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-20 <DIR>
 A;Cross-references: EMBL:X83705; NID:G951023; PIDN:CAAS8678.1; PID:G951024

Query Match 37.5%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFP 5
 |||
 Db 12 PFP 14

RESULT 53
 B53283
 major cat allergen Fel d I beta chain - cat (fragment)
 C;Species: Felis silvestris catus (domestic cat)
 C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 12-May-1994
 C;Accession: B53283
 R;Duffort, O.A.; Carreira, J.; Nitti, G.; Polo, F.; Lombardero, M.
 Mol. Immunol. 28, 301-309, 1991
 A;Title: Studies on the biochemical structure of the major cat allergen Felis domesticus
 A;Reference number: A53283; MUID:91287714; PMID:1712068
 A;Accession: B53283
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <DUF>

Query Match 37.5%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPI 6
 |||
 Db 7 FPI 9

RESULT 54
 A60801
 acrosome stabilizing factor large chain - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: A60801
 R;Wilson, W.L.; Oliphant, G.
 Biol. Reprod. 37, 159-169, 1987
 A;Title: Isolation and biochemical characterization of the subunits of the rabbit spe
 A;Reference number: A60801; MUID:8800873; PMID:3651543
 A;Accession: A60801
 A;Molecule type: protein
 A;Residues: 1-20 <WIL>
 C;Comment: spermatozoa must undergo capacitation and the acrosome reaction to become
 C;Keywords: glycoprotein; semen

Query Match 37.5%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PIL 7
 |||
 Db 16 PIL 18

RESULT 55
 PQ0010
 angiotensin-converting enzyme inhibitor (FLP-3) - common fig
 N;Alternate names: ficus latex peptide 3
 C;Species: Ficus carica (common fig)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: PQ0010
 R;Maruyama, S.; Miyoshi, S.; Tanaka, H.
 Agric. Biol. Chem. 53, 2763-2767, 1989
 A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
 A;Reference number: PQ0008
 A;Accession: PQ0010
 A;Molecule type: protein
 A;Residues: 1-3 <MAR>
 A;Experimental source: latex
 C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 25.0%; Score 2; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LV 8
 |||
 Db 1 LV 2

RESULT 56
 B43848
 cell surface adhesin for heparan sulfate, 60K - Staphylococcus aureus (fragment)
 C;Species: Staphylococcus aureus
 C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 24-Feb-1995
 C;Accession: B43848
 R;Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.
 Infect. Immun. 60, 899-906, 1992
 A;Title: Binding of heparan sulfate to Staphylococcus aureus.
 A;Reference number: A43848; MUID:92176005; PMID:1541563
 A;Accession: B43848
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-4 <LIA>
 A;Note: sequence extracted from NCBI backbone (NCBIP:85444)

Query Match 25.0%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LV 8
 |||
 Db 2 LV 3

RESULT 57

T46627
 hypothetical protein c4 - loblolly pine
 C:Species: Pinus taeda (loblolly pine)
 C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
 C:Accession: T46627
 R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
 submitted to the EMBL Data Library, July 1995
 A;Description: Cloning of a chitinase homolog which lacks chitin binding sites and is do
 A;Reference number: 223105
 A;Accession: T46627
 A;Status: preliminary; translated from GB/EMBL/DDBU
 A:Molecule type: mRNA
 A;Residues: 1-4 <CHA>
 A;Cross-references: EMBL:U1309; NID:g974285; PID:g974292
 A;Experimental source: strain s6Pr2xs6PT3; 8 month seedlings

Query Match 25.0%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LV 8
 ||
 Db 3 LV 4

RESULT 58

S53508
 starvation-induced ribonuclease - tomato
 C:Species: Lycopersicon esculentum (tomato)
 C>Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
 A;Accession: S53508
 R;Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.
 Plant Mol. Biol. 27, 477-485, 1995
 A;Title: cDNA structure and regulatory properties of a family of starvation-induced ribo
 A;Reference number: S53506; MUID:95201242; PMID:7894013
 A;Accession: S53508
 A;Status: preliminary
 A:Molecule type: protein
 A;Residues: 1-4 <KOE>

Query Match 25.0%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FP 5
 ||
 Db 1 FP 2

RESULT 59

PT0675
 T-cell receptor beta chain V-D-J region (140-IAC) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0675
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711358
 A;Accession: PT0675
 A;Status: translation not shown
 A:Molecule type: DNA
 A;Residues: 1-4 <FEE>
 A;Experimental source: day 18 fetal thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 25.0%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3
 ||

Db ||
 3 GP 4

RESULT 60

S47552
 ubiquitin - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
 C;Accession: S47552
 R;Hubbard, M.J.; Carne, A.
 Biochim. Biophys. Acta 1200, 191-196, 1994
 A;Title: Differential feeding-related regulation of ubiquitin and calbindin(9kDa) in
 A;Reference number: S47552; MUID:94304928; PMID:8031840
 A;Accession: S47552
 A;Status: preliminary
 A:Molecule type: protein
 A;Residues: 1-4 <HUB>

Query Match 25.0%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RG 2
 ||
 Db 2 RG 3

RESULT 61

C41225
 copper resistance protein - Pseudomonas syringae pv. tomato (fragment)
 C:Species: Pseudomonas syringae pv. tomato
 C>Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
 C;Accession: C41225
 R;Cha, J.-S.; Cooksey, D.A.
 Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
 A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer
 A;Reference number: A41225; MUID:92020961; PMID:1924351
 A;Accession: C41225
 A;Status: preliminary
 A:Molecule type: protein
 A;Residues: 1-5 <CHA>

Query Match 25.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LV 8
 ||
 Db 4 LV 5

RESULT 62

E60274
 major protein antigen MP763 - Mycobacterium tuberculosis (fragment)
 C:Species: Mycobacterium tuberculosis
 C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
 C;Accession: E60274
 R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
 Infect. Immun. 59, 372-382, 1991
 A;Title: Isolation and partial characterization of major protein antigens in the cult
 A;Reference number: A60274; MUID:91099899; PMID:1898899
 A;Accession: E60274
 A;Status: preliminary
 A:Molecule type: protein
 A;Residues: 1-5 <NAG>

Query Match 25.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PI 6
 ||

Db 3 PI 4

RESULT 63

B37988
acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)
C:Species: Physarum polycephalum
C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
C:Accession: B37988
R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki-Ogawa, J. Biol. Chem. 265, 19898-19903, 1990
A:Title: Purification and characterization of a novel intracellular acid proteinase from Physarum polycephalum
A:Reference number: B37988; MUID:91060608; PMID:2246266
A:Accession: B37988
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <MUR>

Query Match 25.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PI 6
||
Db 4 PI 5

RESULT 64

JS0319
subesophageal ganglion pentapeptide - house cricket
C:Species: Acheta domestica (house cricket)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Accession: JS0319
R:Wicker, C.; Wicker, C.
Comp. Biochem. Physiol. C 88, 185-187, 1987
A:Title: Isolation and structure of a peptide isolated from the subesophageal ganglion of Acheta domestica
A:Reference number: JS0319
A:Accession: JS0319
A:Molecule type: protein
A:Residues: 1-5 <WIC>

Query Match 25.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PF 4
||
Db 4 PF 5

RESULT 65

PT0267
Ig heavy chain CRD3 region (clone 3-94A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0267
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and junctional diversity in the generation of the human antibody repertoire
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0267
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GP 3
||
Db 3 GP 4

RESULT 66

JT0520
Ig kappa chain V-III region (SD1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 16-Aug-1996
C:Accession: JT0520
R:Auker, R.; Conley, M.E.; Pollok, B.A.
J. Exp. Med. 169, 2109-2119, 1989
A:Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia
A:Reference number: JT0511; MUID:89279157; PMID:2786547
A:Accession: JT0520
A:Molecule type: mRNA
A:Residues: 1-5 <ANK>
A>Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangements
A:Note: a stop codon terminates the sequence in the V region
C:Keywords: heterotetramer; immunoglobulin
F:1-5/Domain: V kappa region <VRE>

Query Match 25.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GP 3
||
Db 4 GP 5

RESULT 67

PT0525
T-cell receptor beta chain V-D-J region (100-4J) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0525
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0525
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 25.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RG 2
||
Db 3 RG 4

RESULT 68

PT0608
T-cell receptor beta chain V-D-J region (120-2CP) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0608
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0608
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 25.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0;
QY 1 RG 2
Db 4 RG 5

RESULT 69
PT0669
T-cell receptor beta chain V-D-J region (121-3BH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0669
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0669
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 25.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0;
QY 2 GP 3
Db 4 GP 5

RESULT 70
PT0695
T-cell receptor beta chain V-D-J region (135-1D) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0695
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0695
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 25.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0;
QY 1 RG 2
Db 4 RG 5

RESULT 71
PT0700
T-cell receptor beta chain V-D-J region (161-2A) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0700
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0700
A>Status: translation not shown
A:Molecule type: DNA

A:Residues: 1-5 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 25.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0;
QY 1 RG 2
Db 4 RG 5

RESULT 72
A60986
N-formyl oligopeptide - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
C:Accession: A60986
R;Broom, M.F.; Mellor, D.M.; Chadwick, V.S.
Experientia 45, 1097-1099, 1989
A:Title: Purification and amino acid sequencing of naturally occurring N-formyl-meth:
A:Reference number: A60986; MUID:90092408; PMID:2689204
A:Accession: A60986
A:Molecule type: protein
A:Residues: 1-6 <BRO>
C:Comment: This hexapeptide was the longest of several N-formyl oligopeptides report:
F;1/Modified site: N-formylmethionine #status experimental

Query Match 25.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0;
QY 6 IL 7
Db 4 IL 5

RESULT 73
PQ0008
angiotensin-converting enzyme inhibitor (FLP-1) - common fig
N;Alternate names: ficus latex peptide 1
C:Species: Ficus carica (common fig)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
C:Accession: PQ0008
R;Maruyama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A:Reference number: PQ0008
A:Accession: PQ0008
A:Molecule type: protein
A:Residues: 1-6 <MAR>
A:Experimental source: latex
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 25.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0;
QY 5 PI 6
Db 4 PI 5

RESULT 74
I51317
bHLH transcription factor inhibitor - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51317
R;Zhang, H.; Reynaud, S.; Kloc, M.; Etkin, L.D.; Spohr, G.
Mech. Dev. 50, 119-130, 1995
A:Title: Id gene activity during Xenopus embryogenesis.

A:Reference number: I51316; MUID:95344988; PMID:7619724
A:Accession: I51317
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-6 <ZHA>
A:Cross-references: GB:S79038; NID:g1042006; PIDN:AA014294.1; PID:g4361994
C:Genetics:
A:Gene: Xid1b

Query Match 25.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
||
Db 5 PF 6
||

RESULT 75
I51434
H4 histone - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51434
R:Woodland, H.R.; Warmington, J.R.; Ballantine, J.E.M.; Turner, P.C.
Nucleic Acids Res. 12, 4939-4958, 1984
A:Title: Are there major developmentally regulated H4 gene classes in Xenopus?
A:Reference number: I51391; MUID:84247348; PMID:6330691
A:Accession: I51434
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-6 <WOO>
A:Cross-references: GB:K02304; NID:g214227; PIDN:AAA49738.1; PID:g555517

Query Match 25.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RG 2
||
Db 4 RG 5
||

Search completed: November 25, 2003, 19:36:12
Job time : 5.48837 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 : Search time 2.83721 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-29

Perfect score: 8

Sequence: 1 RGPPPIIV 8

Scoring table: GIGPO 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	37.5	9	1	MGMT_BOVIN
2	3	37.5	13	1	CRBL_VESTR
3	3	37.5	13	1	TEMC_RANTE
4	3	37.5	14	1	JAPI_RANJA
5	3	37.5	15	1	AFIL_MALPA
6	3	37.5	15	1	LPL_TETH
7	3	37.5	15	1	UCO6_MAIZE
8	3	37.5	16	1	AFIS_MALPA
9	3	37.5	16	1	TRYP_FELCA
10	3	37.5	18	1	AHD2_TETPY
11	3	37.5	19	1	DURA_STRGV
12	2	25.0	5	1	PAP2_PARWA
13	2	25.0	5	1	SUGA_ACHDO
14	2	25.0	6	1	E101_LITRU
15	2	25.0	7	1	CGF1_ENTFA
16	2	25.0	7	1	CHAF_ENTFA
17	2	25.0	7	1	FARI_HELTI
18	2	25.0	7	1	MNP1_LEPDE
19	2	25.0	7	1	UF04_MOUSE
20	2	25.0	7	1	UN06_PINPS
21	2	25.0	8	1	AL15_CARNA
22	2	25.0	8	1	AL16_CARMA
23	2	25.0	8	1	ALL5_CALVO
24	2	25.0	8	1	ALL5_CYDFO
25	2	25.0	8	1	AL18_CARMA
26	2	25.0	8	1	ALL9_CARMA
27	2	25.0	8	1	ANG2_BOTJA
28	2	25.0	8	1	CADI_ENTFA
29	2	25.0	8	1	CPD1_ENTFA
30	2	25.0	8	1	FAR7_ASCSU
31	2	25.0	8	1	PKK2_PERAM
32	2	25.0	8	1	PKK3_PERAM
33	2	25.0	8	1	RS7_MYCIT
34	2	25.0	2	1	RT34_BOVIN
35	2	25.0	2	1	UPAA_HUMAN
36	2	25.0	2	1	VGLG_HSV2B
37	2	25.0	2	1	CCAP_CARMA
38	2	25.0	2	1	CONO_CONST
39	2	25.0	2	1	DNF1_LOCM1
40	2	25.0	2	1	FAR5_PANRE
41	2	25.0	2	1	FAR9_ASCSU
42	2	25.0	2	1	FIBB_PAPAN
43	2	25.0	2	1	ISOT_CYPFA
44	2	25.0	2	1	KNL3_BOMVA
45	2	25.0	2	1	LMT3_LOCM1
46	2	25.0	2	1	OXYT_BUPRE
47	2	25.0	2	1	OXYT_CYPFA
48	2	25.0	2	1	OXYT_OCTVU
49	2	25.0	2	1	PGLR_DIAAB
50	2	25.0	2	1	RE42_LITRU
51	2	25.0	2	1	SAMP_MUSCA
52	2	25.0	2	1	TKL1_LOCM1
53	2	25.0	2	1	ULAD_HUMAN
54	2	25.0	2	1	UPA3_HUMAN
55	2	25.0	2	1	UPA7_HUMAN
56	2	25.0	2	1	AH3_PRUSE
57	2	25.0	2	1	ANG1_BOTJA
58	2	25.0	2	1	ANGT_BOVIN
59	2	25.0	2	1	ANGT_CHICK
60	2	25.0	2	1	BPP_VIPAS
61	2	25.0	2	1	COXO_RAT
62	2	25.0	2	1	COXO_THUOB
63	2	25.0	2	1	ESTA_SCHGA
64	2	25.0	2	1	FAR6_PANRE
65	2	25.0	2	1	NS1_MYCTU
66	2	25.0	2	1	PVK_LOCM1
67	2	25.0	2	1	Q2OB_COMTE
68	2	25.0	2	1	RCA_PINPS
69	2	25.0	2	1	RPL_PHODV
70	2	25.0	2	1	SLAP_BACTG
71	2	25.0	2	1	TRP8_LEUMA
72	2	25.0	2	1	UPA5_HUMAN
73	2	25.0	2	1	UXA2_CHLTR
74	2	25.0	2	1	XYNB_DICB4
75	2	25.0	2	1	ANGT_CRIGE
76	2	25.0	2	1	BPP3_BOVIN
77	2	25.0	2	1	BPP4_BOVIN
78	2	25.0	2	1	BPP_AGRHP
79	2	25.0	2	1	BRK_MEGFL
80	2	25.0	2	1	CORZ_PERAM
81	2	25.0	2	1	CS15_BACSU
82	2	25.0	2	1	CX5A_CONAL
83	2	25.0	2	1	ESI_RAT
84	2	25.0	2	1	MORN_HUMAN
85	2	25.0	2	1	RE41_LITRU
86	2	25.0	2	1	TIN1_HOFTI
87	2	25.0	2	1	TIN4_HOFTI
88	2	25.0	2	1	FAR7_PENMO
89	2	25.0	2	1	FREL_LITIN
90	2	25.0	2	1	GRAR_RANRU
91	2	25.0	2	1	NUDM_CANFA
92	2	25.0	2	1	PA2B_VIPBO
93	2	25.0	2	1	RF1_CONSP
94	2	25.0	2	1	TIN2_HOFTI
95	2	25.0	2	1	TIN3_HOFTI
96	2	25.0	2	1	V14K_WSSV
97	2	25.0	2	1	XYLA_STRVN
98	2	25.0	2	1	ACT7_SOYBN
99	2	25.0	2	1	AH4_PRUSE
100	2	25.0	2	1	BLAC_STRGR

ALIGNMENTS

RESULT 1


```

MGMT_BOVIN
ID MGMT_BOVIN STANDARD; PRT; 9 AA.
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-
DE methylguanine-DNA methyltransferase) (Fragment).
GN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=30174912; PubMed=2308822;
RA Rydberg B., Hall J., Karan P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
RT methyltransferase.";
RL Nucleic Acids Res. 18:17-21(1990).
CC -|- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY
CC TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE
CC RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS
CC IRREVERSIBLY INACTIVATED.
CC -|- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) +
CC [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein
CC S-methyl-L-cysteine.
CC -|- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE
CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
CC InterPro; IPR001497; Methyltransf_1.
DR PROSITE; PS00374; MGMT; PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON_TER 1 9 1 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT ACT_SITE 9 9 9
FT NON_TER 9 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 37.5%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PIL 7
Db 4 PIL 6

RESULT 2
CRBL_VESTR
ID CRBL_VESTR STANDARD; PRT; 13 AA.
AC P17231;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vespid chemotactic peptide T (VESCP-T).
OS Vespa tropica (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7450;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Nakajima T., Erspaer V.;
RL (In) Sakakibara S. (eds.);
RL Peptide chemistry 1982, pp.213-218, Protein Research Foundation,
RL Osaka (1983).
CC -|- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD_RES 13 13
FT SEQUENCE 13 AA; 1354 MW; 220140365DFE5338 CRC64;

```

```

Query Match 37.5%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PIL 7
Db 3 PIL 5

RESULT 3
TEMC_RANTE
ID TEMC_RANTE STANDARD; PRT; 13 AA.
AC F56918;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin C.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -|- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
CC -|- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13
FT SEQUENCE 13 AA; 1363 MW; 2201403A65B2448 CRC64;

Query Match 37.5%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PIL 7
Db 3 PIL 5

```

```

RESULT 4
JAP1_RANJA
ID JAP1_RANJA STANDARD; PRT; 14 AA.
AC P83305;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Japonicin-1.
OS Rana japonica (Japanese reddish frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=21826910; PubMed=11835990;
RA Isaacson T., Soto A., Iwamuro S., Knoop F.C., Conlon J.M.;
RT "Antimicrobial peptides with atypical structural features from the
RT skin of the Japanese brown frog Rana japonica.";
RL Peptides 23:419-425(2002).
CC -|- FUNCTION: Antibacterial activity against the Gram-negative
CC bacterium E.coli and the Gram-positive bacterium S.aureus.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.

```

```

CC -!- MASS SPECTROMETRY: MW=2715.4; METHOD=Electrospray.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 8
SQ SEQUENCE 14 AA; 1650 MW; C278625186DBE0B9 CRC64;

Query Match 37.5%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6
DB 2 FPI 4

RESULT 5
AFIL_MALPA
ID AFIL_MALPA STANDARD; PRT; 15 AA.
AC P83141;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Antifungal protein 1 large subunit (CW-1) (Fragment).
OS Malva parviflora (Little mallow) (Cheeseweed).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Malvoideae; Malva.
OX NCBI_TaxID=145753;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Seed.
RX MEDLINE=20568734; PubMed=11118343;
RA Wang X., Bunkers G.J.;
RT "Potent heterologous antifungal proteins from cheeseweed (Malva parviflora).";
RL Biochem. Biophys. Res. Commun. 279:669-673(2000).
CC -!- FUNCTION: Possesses antifungal activity against P.infestans but not F.graminearum.
CC -!- SUBUNIT: Heterodimer of a large and a small subunit.
CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt concentration.
DR GO; GO:0003799; F:antifungal peptide activity; IDA.
KW Fungicide; Antibiotic.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1783 MW; 2CB3079F53CC70F9 CRC64;

Query Match 37.5%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GFP 4
DB 3 GFP 5

RESULT 6
LPL_THETH
ID LPL_THETH STANDARD; PRT; 15 AA.
AC P21234;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu leader peptide.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=88121725; PubMed=3323845;
RA Croft J.E., Love D.R., Bergquist P.L.;
RT "Expression of leucine genes from an extremely thermophilic bacterium in Escherichia coli.";
```

```

Mol. Genet. 210:490-497(1987).
-!- FUNCTION: Involved in control of the biosynthesis of leucine.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; X06604; CAA29823.1; -.
KW Leucine biosynthesis; Leader peptide.
SQ SEQUENCE 15 AA; 1666 MW; C2F107A386D7620B CRC64;

Query Match 37.5%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 6 ILV 8

RESULT 7
UC06_MAIZE
ID UC06_MAIZE STANDARD; PRT; 15 AA.
AC P80612;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 1131) (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Penollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated genome analysis program.";
RT Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.8, ITS MW IS: 71.0 kDa.
DR Maize-2DPAGE; P80612; COLEOPTILE.
DR MaizeDB; 123930; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1390 MW; 7005E22830F23D61 CRC64;

Query Match 37.5%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
DB 8 RGP 10

RESULT 8
AFIS_MALPA
ID AFIS_MALPA STANDARD; PRT; 16 AA.
AC P83140;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antifungal protein 1 small subunit (CW-1) (Fragment).
OS Malva parviflora (Little mallow) (Cheeseweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosidids II; Malvales; Malvaceae; Malvoideae; Malva.
 OX NCBI_TaxID=145753;
 [1]
 RN SEQUENCE, AND FUNCTION.
 RC TISSUE=Seed;
 RC MEDLINE=20568734; PubMed=11118343;
 RA Wang X., Bunkers G.J.;
 RA "Potent heterologous antifungal proteins from cheeseweed (Malva
 RT parviflora).";
 RL Biochem. Biophys. Res. Commun. 279:669-673 (2000).
 CC -|- FUNCTION: Possesses antifungal activity against F.graminearum.
 CC -|- SUBUNIT: Heterodimer of a large and a small subunit.
 CC -|- MISCELLANEOUS: Antimicrobial activity is not affected by salt
 CC concentration.
 DR GO: 0003799; F:antifungal peptide activity; IDA.
 KW Fungicide; Antibiotic.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1888 MW; 2893A1C66F5D3F57 CRC64;
 Query Match 37.5%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GPF 4
 |||
 Db 3 GPF 5
 RESULT 9
 TRYP_FELCA STANDARD; PRT; 16 AA.
 ID TRYP_FELCA
 AC P81071; 1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trypsin precursor (EC 3.4.21.4) (Fragment).
 CC Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RC MEDLINE=97235546; PubMed=9080665;
 RA Steiner J.M., Medinger T.L., Williams D.A.;
 RT "Purification and partial characterization of feline trypsin.";
 RL Comp. Biochem. Physiol. 116B:87-93 (1997).
 CC -|- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
 CC -|- SUBCELLULAR LOCATION: Extracellular.
 CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR InterPro; IPR001254; Ser.protease TRY.
 DR PROSITE; PS00240; TRYPSIN_DOM; PARTIAL.
 DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
 DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
 KW Hydrolase; Serine protease; Digestion; Pancreas; Zymogen.
 FT PROPEP 1 8
 CHAIN 9 >16
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1825 MW; A6D751BB58760A86 CRC64;
 Query Match 37.5%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 FPI 6
 |||
 Db 1 FPI 3
 RESULT 10
 AHD2_TETPY STANDARD; PRT; 18 AA.
 ID AHD2_TETPY

AC P35430;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE 20-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.149) (20-alpha-HSD)
 DE (Fragment).
 CC Tetrahymena pyriformis.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
 OC Tetrahymenina; Tetrahymena.
 OX NCBI_TaxID=5908;
 [1]
 RN SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN=W;
 RC MEDLINE=94107273; PubMed=8280099;
 RA Inazu A., Sato K., Nakayama Y., Hara A., Nozawa Y.;
 RT "Purification and characterization of a novel dimeric 20 alpha-
 RT hydroxysteroid dehydrogenase from Tetrahymena pyriformis.";
 RL Biochem. J. 297:195-200 (1994).
 CC -|- FUNCTION: SPECIFIC FOR THE OXIDATION OF THE 20-ALPHA HYDROXY
 CC GROUP OF 17-ALPHA-HYDROXYPROGESTERONE AND 17-ALPHA-
 CC HYDROXYPREGNENOLONE.
 CC -|- CATALYTIC ACTIVITY: 17-alpha,20-alpha-dihydroxypregn-4-en-3-one +
 CC NAD(P)(+) = 17-alpha-hydroxyprogesterone + NAD(P)H.
 CC -|- SUBUNIT: Homodimer.
 DR PIR; S40502; S40502.
 KW Oxidoreductase; NADP.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 1861 MW; 16DF6B287E3B0A0D CRC64;
 Query Match 37.5%; Score 3; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 FPI 6
 |||
 Db 13 FPI 15
 RESULT 11
 DURA_STRGV STANDARD; PRT; 19 AA.
 ID DURA_STRGV
 AC P36504;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Lantibiotic duramycin (leucopeptin) (Antibiotic PA48009).
 CC Streptovorticillum griseovorticillatum.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=68215;
 [1]
 RN SEQUENCE, AND STRUCTURE BY NMR.
 RC STRAIN=PA-48009;
 RC MEDLINE=91107438; PubMed=2272918;
 RA Hayaashi F., Nagashima K., Terui Y., Kawamura Y., Matsumoto K.,
 RA Itazaki H.;
 RT "The structure of PA48009: the revised structure of duramycin.";
 RL J. Antibiot. 43:1421-1430 (1990).
 [2]
 RN SEQUENCE.
 RC MEDLINE=91107436; PubMed=2125590;
 RA Fredenhagen A., Fendrich G., Marki F., Marki W., Gruner J.,
 RA Raschdorf F., Peter H.H.;
 RT "Duramycins B and C, two new lanthionine containing antibiotics as
 RT inhibitors of phospholipase A2. Structural revision of duramycin and
 RT cinnamycin.";
 RL J. Antibiot. 43:1403-1412 (1990).
 CC -|- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
 CC -|- PTM: Maturation of lantibiotics involves the enzymic conversion of
 CC Thr, and Ser into dehydrated AA and the formation of thioether
 CC bonds with cysteine or the formation of dialkylamine bonds with
 CC lysine. This is followed by membrane translocation and cleavage of
 CC the modified precursor.

CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
 KW Antibiotic; Bacteriocin; Lantibiotic; D-amino acid; Thioether bond.
 FT CROSSLNK 1 18 Beta-methylanthionine (Cys-Thr).
 FT CROSSLNK 4 14 Lanthionine (Ser-Cys).
 FT CROSSLNK 5 11 Beta-methylanthionine (Cys-Thr).
 FT CROSSLNK 6 19 Lysinoalanine (Ser-Lys).
 SQ SEQUENCE 19 AA; 2069 MW; 012951AE27362F00 CRC64;

Query Match 37.5%; Score 3; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
 Db 8 GPF 10

RESULT 12
 PAP2 PARMA STANDARD; PRT; 5 AA.
 AC P81864;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Pardaxin II (PXII) (Fragment).
 OS Pardachirus marmoratus (Red sea moses sole).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
 CC Soleiidae; Soleidae; Pardachirus.
 CC NCBI_TaxID=31087;
 [1]
 RP SEQUENCE.

RC TISSUE=Skin secretion;
 RX MEDLINE=87057369; PubMed=3782138;
 RA Lazarovici P., Primor N., Loew L.M.;
 "Purification and pore-forming activity of two hydrophobic
 RT polypeptides from the secretion of the Red sea moses sole (Pardachirus
 RT marmoratus).";
 RL J. Biol. Chem. 261:16704-16713 (1986).
 CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
 CC properties. Forms voltage-dependent, ion-permeable channels
 CC in membranes. At high concentration causes cell membrane lysis.
 CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
 KW Toxin.
 FT NON TER
 SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PF 5
 Db 4 PF 5

RESULT 13
 SUGA ACHDO STANDARD; PRT; 5 AA.
 AC P19951;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Subesophageal ganglion pentapeptide.
 CC Acheta domestica (House cricket).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
 CC Acheta.
 CC NCBI_TaxID=6997;
 [1]

RP SEQUENCE.
 RA Wicker C., Wicker C.;
 RT "Isolation and structure of a peptide isolated from the
 RT subesophageal ganglion of Acheta domestica (orthoptera).";
 RL Comp. Biochem. Physiol. 88C:185-187(1987).
 CC -!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL
 CC GANGLIA.
 DR PIR; JS0319; JS0319.
 SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
 Db 4 PF 5

RESULT 14
 EI01 LITRU STANDARD; PRT; 6 AA.
 AC P82096;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Electrin 1.
 OS Litoria rubella (Desert tree frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 CC Pelodyadinae; Litoria.
 CC NCBI_TaxID=104895;
 [1]
 RP SEQUENCE.

RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645 (1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 KW Amphibian defense peptide; Amidation.
 FT MOD RES 6
 SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6
 Db 3 PF 4

RESULT 15
 CCF1 ENTFA STANDARD; PRT; 7 AA.
 AC P20104;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone ccf10.
 OS Enterococcus faecalis (Streptococcus faecalis).
 CC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 CC NCBI_TaxID=1351;
 [1]
 RP SEQUENCE.
 RX MEDLINE=89008313; PubMed=3139658;
 RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
 RA Adsit J.C., Dunny G.M., Suzuki A.;
 RT "Structure of ccf10, a peptide sex pheromone which induces
 RT conjugative transfer of the Streptococcus faecalis tetracycline

```

RT resistance plasmid, pCF10."
RL J. Biol. Chem. 263:14574-14578 (1988).
CC -1- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID PCF10.
DR PIR; A30812; A30812.
KW Pheromone.
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LV 8
DB 1 LV 2

RESULT 16
CIA_ENTFA
ID CIA_ENTFA STANDARD; PRT; 7 AA.
AC P11932;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=87005252; PubMed=3093276;
RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
RA White B.A., An F.Y., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the Streptococcus faecalis sex pheromone,
RT CAM373."
RL FEBS Lett. 206:69-72 (1986).
CC -1- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
CC HARBORING PAM373.
CC -1- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR
CC SPECIFICITY OF PHEROMONES TO PLASMIDS.
CC -1- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
DR PIR; A25269; A25269.
KW Pheromone.
SQ SEQUENCE 7 AA; 734 MW; 75BDD72059C05D80 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IL 7
DB 4 IL 5

RESULT 17
FARI_HELTI
ID FARI_HELTI STANDARD; PRT; 7 AA.
AC P41871;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRamide-like neuropeptide GDPFLRF-amide.
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Planorbidae; Helisoma.
OX NCBI_TaxID=27815;
RN [1]
RP SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis."

```

```

RL Peptides 15:31-36 (1994).
CC -1- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
CC THE KIDNEY, MANTLE AND SKIN.
CC -1- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
DB 3 PF 4

RESULT 18
MNPI_LEPDE
ID MNPI_LEPDE STANDARD; PRT; 7 AA.
AC P42984;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Myotropic neuropeptide 1 (Ld-MNP-1).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
OC Chrysomelini; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE AND SYNTHESIS.
RC TISSUE=Head.
RX MEDLINE=95380343; PubMed=7651886;
RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RA Grauwels L., van Leuven F., de Loof A.;
RT "Identification, characterization, and immunological localization of
RT a novel myotropic neuropeptide in the Colorado potato beetle,
RT Leptinotarsa decemlineata."
RL Peptides 16:365-374 (1995).
CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 705 MW; 6DD737687458DB0 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3
DB 4 GP 5

RESULT 19
UF04_MOUSE
ID UF04_MOUSE STANDARD; PRT; 7 AA.
AC F38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (p46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;

```

RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
 FT NON TER 7
 SQ SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RG 2
 ||
 DB 6 RG 7

RESULT 20
 UN06 PINPS STANDARD; PRT; 7 AA.
 ID _UN06 PINPS STANDARD; PRT; 7 AA.
 AC P81675;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of needles (N141) (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=9274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 proteins";
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
 FT NON TER 1
 FT NON TER 7
 SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
 ||
 DB 6 PF 7

RESULT 21
 AL15 CARMA STANDARD; PRT; 8 AA.
 ID _AL15 CARMA STANDARD; PRT; 8 AA.
 AC P81818;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 15.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestros J.-L., Scott A.G., Jaros P.P.,

RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 811 MW; 922879D5AB47687D CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3
 ||
 DB 2 GP 3

RESULT 22
 AL16 CARMA STANDARD; PRT; 8 AA.
 ID _AL16 CARMA STANDARD; PRT; 8 AA.
 AC P81819;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 16.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestros J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3
 ||
 DB 2 GP 3

RESULT 23
 ALL5 CALVO STANDARD; PRT; 8 AA.
 ID _ALL5 CALVO STANDARD; PRT; 8 AA.
 AC P41841;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=93211980; PubMed=8460157;
 RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,

RA Thorpe A.;
 RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria
 with sequence homology to cockroach allatostatins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
 RN [2]
 RP CHARACTERIZATION, AND HYDROXYLATION.
 RC TISSUE=Head;
 RX MEDLINE=94342269; PubMed=8063725;
 RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
 RT "[Hyp3]Met-callatostatin. Identification and biological properties of
 a novel neuropeptide from the blowfly Calliphora vomitoria.";
 RL J. Biol. Chem. 269:21059-21066(1994).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
 A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
 INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
 BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
 FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
 CC -!- TISSUE SPECIFICITY. NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 DR PIR; E47393;
 KW Neuropeptide; Amidation; Hydroxylation.
 FT MOD RES 3 3 HYDROXYLATION (20%).
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB47768 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3
 ||
 DB 1 GP 2

RESULT 24

ALL5 CYDPO STANDARD; PRT; 8 AA.
 AC P82156;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiastatin 5.
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 898 MW; 922879CABB58640D CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RG 2
 ||
 DB 2 RG 3

RESULT 25

ALL8 CARMA STANDARD; PRT; 8 AA.
 AC P81811;

DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 8.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Brachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 795 MW; 922879CDCB47687D CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3
 ||
 DB 2 GP 3

RESULT 26

ALL9 CARMA STANDARD; PRT; 8 AA.
 AC P81812;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 9.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Brachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 781 MW; 7C2879CDCB476878 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3
 ||
 DB 2 GP 3

RESULT 27

ANG2 BOTJA STANDARD; PRT; 8 AA.
 ID _ANG2_BOTJA

```

AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Luca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca."
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON TER 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
DB 7 PF 8

RESULT 28
CAD1_ENTFA
ID CAD1_ENTFA STANDARD; PRT; 8 AA.
AC P13268;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CAD1.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85051889; PubMed=6437872;
RA Mori M., Sagakami Y., Nariya M., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the bacterial sex pheromone, cad1, that
RT induces plasmid transfer in Streptococcus faecalis."
RL FEBS Lett. 178:97-100(1984).
CC -!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID PAD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LV 8
DB 4 LV 5

RESULT 29
CPD1_ENTFA
ID CPD1_ENTFA STANDARD; PRT; 8 AA.
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)

```

```

DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CPD1.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, cpd1."
RL Science 226:849-850(1984).
CC -!- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOCIN PLASMID PPD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LV 8
DB 2 LV 3

RESULT 30
FAR7_ASCSU
ID FAR7_ASCSU STANDARD; PRT; 8 AA.
AC P43171;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AF7.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum."
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 963 MW; 9CD40059D417687D CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3
DB 2 GP 3

RESULT 31
PPK2_PERAM
ID PPK2_PERAM STANDARD; PRT; 8 AA.
AC P82692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-2 (Pea-PK-2) (FxrRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;

```


RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RA MEDLINE=9735323; PubMed=9210163;
 RX Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of two pyrokinins from the
 retrocerebral complex of the American cockroach.";
 RL Peptides 18:473-478(1997).
 RN [2]
 RN TISSUE SPECIFICITY.
 RP MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of EXPRlamides in the nervous system of
 the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 (MYOTROPIC ACTIVITY).
 CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
 CC -!- MASS SPECTROMETRY: MW=883; METHOD=WALDI.
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; FALSE NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 884 MW; C934176D9D7775 CRC64;

 Query Match 25.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 PF 4
 DB 3 PF 4

 RESULT 32
 ID -PK3_PERAM STANDARD; PRT; 8 AA.
 AC P82618;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-3 (Pea-PK-3) (FXPRU-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;
 OC Blattidae; Periplaneta.
 CX NCBI_TaxID=6978;
 RN [1]
 RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Retrocerebral complex;
 RX MEDLINE=99212469; PubMed=10196736;
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and
 abdominal neurohemal organs of the American cockroach.";
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).
 RN [2]
 RN TISSUE SPECIFICITY.
 RP MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of EXPRlamides in the nervous system of
 the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 (MYOTROPIC ACTIVITY).
 CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
 CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=WALDI.
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

 Query Match 25.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 7 LV 8
 DB 1 LV 2

 RESULT 33
 ID -RS7_MYCIT STANDARD; PRT; 8 AA.
 AC P33564;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S7 (Fragment).
 GN RPSG.
 OS Mycobacterium intracellulare.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 CX NCBI_TaxID=1767;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=93197130; PubMed=8451173;
 RX Nair J., Rouse D.A., Morris S.L.;
 RT "Nucleotide sequence analysis of the ribosomal S12 gene of
 Mycobacterium intracellulare.";
 RL Nucleic Acids Res. 21:1039-1039(1993).
 CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
 directly to 16S rRNA where it nucleates assembly of the head
 domain of the 30S subunit. Is located at the subunit interface
 close to the decoding center, probably blocks exit of the E-site
 tRNA (By similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
 and S11 (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See http://www.isb-sib.ch/announce/
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L08171; AAA5376.1; -
 DR PIR; S35538; S35538.
 DR HAMAP; MF 00480; -; 1.
 DR InterPro; IPR000235; Ribosomal S7.
 DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
 KW Ribosomal protein; RNA-binding; rRNA-binding; tRNA-binding.
 FT INIT MET 0 0 BY SIMILARITY.
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

 Query Match 25.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 GP 3
 DB 4 GP 5

 RESULT 34
 ID -RT34_BOVIN STANDARD; PRT; 8 AA.
 AC P82929;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitochondrial 28S ribosomal protein S34 (S34mt) (MRP-S34) (Fragment).
 GN MRPS34.

```

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C.; Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IL 7
DB 4 IL 5

RESULT 35
UPAA HUMAN STANDARD; PRT; 8 AA.
ID UPAA HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7, ITS MW IS: 12 kDa.
DR SWISS-2DPAGE; P30096; HUMAN.
FT NON_TER 1 1
FT VARIANT 5 5 F -> P.
FT NON_TER 8 8 /FTID=VAR_000004.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IL 7
DB 2 IL 3

RESULT 36
VGLG HSV2B STANDARD; PRT; 8 AA.
ID VGLG HSV2B STANDARD; PRT; 8 AA.
AC P81780;

```

```

DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Glycoprotein G (Fragment).
OS Herpes simplex virus (type 2 / strain B4327UR).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=103921;
RN [1]
RP SEQUENCE.
RA Liljeqvist J.-A., Svennerholm B., Bergstrom T.;
RL Submitted (APR-1999) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GD, GI, AND GE.
CC -!- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
CC HSV-1.
KW Glycoprotein.
FT NON_TER 8 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 683 MW; 7B47686772C865B8 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3
DB 6 GP 7

RESULT 37
CCAP CARMA STANDARD; PRT; 9 AA.
ID CCAP CARMA STANDARD; PRT; 9 AA.
AC P38556;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cardioactive peptide (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759, 7130, 7067, 37547;
RN [1]
RP SEQUENCE.
RC SPECIES=C.maenas; TISSUE=Pericardial organs;
RA Stangier J., Hilbich C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
RT shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=M.sexta;
RX MEDLINE=93050243; PubMed=1426284;
RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
RT hawkmoth, Manduca sexta.";
RL FEBS Lett. 313:165-168(1992).
RN [3]
RP SEQUENCE.
RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RX MEDLINE=94176032; PubMed=8129851;
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
RT molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
CC INTO THE HEMOLYMPH.
DR PIR; A26363; A26363.

```

DR PIR; S27233; S27233.
 KW Neuropeptide; Amidation.
 FT DISULFID 3 9
 FT MOD RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 959 MW; CSA861A9CDD44EB9 CRC64;
 Query Match 25.0%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PF 4
 Db 1 PF 2
 RESULT 38
 CONO CONST STANDARD; PRT; 9 AA.
 AC P05487;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Arg-conopressin S.
 OS Conus striatus (Striated cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6493;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=8805832; PubMed=3680228;
 RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
 RA Gray W.R., Olivera B.M.;
 RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
 RT peptides from Conus geographus and Conus striatus venoms.";
 RL J. Biol. Chem. 262:15821-15824(1987).
 RN [2]
 RP REVIEW.
 RX MEDLINE=89024586; PubMed=3052286;
 RA Gray W.R., Olivera B.M., Cruz L.J.;
 RT "Peptide toxins from venomous Conus snails.";
 RL Annu. Rev. Biochem. 57:665-700(1988).
 CC -!- FUNCTION: Targets vasopressin-oxytocin related receptors.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR; B28495; B28495.
 DR InterPro; IPR000981; Neurohyp_horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD RES 9 9
 SQ SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;
 Query Match 25.0%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RG 2
 Db 8 RG 9
 RESULT 39
 DNFI LOCFMI STANDARD; PRT; 9 AA.
 AC P16339;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Locupressin (Diuretic neuropeptide F1/F2).
 OS Locusta migratoria (Migratory locust).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Suboesophageal ganglion, and Thoracic ganglion;
 RX MEDLINE=8807077; PubMed=3689410;
 RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
 RA Delaage M., Schooley D.A.;
 RT "Identification of an arginine vasopressin-like diuretic hormone from
 RT Locusta migratoria.";
 RL Biochem. Biophys. Res. Commun. 149:180-186(1987).
 CC -!- FUNCTION: DIURETIC HORMONE.
 CC -!- SUBUNIT: F2 IS AN ANTI-PARALLEL DISULFIDE LINKED DIMER OF F1.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR; A29477; A29477.
 DR InterPro; IPR000981; Neurohyp_horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT DISULFID 1 6 IN F1.
 FT DISULFID 1 1 INTERCHAIN (WITH C-6') (IN F2).
 FT DISULFID 6 6 INTERCHAIN (WITH C-1') (IN F2).
 FT MOD RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;
 Query Match 25.0%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RG 2
 Db 8 RG 9
 RESULT 40
 FARS PANRE STANDARD; PRT; 9 AA.
 ID -FARS PANRE
 AC P82661;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FMRamide-like neuropeptide PF5 (AMRNALVRP-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE, FUNCTION, AND AMIDATION.
 RA Moffet C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
 RA Maule A.G.;
 RT "Isolation, characterization and pharmacology of FMRamide-related
 RT peptides (FARPs) from free-living nematode, Panagrellus redivivus.";
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.
 CC -!- FUNCTION: MYOACTIVE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC -!- FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1077 MW; A0D112C72DD45406 CRC64;
 Query Match 25.0%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 LV 8
 Db 6 LV 7
 RESULT 41
 FAR9_ASCSU

```

ID FAR9_ASCSU STANDARD; PRT; 9 AA.
AC P43172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRamide-like neuropeptide AF9.
OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3
||
DB 3 GP 4

RESULT 42
FIBB_PAPAN
ID FIBB_PAPAN STANDARD; PRT; 9 AA.
AC P19344;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D28854; D28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1076 MW; DDFE6409C7287B06 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

ID ISOT_CYPCA STANDARD; PRT; 9 AA.
AC P42993;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Isotocin.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishes.";
RL Comp. Biochem. Physiol. 14:245-254(1965).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A61364; A61364.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PI 6
||
DB 7 PI 8

RESULT 44
KNL3_BOMVA
ID KNL3_BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE. SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Bjorson A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.

```

SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
DB 7 PF 8

RESULT 45

LMT3 LOOMI
ID -LMT3_LOOMI STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamytotropin 3 (LOW-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamytotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamytotropin peptide family.";
RT Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -1- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR INTERPRO; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 9 9
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
DB 4 PF 5

RESULT 46

OXYT BUPRE
ID -OXYT_BUPRE STANDARD; PRT; 9 AA.
AC P42955;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Seritocin ([Ser5, Ile8]-oxytocin).
OS Bufo regularis (leopard toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;
OX NCBI_TaxID=8390;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary neurointermediate lobe;
RX MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
RT "A new neurohypophysial peptide, seritocin ([Ser5, Ile8]-oxytocin),
RT identified in a dryness-resistant African toad, Bufo regularis.";
RT Int. J. Pept. Protein Res. 45:482-487(1995).

CC -1- FUNCTION: Devoid of oxytocic activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neuhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9 9
FT MOD RES 9 9 9
SQ SEQUENCE 9 AA; 983 MW; 17FF476EA5A6D04B CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PI 6
DB 7 PI 8

RESULT 47

OXYT CYPCA
ID -OXYT_CYPCA STANDARD; PRT; 9 AA.
AC P23879;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Vasotocin.
OS Cyprinus carpio (Common carp), and
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962, 7757;
RN [1]
RP SEQUENCE.
RC SPECIES=Carpio; TISSUE=Pituitary;
RA Acher R., Chauvet J., Chauvet M.-I., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishes.";
RL Comp. Biochem. Physiol. 14:245-254(1965).
RN [2]

RP SEQUENCE.
RC SPECIES=P. marinus; TISSUE=Pituitary;
RX MEDLINE=88225976; PubMed=3371648;
RA Lane T.F., Sower S.A., Kawauchi H.;
RT "Arginine vasotocin from the pituitary gland of the lamprey
RT (Petromyzon marinus): isolation and amino acid sequence.";
RL Gen. Comp. Endocrinol. 70:152-157(1988).

CC -1- FUNCTION: ANTIDIURETIC HORMONE.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; B61364; B61364.
DR PIR; S06375; S06375.
DR InterPro; IPR000981; Neuhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9 9
FT MOD RES 9 9 9
SQ SEQUENCE 9 AA; 1053 MW; 17EB176EB456D04B CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RG 2
DB 8 RG 9

RESULT 48

OXYT_OCTVU

```

Qy 1 RG 2
   ||
Db 8 RG 9

RESULT 50
RE42_LITRU STANDARD; PRT; 9 AA.
ID RE42_LITRU STANDARD; PRT; 9 AA.
AC P82075; P82093;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 4.2/4.3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RN SEQUENCE, AND MASS SPECTROMETRY.
RP TISSUE=Skin secretion;
RC Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
RN [2]
RN SEQUENCE
RP TISSUE=Skin secretion;
RC Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RA "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -1- PTM: Rubellidin 4.2 seems to differ from Rubellidin 4.3 by its C-
CC terminal amidation.
CC -1- MASS SPECTROMETRY: MW=883; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MOD RES 9
FT SEQUENCE 9 AA; 884 MW; 2C2D77205AA72738 CRC64;
Qy 6 IL 7
   ||
Db 6 IL 7

Query Match 25.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 51
SAMP MUSCA
ID _SAMP MUSCA STANDARD; PRT; 9 AA.
AC P19035;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum amyloid P-component (SAP) (Fragment).
OS Mustelus canis (Smooth dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes; Triakidae;
OC Mustelus.
OX NCBI_TaxID=7812;
RN [1]
RN SEQUENCE
RP MEDLINE=83160932; PubMed=6403520;
RX Robey F.A., Tanaka T., Liu T.-Y.;
RT "Isolation and characterization of two major serum proteins from the

```

RT dogfish, Mustelus canis, C-reactive protein and amyloid P component.";
 RL J. Biol. Chem. 258:3889-3894(1983).
 CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
 CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
 CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
 CC PIR; B20569; B20569.
 DR InterPro: IPR001759; Pentaxin.
 DR PROSITE: PS00289; PENTAXIN; PARTIAL.
 KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
 FT DOMAIN 1 >9 PENTAXIN.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FP 5
 ||
 Db 2 FP 3

RESULT 52
 TKL1 LOCMI
 ID TKL1 LOCMI STANDARD; PRT; 9 AA.
 AC P16223;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Locustatachykinin I (TK-I).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=90184489; PubMed=2311766;
 RA Schoofs L., Holman G.M., Hayes I.K., Nachman R.J., de Loof A.;
 RT "Locustatachykinin I and II, two novel insect neuropeptides with
 RT homology to peptides of the vertebrate tachykinin family.";
 RL PDBS Lett. 261:397-401(1990).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
 CC OVIDUCT AND FOREGUT.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 9
 FT AMIDATION.
 SQ SEQUENCE 9 AA; 939 MW; 2389C86B59C865A7 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3
 ||
 Db 1 GP 2

RESULT 53
 ULAD HUMAN
 ID ULAD HUMAN STANDARD; PRT; 9 AA.
 AC P31929;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of liver tissue (Spot 106) (Fragment).
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94147969; PubMed=8313870;
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
 RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
 RT "Human liver protein map: update 1993.";
 RL Electrophoresis 14:1216-1222(1993).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6, ITS MW IS: 15 kDa.
 DR SWISS-2DPAGE; P31929; HUMAN.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1129 MW; D02DFB41B6D33322 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LV 8
 ||
 Db 1 LV 2

RESULT 54
 UP3 HUMAN
 ID UP3 HUMAN STANDARD; PRT; 9 AA.
 AC P30089;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
 DR SWISS-2DPAGE; P30089; HUMAN.
 FT NON_TER 1
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FP 5
 ||
 Db 4 FP 5

RESULT 55
 UP7 HUMAN
 ID UP7 HUMAN STANDARD; PRT; 9 AA.
 AC B30053;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 18) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 DR PROTEIN IS: 5.05, ITS MW IS: 37 kDa.
 CC SWISS-2DPAGE; P30093; HUMAN.
 FT NON_TER 1 1
 FT UNSURE 5 5
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;
 Query Match 25.0%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 LV 8
 DB 2 LV 3
 RESULT 56
 AH3_PRUSE STANDARD; PRT; 10 AA.
 AC P29261;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
 DE isozyme II) (AH II) (Fragment).
 OS Prunus serotina (Black cherry).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 OX NCBI_TaxID=23207;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RA Li C.P., Swain E., Poulton J.E.;
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
 RL Plant Physiol. 100:282-290(1992).
 CC -!- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
 CC glucose.
 CC -!- SUBUNIT: Monomer.
 CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
 CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
 CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
 CC EMBRYONAL TISSUES.
 CC -!- PTM: GLYCOSYLATED.
 KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;
 Query Match 25.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PI 6
 DB 4 PI 5
 RESULT 57
 ANGL_BOTJA STANDARD; PRT; 10 AA.
 ID ANGL_BOTJA
 AC Q10581;

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Angiotensin-like peptide I (Fragment).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scieroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=96208932; PubMed=8829801;
 RA Borgheresi R.A.M.B., Dalle Luca J., Carmona E., Picarelli Z.P.;
 RT "Isolation and identification of angiotensin-like peptides from the
 RT plasma of the snake Bothrops jararaca.";
 RL Comp. Biochem. Physiol. 113B:467-473(1996).
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;
 Query Match 25.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PF 4
 DB 7 PF 8
 RESULT 58
 ANGT_BOVIN STANDARD; PRT; 10 AA.
 ID ANGT_BOVIN
 AC P01017;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
 DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]
 DE (Fragment).
 GN AGT OR SERPIN A8.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RA Elliott D.F., Peart W.S.;
 RT "The amino acid sequence in a hypertensin.";
 RL Biochem. J. 85:246-254(1957).
 CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
 CC plasma.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR PIR; A90345; A90345.
 DR PDB; 3ER5; 15-JUL-92.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin; 3D-structure.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT PEPTIDE 1 8 ANGIOTENSIN II.
 FT PEPTIDE 2 8 ANGIOTENSIN III.
 FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1282 MW; CEEFBDD761F2DB42 CRC64;
 Query Match 25.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PF 4
 ||
 7 PF 8
 Db
 RESULT 59
 ANGT_CHICK
 ID ANGT_CHICK STANDARD; PRT; 10 AA.
 AC P01018;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II) (Fragment).]
 DE II; Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]
 GN ACT OR SERPINAB.
 OS Gallus gallus (Chicken), and
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 NCBI_TaxID=9031, 93934;
 RN [1]
 RP SEQUENCE
 RC SPECIES=Chicken;
 RX MEDLINE=74127845; PubMed=4361802;
 RA Nakayama T., Nakajima T., Sokabe H.;
 RT "Comparative studies on angiotensins. 3. Structure of fowl
 angiotensin and its identification by DNS-method.";
 RL Chem. Pharm. Bull. 21:2085-2087(1973).
 RN [2]
 RP SEQUENCE
 RC SPECIES=C.c.japonica;
 RX MEDLINE=90284684; PubMed=2191893;
 RA Takei Y., Haegawa Y.;
 RT "Vasopressor and depressor effects of native angiotensins and
 inhibition of these effects in the Japanese quail.";
 RL Gen. Comp. Endocrinol. 79:12-22(1990).
 CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CLEAVES ANGIOTENSIN I. FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II. THE MOST POTENT
 PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 BALANCE OF BODY FLUIDS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR PIR; A60624; A60624.
 DR PIR; A90917; A90917.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT PEPTIDE 1 8 ANGIOTENSIN II.
 FT PEPTIDE 2 8 ANGIOTENSIN III.
 FT NON TER 10 1232 MW; CEEFBDD761F2DB42 CRC64;
 SQ SEQUENCE 10 AA; 1232 MW; CEEFBDD761F2DB42 CRC64;
 Query Match 25.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PF 4
 ||
 7 PF 8
 Db

RESULT 60
 BPP VIPAS
 ID BPP VIPAS STANDARD; PRT; 10 AA.
 AC P31351;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide (Angiotensin-converting
 enzyme inhibitor).
 DE Vipera aspis (Aspic viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Vipera.
 NCBI_TaxID=8706;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Venom;
 RX MEDLINE=90382616; PubMed=2169439;
 RA Komori Y., Sugihara H.;
 RT "Characterization of a new inhibitor for angiotensin converting
 enzyme from the venom of Vipera aspis aspis.";
 RL Int. J. Biochem. 22:767-771(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 angiotensin-converting enzyme and enhances the action of
 bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; A60377; XASNPC.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;
 Query Match 25.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GP 3
 ||
 5 GP 6
 Db
 RESULT 61
 COXO RAT
 ID COXO RAT STANDARD; PRT; 10 AA.
 AC P80432;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIIC, mitochondrial (EC 1.9.3.1)
 DE (VIIIA) (Fragment).
 DE COX7C OR COX7C1.
 GN Rattus norvegicus (Rat).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE
 RC STRAIN=Wistar; TISSUE=Heart, and Liver;
 RX MEDLINE=95324529; PubMed=7601105;
 RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
 RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
 amino-terminal sequences suggest identity of the fetal heart and the
 adult liver isoform.";
 RL Eur. J. Biochem. 230:235-241(1995).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocchrome c + O(2) = 4 ferricytochrome
 c + 2 H(2)O.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
 DR PIR; S65388; S65388.
 KW Oxidoreductase; Mitochondrion.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1117 MW; 126DE767687B1B0B CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred.No. 1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3
 ||
 6 GP 7

Db

RESULT 62

COCO THUOB
 ID _COCO THUOB STANDARD; - PRT; 10 AA.
 AC P80982;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIIC (EC 1.9.3.1) (Fragment).
 OS Thunnus obesus (Bigeye tuna).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 CC Scombridae; Thunnus.
 OX NCBI_TaxID=8241;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Heart, and Liver;
 RX MEDLINE=97454291; PubMed=9310366;
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver";
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferrocycytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
 DR PIR; S77990; S77990.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1059 MW; 126DE767687B1DCB CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred.No. 1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3
 ||
 6 GP 7

Db

RESULT 63

ESTA SCHGA
 ID _ESTA SCHGA STANDARD; PRT; 10 AA.
 AC P81012;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Esterase 52 kDa subunit (EC 3.1.1.1) (Carboxylic-ester hydrolase)
 DE (Fragment).
 OS Schizaphis graminum (Aphid).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
 CC Aphidoidea; Aphididae; Aphidini; Schizaphis.
 OX NCBI_TaxID=13262;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=97468499; PubMed=9327586;
 RA Siegfried B.D., Ono M., Swanson J.J.;
 RT "Purification and characterization of a carboxylesterase associated

with organophosphate resistance in the greenbug, Schizaphis graminum
 RT (Homoptera: Aphididae).";
 RL Arch. Insect Biochem. Physiol. 36:229-240(1997).
 CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
 CC carboxylic anion.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR InterPro; IPR002018; Carboxylesterase_B_1; PARTIAL.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; PARTIAL.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
 KW Hydrolase; Serine esterase.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1025 MW; 018ABE587865A2C0 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred.No. 1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PI 6
 ||
 2 PI 3

Db

RESULT 64

FAR6 PANRE
 ID _FAR6 PANRE STANDARD; PRT; 10 AA.
 AC P82660;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FMRFamide-like neuropeptide PF6 (NGAPQPPVRF-amide).
 OS Panagrellus redivivus.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 CC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE, FUNCTION, AND AMIDATION.
 RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
 RA Maule A.G.;
 RT "Isolation, characterization and pharmacology of FMRFamide-related
 RT peptides (FARPs) from free-living nematode, Panagrellus redivivus.";
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.
 CC -!- FUNCTION: MYOACTIVE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 10 10
 SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred.No. 1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
 ||
 6 PF 7

Db

RESULT 65

NS1 MYCTU
 ID _NS1 MYCTU STANDARD; PRT; 10 AA.
 AC P81135;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 30 kDa non-secretory protein 1 (Fragment).
 OS Mycobacterium tuberculosis
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=H37Rv;

```

RA Prasad H.K., Annapurna P.S.;
RL Submitted (DEC-1997) to the SWISS-PROT data bank.
CC -!- CAUTION: We are unable to find this protein in the translation of
CC the genome of strain H37Rv.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1042 MW; 8767FE6AB2C73771 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LV 8
DB 5 LV 6

RESULT 66
ID PVK LOCOMI STANDARD; PRT; 10 AA.
AC P83382;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Periviscerokinin (hom-PVK-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
TISSUE=Abdominal perisymphathetic organs;
MEDLINE=21896327; PubMed=11897380;
RA Predel R., Gaede G.;
RT Identification of the abundant neuropeptide from abdominal
RT perisymphathetic organs of locusts.";
RL Peptides 23:621-627(2002).
CC -!- FUNCTION: Myotropic peptide; increases the frequency of
CC contraction of the heart and stimulates amplitude and tonus of the
CC foregut.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1104.5; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:0005184; F:neuropeptide hormone activity; IDA.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD_RES 10
FT MOD_RES 10 AMIDATION.
SQ SEQUENCE 10 AA; 1105 MW; 39811269D6D9C728 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FP 5
DB 7 FP 8

RESULT 67
ID Q2OB COMTE STANDARD; PRT; 10 AA.
AC P80455;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinoline 2-oxidoreductase, beta chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
SEQUENCE.

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

RC STRAIN=63;
RX MEDLINE=9603589; PubMed=7556204;
RA Schach S., Tshisuka B., Fetzner S., Lingens F.;
RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT quinoline and 3-methylquinoline degradation.";
RL Eur. J. Biochem. 232:536-544(1995).
CC -!- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-
CC 1,2-DIHYDROQUINOLINE.
CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-
CC 1(2H)-one + reduced acceptor.
CC -!- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)quinoline; first
CC step.
CC -!- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
CC TWO GAMMA CHAINS (PROBABLE).
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1241 MW; C2E2C25DD9CDC769 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FP 5
DB 3 FP 4

RESULT 68
ID RCA PINPS STANDARD; PRT; 10 AA.
AC P81084;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable ribulose biphosphate carboxylase/oxygenase activase (RuBisCO
DE activase) (RA) (Water stress responsive protein 4) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
SEQUENCE.
TISSUE=Needle;
RX MEDLINE=98418576; PubMed=9747804;
RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water-deficit-responsive proteins in maritime pine.";
RL Plant Mol. Biol. 38:587-596(1998).
RN [2]
SEQUENCE.
TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- FUNCTION: ACTIVATION OF RUBISCO (RIBULOSE-1,5-BISPHOSPHATE
CC CARBOXYLASE/OXYGENASE; EC 4.1.1.39) INVOLVES THE ATP-DEPENDENT
CC CARBOXYLATION OF THE EPSILON-AMINO GROUP OF LYSINE LEADING TO A
CC CARBAMATE STRUCTURE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Chloroplast stroma (By similarity).
CC -!- INDUCTION: By water stress.
CC -!- SIMILARITY: BELONGS TO THE RUBISCO ACTIVASE FAMILY.
KW Chloroplast; ATP-binding.
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1171 MW; C0A506D2C72B1EA6 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Qy 7 LV 8
    ||
Db 6 LV 7

RESULT 69
RRPL PHODV
ID RPL PHODV STANDARD; PRT; 10 AA.
AC P35946;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase beta subunit (EC 2.7.7.48) (large structural protein)
DE (L protein) (Fragment).
GN L.
OS Phocine distemper virus (PDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_TaxID=11240;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=U1ster/88;
RX MEDLINE=92268877; PubMed=1588321;
RA Curran M.D., O'Loan D., Kennedy S., Rima B.K.;
RT "Molecular characterization of phocine distemper virus: gene order
and sequence of the gene encoding the attachment (H) protein.";
RL J. Gen. Virol. 73:1189-1194(1992).
CC -!- FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY
CC FUNCTION IN MRNA SYNTHESIS, CAPPING, METHYLATION AND POLY(A)
CC SYNTHESIS OF NEWLY SYNTHESIZED VIRAL MRNAS. RNA EDITING OF THE P
CC GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}(N).
CC -!- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DE EMBL; D10371; BAA01208.1; -
KW Transferase; RNA-directed RNA polymerase.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1105 MW; 9C2B7FD452D5A2D5 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 IL 7
    ||
Db 9 IL 10

RESULT 70
SLAP BACTG
ID SLAP BACTG STANDARD; PRT; 10 AA.
AC P49325;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE S-layer protein (surface layer protein) (Fragment).
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29338;
RN [1]
RP SEQUENCE
RX STRAIN=NRRL 4045; PubMed=2592346;
RX MEDLINE=90078111; PubMed=2592346;
```

```
RA Luckevich M.D., Beveridge T.J.;
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";
RL Bacteriol. 171:6656-6667(1989).
CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH OBLIQUE (P2) SYMMETRY.
DR PIR; A60476; A60476.
KW Cell wall; S-layer.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FP 5
    ||
Db 5 FP 6

RESULT 71
TRP8 LEUMA
ID TRP8 LEUMA STANDARD; PRT; 10 AA.
AC P81740;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tachykinin-related peptide 8 (LemTRP 8).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX TISSUE=Brain;
RX MEDLINE=97269266; PubMed=9114447;
RA Muren J.E., Maessel D.R.;
RT "Seven tachykinin-related peptides isolated from the brain of the
RT madeira cockroach; evidence for tissue-specific expression of
RT isoforms.";
RL Peptides 18:7-15(1997).
CC -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: BRAIN.
CC -!- MASS SPECTROMETRY: MW=1076.9; METHOD=MALDI.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1076 MW; 9E410371E9C87685 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GP 3
    ||
Db 1 GP 2

RESULT 72
UPAS HUMAN
ID UPAS HUMAN STANDARD; PRT; 10 AA.
AC P30091;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX TISSUE=Plasma;
RC MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC -1- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
CC PROTEIN.
DR SWISS-2DPAGE; P30091; HUMAN.
FT NON TER 1 1 G -> Y.
FT VARIANT 9 9 /FTId=VAR_000002.
FT NON TER 10 10
FT SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LV 8
Db 7 LV 8

RESULT 73
UXA2 CHLTR
ID UXA2 CHLTR STANDARD; PRT; 10 AA.
AC P38003;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Unknown protein from 2D-page from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/Bu;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christensen G., Birkelund S., Vretou E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.65, ITS MW IS: 26.5 kDa.
DR Siena-2DPAGE; P38003; -.
FT NON TER 10 10
FT SEQUENCE 10 AA; 1019 MW; 49C285C6CAE862C7 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LV 8
Db 3 LV 4

RESULT 74
XYNB DICB4
ID XYNB DICB4 STANDARD; PRT; 10 AA.
AC P80717;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase B (EC 3.2.1.8) (Xylanase B)
DE (1,4-beta-D-xylan xylanhidrolase B) (Fragment).

```

```

OS Dictyoglomus sp. (strain B4).
OC Bacteria; Dictyoglomi; Dictyoglomales; Dictyoglomaceae; Dictyoglomus.
OX NCBI_TaxID=69007;
RN [1]
RP SEQUENCE.
RA Adansen A.K., Jacobsen S., Ahring B.K.;
RL Submitted (OCT-1996) to the SWISS-PROT data bank.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL
CC HYDROLASES).
DR InterPro; IPR001000; Glyco_hydro_10.
DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; PARTIAL.
KW Xylan degradation; Hydrolase; Glycosidase.
FT NON TER 10 10
FT SEQUENCE 10 AA; 1144 MW; 4554322AA72041A3 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IL 7
Db 5 IL 6

RESULT 75
ANGT CRIGE
ID ANGT CRIGE STANDARD; PRT; 11 AA.
AC P09037;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Crinia-angiotensin II.
OS Crinia georgiana (Quacking frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Crinia.
OX NCBI_TaxID=8374;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=80024575; PubMed=488254;
RA Espamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
RT "Amino acid composition and sequence of crinia-angiotensin, an
RT angiotensin II-like endopeptide from the skin of the Australian
RT frog Crinia georgiana.";
RL Experientia 35:1132-1133(1979).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
DR PIR; S07207; S07207.
KW Vasoconstrictor.
FT NON TER 10 10
FT SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 25.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
Db 10 PF 11

```

Search completed: November 25, 2003, 19:28:25
Job time : 2.90864 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 : Search time 15.0233 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-29

Perfect score: 8

Sequence: 1 RGPFPILV 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTRMBL23.*

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	3	37.5	9	5	Q9TWD6	Q9twd6 leptinotars
2	3	37.5	10	13	Q90Y93	Q90y93 gallus gall
3	3	37.5	11	5	P82700	P82700 leucophaea
4	3	37.5	11	6	Q9TRR7	Q9trr7 oryctolagus
5	3	37.5	11	11	Q9QVC5	Q9qvc5 rattus norv
6	3	37.5	12	6	Q8MJQ0	Q8mjq0 saguinus fu
7	3	37.5	12	6	Q8MJP8	Q8mjp8 callimico g
8	3	37.5	12	6	Q8MJP7	Q8mjp7 callithrix
9	3	37.5	12	6	Q8MJP9	Q8mjp9 leontopithe
10	3	37.5	12	6	Q8MJP6	Q8mjp6 cebuella py
11	3	37.5	12	6	Q8MJE3	Q8mje3 samiri sci
12	3	37.5	12	6	Q8MJQ1	Q8mjql ateles fusc
13	3	37.5	12	6	Q8MJE2	Q8mje2 cebus apell
14	3	37.5	12	6	Q8MJE4	Q8mje4 aotus azara
15	3	37.5	12	11	Q8K3U3	Q8k3u3 mus musculu
16	3	37.5	13	2	Q53693	Q53693 streptomyce

17	3	37.5	13	2	Q34622	Q34622 borrelia bu
18	3	37.5	13	2	Q31365	Q31365 borrelia ga
19	3	37.5	13	2	Q31364	Q31364 borrelia ga
20	3	37.5	13	3	Q93824	Q93824 candida tro
21	3	37.5	14	2	O52220	O52220 salmonella
22	3	37.5	14	4	Q16045	Q16045 homo sapien
23	3	37.5	14	13	P82832	P82832 kana luteiv
24	3	37.5	15	2	Q9R5D5	Q9r5d5 chromatium
25	3	37.5	15	4	Q8TCS7	Q8tcs7 homo sapien
26	3	37.5	15	6	Q8WNQ2	Q8wnq2 sus scrofa
27	3	37.5	15	6	Q9TRN2	Q9trn2 sus scrofa
28	3	37.5	15	6	Q9TRN5	Q9trn5 sus scrofa
29	3	37.5	15	6	Q9TRN4	Q9trn4 sus scrofa
30	3	37.5	15	8	Q9T2K8	Q9t2k8 spinacia ol
31	3	37.5	15	8	Q35921	Q35921 salmo salar
32	3	37.5	15	10	Q9S929	Q9s929 glycine max
33	3	37.5	15	11	Q9Z114	Q9z114 mus musculu
34	3	37.5	15	13	Q9PS10	Q9ps10 gallus gall
35	3	37.5	16	4	Q9UCL0	Q9ucl0 homo sapien
36	3	37.5	16	4	Q9UCK9	Q9uck9 homo sapien
37	3	37.5	16	5	Q9TZR1	Q9tzzr1 haliotis fu
38	3	37.5	16	6	Q28324	Q28324 capra hircu
39	3	37.5	16	8	Q8MC35	Q8mc35 sonneratia
40	3	37.5	16	8	Q8MC39	Q8mc39 ammannia ba
41	3	37.5	16	8	Q8LVE1	Q8lve1 punica gran
42	3	37.5	16	8	Q8MC53	Q8mc53 woodfordia
43	3	37.5	16	8	Q8MC17	Q8mc17 ludwigia hy
44	3	37.5	16	8	Q8LVE2	Q8lve2 lythrum sal
45	3	37.5	16	8	Q8LVE0	Q8lve0 trapa maxim
46	3	37.5	16	8	Q8MET2	Q8met2 saxifraga s
47	3	37.5	16	8	Q8MC45	Q8mc45 decodon ver
48	3	37.5	16	8	Q8MC21	Q8mc21 combreum w
49	3	37.5	16	8	Q8MC51	Q8mc51 cuphea lanc
50	3	37.5	16	8	Q8MC33	Q8mc33 rotala indi
51	3	37.5	16	8	Q8MC19	Q8mc19 quiscualis
52	3	37.5	16	8	Q8MC49	Q8mc49 pemphis aci
53	3	37.5	16	8	Q8MC27	Q8mc27 lagerstroem
54	3	37.5	16	8	Q8MET0	Q8met0 cercidiphyll
55	3	37.5	16	8	Q8MC33	Q8mc33 sonneratia
56	3	37.5	16	8	Q8MC41	Q8mc41 nesaea lued
57	3	37.5	16	8	Q8MC15	Q8mc15 fuchsia hyb
58	3	37.5	16	8	Q8MC43	Q8mc43 sonneratia
59	3	37.5	16	8	Q8MC47	Q8mc47 peplis port
60	3	37.5	16	8	Q8MC37	Q8mc37 lawsonia in
61	3	37.5	16	8	Q8MC39	Q8mc39 duabanga gr
62	3	37.5	16	8	Q8MC31	Q8mc31 lagerstroem
63	3	37.5	16	8	Q8MES8	Q8mes8 daphniophyll
64	3	37.5	16	8	Q8MC35	Q8mc35 heimia myrt
65	3	37.5	17	4	Q92727	Q92727 homo sapien
66	3	37.5	17	4	Q96RT3	Q96rt3 homo sapien
67	3	37.5	17	6	Q8MIG8	Q8mic8 orycteropus
68	3	37.5	17	6	Q8M1C1	Q8mic1 physeter ca
69	3	37.5	17	6	Q8M1D3	Q8mid3 manis sp. p
70	3	37.5	17	6	Q8MIG3	Q8mig3 dicros bic
71	3	37.5	17	6	Q9TRH5	Q9trh5 bos taurus
72	3	37.5	17	6	Q8MIF6	Q8mif6 equus cabal
73	3	37.5	17	6	Q8MI97	Q8mi97 trichechus
74	3	37.5	17	6	Q8MIG9	Q8mig9 cynopterus
75	3	37.5	17	6	Q8MIF2	Q8mif2 elephas max
76	3	37.5	17	8	Q9XQN9	Q9xqn9 sinapis alb
77	3	37.5	17	12	Q8S673	Q8s673 reovirus (t
78	3	37.5	17	16	Q8X4A4	Q8x4a4 escherichia
79	3	37.5	18	4	Q9BZM7	Q9bzm7 homo sapien
80	3	37.5	18	13	Q90790	Q90790 gallus gall
81	3	37.5	18	13	Q90XC9	Q90xc9 gallus gall
82	3	37.5	19	2	P74875	P74875 salmonella
83	3	37.5	19	2	Q9RLU4	Q9rlu4 lactococcus
84	3	37.5	19	2	Q51278	Q51278 neisseria m
85	3	37.5	19	4	Q8TCB2	Q8tcb2 homo sapien
86	3	37.5	19	6	Q9TR01	Q9trr01 sus scrofa
87	3	37.5	19	10	Q9S8M0	Q9s8m0 triticum ae
88	3	37.5	19	10	Q9S8Q0	Q9s8q0 pinus sylve
89	3	37.5	19	11	Q925G8	Q925g8 mus musculu

-90 3 37.5 19 12 Q90633 baboon herp
 91 3 37.5 19 12 Q90630 baboon herp
 92 3 37.5 19 13 Q9DE21 gallus gall
 93 3 37.5 19 15 Q905K0 human immun
 94 3 37.5 19 15 Q905G4 human immun
 95 3 37.5 19 15 Q905I4 human immun
 96 3 37.5 19 15 Q90RG5 human immun
 97 3 37.5 19 15 Q905E4 human immun
 98 3 37.5 19 15 Q905L2 human immun
 99 3 37.5 20 2 Q9R4V3
 100 3 37.5 20 2 Q53346 pseudomonas

ALIGNMENTS

RESULT 1
 Q9TWD6 PRELIMINARY; PRT; 9 AA.
 AC Q9TWD6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE LED-NPF-1-NEUROPEPTIDE F-related peptide
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Phytophaga; Chrysomelidae; Chrysomelidae; Chrysomelinae;
 OC Chrysomelini; Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96245438; PubMed=8814784;
 RA Spittaels K., Verhaert P., Shaw C., Johnston R.N., Devreese B.,
 RA Van Beumen J., De Loof A.;
 RT "Insect neuropeptide F (NPF)-related peptides: isolation from Colorado
 RT potato beetle (Leptinotarsa decemlineata) brain."
 RL Insect Biochem. Mol. Biol. 26:375-382(1996).
 SQ SEQUENCE 9 AA; 1066 MW; 7E02340736C76864 CRC64;

Query Match 37.5%; Score 3; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
 Db 2 RGP 4

RESULT 2
 Q90Y93 PRELIMINARY; PRT; 10 AA.
 AC Q90Y93;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Growth hormone (fragment).
 GN GH.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kansaku N., Nakada A., Yagi E., Okabayashi H., Guemene D.;
 RT "Genetic variation of chicken growth hormone gene."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB061722; BAB69037.1; -.
 FT NON TER 1
 FT NON TER 10
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1155 MW; 6841751775A40AAB CRC64;

Query Match 37.5%; Score 3; DB 13; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
 Db 8 RGP 10

RESULT 3
 P82700 PRELIMINARY; PRT; 11 AA.
 AC P82700;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Periviscerokinin-3 (LEM-PVK-3).
 OS Leucophaea maderae (Madeira cockroach).
 OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
 OS Blaberus craniifer,
 OS Blaptica dubia (Argentinian wood cockroach), and
 OS Gromphadorina portentosa (Cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blabridae; Leucophaea.
 OX NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
 RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
 RX MEDLINE=20307624; PubMed=10849006;
 RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
 RT Identification of novel periviscerokinins from single neurohaemal
 RT release sites in insects. MS/MS fragmentation complemented by Edman
 RT degradation.";
 RL Eur. J. Biochem. 267:3869-3873(2000).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -1- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI.
 KW Neuropeptide; Amidation.
 FT MOD RES 11 11
 FT SEQUENCE 11 AA; 1147 MW; 2F4D9FF2D7605698 CRC64;

Query Match 37.5%; Score 3; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFP 5
 Db 7 PFP 9

RESULT 4
 Q9TRR7 PRELIMINARY; PRT; 11 AA.
 AC Q9TRR7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Calcyclin-associated protein, CAP50=CA2+/phospholipid-binding protein
 DE L-13 fragment (fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=92250478; PubMed=1533622;
 RA Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;
 RT "A calcyclin-associated protein is a newly identified member of the
 RT Ca2+/phospholipid-binding proteins, annexin family."
 RL J. Biol. Chem. 267:8919-8924(1992).
 FT NON TER 1
 FT NON TER 11
 FT NON TER 11

```

SQ SEQUENCE 11 AA; 1310 MW; 55580B0F5DDAA9C7 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7
   |||
DB 2 PIL 4

RESULT 5
Q9QVC5 PRELIMINARY; PRT; 11 AA.
AC Q9QVC5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE DM53 protein (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RX MEDLINE=92291078; PubMed=1601872;
RA Subramaniam V.N., bin Mohd Yusoff A.R., Wong S.H., Lim G.B., Chew M.,
RA Hong W.;
RT "Biochemical fractionation and characterization of proteins from
RT Golgi-enriched membranes.";
RL J. Biol. Chem. 267:12016-12021(1992).
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1210 MW; 5B61C10B9DDAB2C7 CRC64;

Query Match 37.5%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
   |||
DB 1 ILV 3

RESULT 6
Q8MJQ0 PRELIMINARY; PRT; 12 AA.
AC Q8MJQ0;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE Stem cell tyrosine kinase 1 (Fragment).
GN STK-1.
OS Saguinus fuscicollis (Brown-headed tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=9487;
RN [1]
RP SEQUENCE FROM N.A.
RA Singer S.S., Schmitz J., Schwieck C., Zischler H.;
RT "Molecular cladiatic markers in New World monkey phylogeny.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368142; AAN01092.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1290 MW; 5FBA3924FAB44727 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
   |||
DB 10 GPF 12

RESULT 7
Q8MJP8 PRELIMINARY; PRT; 12 AA.
AC Q8MJP8;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE Stem cell tyrosine kinase 1 (Fragment).
GN STK-1.
OS Callimico goeldii (Goeldi's marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callimico.
OX NCBI_TaxID=9495;
RN [1]
RP SEQUENCE FROM N.A.
RA Singer S.S., Schmitz J., Schwieck C., Zischler H.;
RT "Molecular cladiatic markers in New World monkey phylogeny.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368144; AAN01094.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1290 MW; 5FBA3924FAB44727 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
   |||
DB 10 GPF 12

RESULT 8
Q8MJP7 PRELIMINARY; PRT; 12 AA.
AC Q8MJP7;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE Stem cell tyrosine kinase 1 (Fragment).
GN STK-1.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RA Singer S.S., Schmitz J., Schwieck C., Zischler H.;
RT "Molecular cladiatic markers in New World monkey phylogeny.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368145; AAN01095.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1290 MW; 5FBA3924FAB44727 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
   |||
DB 10 GPF 12

RESULT 9
Q8MJP9 PRELIMINARY; PRT; 12 AA.
AC Q8MJP9;

```


DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Stem cell tyrosine kinase 1 (Fragment).
 GN STK-1.
 OS Leontopithecus rosalia (Golden lion tamarin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
 OC Neotopithecus.
 OC Leontopithecus.
 OX NCBI_TaxID=30588;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Singer S.S., Schmitz J., Schwiegk C., Zischler H.;
 RT "Molecular cladistic markers in New World monkey phylogeny."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF368143; AA01093.1; -.
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1290 MW; 5FBA3924FAB44727 CRC64;
 Query Match 37.5%; Score 3; DB 6; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 GPF 4
 Db 10 GPF 12
 RESULT 10
 Q8MJP6
 ID Q8MJP6 PRELIMINARY; PRT; 12 AA.
 AC Q8MTP6;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Stem cell tyrosine kinase 1 (Fragment).
 GN STK-1.
 OS Cebus pygmaea (Pygmy marmoset) (Callithrix pygmaea).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
 OX NCBI_TaxID=9493;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Singer S.S., Schmitz J., Schwiegk C., Zischler H.;
 RT "Molecular cladistic markers in New World monkey phylogeny."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF368146; AA01096.1; -.
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1321 MW; 5FBA39254AB44727 CRC64;
 Query Match 37.5%; Score 3; DB 6; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 GPF 4
 Db 10 GPF 12
 RESULT 11
 Q8MJJE3
 ID Q8MJJE3 PRELIMINARY; PRT; 12 AA.
 AC Q8MJJE3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Stem cell tyrosine kinase 1 (Fragment).
 GN STK-1.
 OS Saimiri sciureus (Common squirrel monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Singer S.S., Schmitz J., Schwiegk C., Zischler H.;
 RT "Molecular cladistic markers in New World monkey phylogeny."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF489261; AA01126.1; -.
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1290 MW; 5FBA3924FAB44727 CRC64;
 Query Match 37.5%; Score 3; DB 6; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 GPF 4
 Db 10 GPF 12
 RESULT 12
 Q8MUQ1
 ID Q8MUQ1 PRELIMINARY; PRT; 12 AA.
 AC Q8MUQ1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Stem cell tyrosine kinase 1 (Fragment).
 GN STK-1.
 OS Ateles fusciceps (Brown-headed spider monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateles.
 OX NCBI_TaxID=9508;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Singer S.S., Schmitz J., Schwiegk C., Zischler H.;
 RT "Molecular cladistic markers in New World monkey phylogeny."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF368141; AA01091.1; -.
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1290 MW; 5FBA3924FAB44727 CRC64;
 Query Match 37.5%; Score 3; DB 6; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 GPF 4
 Db 10 GPF 12
 RESULT 13
 Q8MJJE2
 ID Q8MJJE2 PRELIMINARY; PRT; 12 AA.
 AC Q8MJJE2;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Stem cell tyrosine kinase 1 (Fragment).
 GN STK-1.
 OS Cebus apella (Brown-capped capuchin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebus.
 OX NCBI_TaxID=9515;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Singer S.S., Schmitz J., Schwiegk C., Zischler H.;
 RT "Molecular cladistic markers in New World monkey phylogeny."

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF489262; AAN01127.1; --

KW Kinase.

FT NON_TER 1

FT NON_TER 12

SQ SEQUENCE 12 AA; 1290 MW; 5FBA3924FAB44727 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 12;

Best Local Similarity 100.0%; Pred. No. 5.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4

DB 10 GPF 12

RESULT 14

ID Q8MJE4

AC Q8MJE4; PRELIMINARY; PRT; 12 AA.

DT 01-OCT-2002 (TReMBLrel. 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)

DE Stem cell tyrosine kinase 1 (Fragment).

GN STK-1.

OS Aotus azarai (Aotus azarai).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.

OX NCBI_TaxID=30591;

RN [1]

RP SEQUENCE FROM N.A.

RA Singer S.S., Schmitz J., Schwiegg C., Zischler H.;

RT "Molecular cladiatic markers in New World monkey phylogeny."

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF489260; AAN01125.1; --

KW Kinase.

FT NON_TER 1

FT NON_TER 12

SQ SEQUENCE 12 AA; 1314 MW; EBBA3924FAB44721 CRC64;

Query Match

Best Local Similarity 37.5%; Score 3; DB 6; Length 12;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4

DB 10 GPF 12

RESULT 15

ID Q8K3U3

AC Q8K3U3; PRELIMINARY; PRT; 12 AA.

DT 01-OCT-2002 (TReMBLrel. 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)

DE Lectin Ym1 (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6;

RA Welch J.S., Escoubet-Lozach L., Sykes D.B., Glass C.K.;

RT "TH2 cytokines and allergic challenge induce yml expression in

macrophages by a STAT6-dependent mechanism."

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF533510; AAN04032.1; --

FT NON_TER 12

FT NON_TER 12

SQ SEQUENCE 12 AA; 1301 MW; 1373DC4258B2C720 CRC64;

Query Match

Best Local Similarity 37.5%; Score 3; DB 11; Length 12;

Best Local Similarity 100.0%; Pred. No. 5.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8

DB 5 ILV 7

RESULT 16

ID Q53693

AC Q53693; PRELIMINARY; PRT; 13 AA.

DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)

DE Leader peptide.

OS Streptomyces avermitilis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=33903;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CU-18;

RA De Rossi E., Leva R., Gusberti L., Manachini P.L., Riccardi G.;

RT "Cloning, sequencing and expression of the ilvBNC gene cluster from

Streptomyces avermitilis."

RL Gene 166:127-132 (1995).

DR EMBL; L39268; AAA93097.1; --

SQ SEQUENCE 13 AA; 1499 MW; 5E080E40FD4E32C7 CRC64;

Query Match

Best Local Similarity 37.5%; Score 3; DB 2; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8

DB 5 ILV 7

RESULT 17

ID O34622

AC O34622; PRELIMINARY; PRT; 13 AA.

DT 01-JAN-1998 (TReMBLrel. 05, Created)

DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)

DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)

DE GUA (Fragment).

GN GUA.

OS Borrelia burgdorferi (Lyme disease spirochete).

OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.

OX NCBI_TaxID=139;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CT39, DN127CL9-2, and 25015;

RX MEDLINE=97426044; PubMed=9282748;

RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,

Rosa P.;

RT "The Borrelia burgdorferi circular plasmid cp26: conservation of

plasmid structure and targeted inactivation of the ospC gene."

RL Mol. Microbiol. 25:361-374 (1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=DN127CL9-2, and 25015;

RX MEDLINE=95154673; PubMed=7851744;

RA Stevenson B., Barthold S.W.;

RT "Expression and sequence of outer surface protein C among North

American isolates of Borrelia burgdorferi."

RL FEMS Microbiol. Lett. 124:367-372 (1994).

DR EMBL; U93694; AAC45522.1; --

DR EMBL; U04280; AAC45543.1; --

DR EMBL; U04282; AAC45541.1; --

FT NON_TER 13

```

SQ SEQUENCE 13 AA; 1407 MW; 08FAB3930E0BC720 CRC64;
Query Match 37.5%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db 6 ILV 8

RESULT 18
O31365 PRELIMINARY; PRT; 13 AA.
ID O31365;
AC O31365;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GuAA (Fragment).
GN GUAA.
OS Borrelia garinii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=29519;
RN [1]_TaxID=29519;
RP SEQUENCE FROM N.A.
RC STRAIN=IP90;
RX MEDLINE=97426044; PubMed=9282748;
RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
RA Rosa P.;
RT "the Borrelia burgdorferi circular plasmid cp26: conservation of
RT plasmid structure and targeted inactivation of the ospC gene.";
RL Mol. Microbiol. 25:361-374(1997).
DR EMBL; U93701; AAC45536.1; -.
FT NON_TER 13
FT SEQUENCE 13 AA; 1382 MW; 08BFB4180E0BC720 CRC64;

Query Match 37.5%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db 6 ILV 8

RESULT 19
O31364 PRELIMINARY; PRT; 13 AA.
ID O31364;
AC O31364;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GuAA (Fragment).
GN GUAA.
OS Borrelia garinii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=29519;
RN [1]_TaxID=29519;
RP SEQUENCE FROM N.A.
RC STRAIN=G25;
RX MEDLINE=97426044; PubMed=9282748;
RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
RA Rosa P.;
RT "the Borrelia burgdorferi circular plasmid cp26: conservation of
RT plasmid structure and targeted inactivation of the ospC gene.";
RL Mol. Microbiol. 25:361-374(1997).
DR EMBL; U93700; AAC45534.1; -.
FT NON_TER 13
FT SEQUENCE 13 AA; 1449 MW; 08FAB9BB0E0BC720 CRC64;

Query Match 37.5%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ SEQUENCE 13 AA; 1407 MW; 08FAB3930E0BC720 CRC64;
Query Match 37.5%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db 6 ILV 8

RESULT 20
O93824 PRELIMINARY; PRT; 13 AA.
ID O93824;
AC O93824;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE UDP-galactose-4-epimerase (Fragment).
GN GAL10.
OS Candida tropicalis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5482;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PK233;
RA Kanai T., Ueda M., Tanaka A.;
RT "Candida tropicalis promoter region of GAL1 and GAL10 gene.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB019434; BAA34351.1; -.
FT NON_TER 1
FT NON_TER 13
FT SEQUENCE 13 AA; 1312 MW; 0B559D6AE18BC720 CRC64;

Query Match 37.5%; Score 3; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db 6 ILV 8

RESULT 21
O52220 PRELIMINARY; PRT; 14 AA.
ID O52220;
AC O52220;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE YecG (Fragment).
GN YECG.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RA Toguchi A., Harshay R.M.;
RT "Flagellar master operon (fliH and fliC) from Salmonella typhimurium
RT LT2 (includes partial upstream yecG sequence and downstream mocha
RT promoter sequence).";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029300; AAB96642.1; -.
FT NON_TER 14
FT SEQUENCE 14 AA; 1561 MW; 42679A87F94DFBC7 CRC64;

Query Match 37.5%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db 6 ILV 8

```

```
RESULT 22
Q16045          PRELIMINARY;      PRT;      14 AA.
AC Q16045;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE D3 dopamine receptor (Fragment).
GN D3R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93326145; PubMed=7916609;
RA Nagai Y., Ueno S., Saeki Y., Soga F., Yanagihara T.;
RT "Expression of the D3 dopamine receptor gene and a novel variant
RT transcript generated by alternative splicing in human peripheral blood
RT lymphocytes.";
RL Biochem. Biophys. Res. Commun. 194:368-374(1993).
DR EMBL; S63845; AAB27543.2; -.
FT NON_TER
SQ SEQUENCE 1 1 1586 MW; EA310BEP94CF1B1 CRC64;

Query Match 37.5%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
DB 4 RGP 6

RESULT 23
P82832          PRELIMINARY;      PRT;      14 AA.
ID P82832;
AC P82832;
DT 01-WAR-2001 (TrEMBLrel. 16, Created)
DT 01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Temporin-11C.
OS Rana luteiventris.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=58176;
RN [1]_TaxID=58176;
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=SKIN;
RX MEDLINE=20117700; PubMed=10651828;
RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
RA Conlon J.M.;
RT "Peptides with antimicrobial activity from four different families
RT isolated from the skins of the North American frogs Rana luteiventris,
RT Rana berlandieri and Rana pipiens.";
RL Eur. J. Biochem. 267:894-900(2000).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S. AUREUS. WEAK ACTIVITY AGAINST GRAM-NEGATIVE BACTERIUM E. COLI AND
CC THE YEAST C. ALBICANS.
CC -!- MASS SPECTROMETRY: MW=1603.1; METHOD=ELECTROSPRAY.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAegurin/RUGOSIN
CC FAMILY.
KW Antibiotic; Amidation; Fungicide.
FT MOD_RES 14 14 AMIDATION
SQ SEQUENCE 14 AA; 1604 MW; 0B540E1B7FCA8924 CRC64;

Query Match 37.5%; Score 3; DB 13; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7
```

```
Db 3 PIL 5

RESULT 24
Q9R5D5          PRELIMINARY;      PRT;      15 AA.
ID Q9R5D5;
AC Q9R5D5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE POLY(3-HYDROXYBUTYRIC acid) granule-associated 40 kDa protein
DE (Fragment).
OS Chromatium vinosum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC Chromatiaceae; Allochromatium.
OX NCBI_TaxID=1049;
RN [1]_TaxID=1049;
RP SEQUENCE.
RX MEDLINE=93146381; PubMed=1490603;
RA Liebergesell M., Schmidt B., Steinbuechel A.;
RT "Isolation and identification of granule-associated proteins relevant
RT for poly(3-hydroxyalkanoic acid) biosynthesis in Chromatium vinosum
RT D.";
RL FEMS Microbiol. Lett. 78:227-232(1992).
SQ SEQUENCE 15 AA; 1834 MW; 215B7FCFCF65BB8E CRC64;

Query Match 37.5%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPI 6
DB 2 PPI 4

RESULT 25
Q8TCS7          PRELIMINARY;      PRT;      15 AA.
ID Q8TCS7;
AC Q8TCS7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Complement component C7 (Fragment).
GN C7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Gonzalez S., Martinez Borra J., Lopez Larrea C.;
RT "Cloning and characterization of human complement component C7
RT promoter.";
RL Genes Immun. 0:0-0(2002).
DR EMBL; Y11720; CAA72407.1; -.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1666 MW; 10984ADCA7B43F19 CRC64;

Query Match 37.5%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 8 ILV 10

RESULT 26
Q8WNQ2          PRELIMINARY;      PRT;      15 AA.
ID Q8WNQ2;
AC Q8WNQ2;
```

DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE Niemann-Pick type C1 protein (Fragment).
 OS Sus scrofa (Pig).
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gevry N.Y., Murphy B.D.;
 RT "Porcine Niemann-Pick type C1 gene, promoter region.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF329087; AAL37473.1; -.
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1572 MW; D96760FBEDE64A840 CRC64;

 Query Match 37.5%; Score 3; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 RGP 3
 Db ||||
 4 RGP 6

 RESULT 27
 ID Q9TRN2 PRELIMINARY; PRT; 15 AA.
 AC Q9TRN2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE LOW MR zona pellucida binding protein (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92378826; PubMed=1510840;
 RA Parry R.V., Barker P.J., Jones R.;
 RT "Characterization of low Mr zona pellucida binding proteins from boar
 spermatozoa and seminal plasma.";
 RL Mol. Reprod. Dev. 33:108-115(1992).
 SQ SEQUENCE 15 AA; 1572 MW; 7FBC9786771A722E CRC64;

 Query Match 37.5%; Score 3; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 RGP 3
 Db ||||
 4 RGP 6

 RESULT 28
 ID Q9TRN5 PRELIMINARY; PRT; 15 AA.
 AC Q9TRN5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE LOW MR zona pellucida binding protein (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92378826; PubMed=1510840;
 RA Parry R.V., Barker P.J., Jones R.;
 RT "Characterization of low Mr zona pellucida binding proteins from boar

RT spermatozoa and seminal plasma.";
 RL Mol. Reprod. Dev. 33:108-115(1992).
 SQ SEQUENCE 15 AA; 1604 MW; 7FAA10E0E0CA722E CRC64;

 Query Match 37.5%; Score 3; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 RGP 3
 Db ||||
 4 RGP 6

 RESULT 29
 ID Q9TRN4 PRELIMINARY; PRT; 15 AA.
 AC Q9TRN4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE LOW MR zona pellucida binding protein (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92378826; PubMed=1510840;
 RA Parry R.V., Barker P.J., Jones R.;
 RT "Characterization of low Mr zona pellucida binding proteins from boar
 spermatozoa and seminal plasma.";
 RL Mol. Reprod. Dev. 33:108-115(1992).
 SQ SEQUENCE 15 AA; 1768 MW; 7FA2379E1461610E CRC64;

 Query Match 37.5%; Score 3; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 RGP 3
 Db ||||
 4 RGP 6

 RESULT 30
 ID Q9T2K8 PRELIMINARY; PRT; 15 AA.
 AC Q9T2K8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE LHCII kinase, 64 kDa kinase (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92183823; PubMed=1544419;
 RA Gal A., Herrmann R.G., Lottspeich F., Ohad I.;
 RT "Phosphorylation of cytochrome b6 by the LHC II kinase associated with
 the cytochrome complex.";
 RL FEBS Lett. 298:33-35(1992).
 FT NON TER 1
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1556 MW; 6E00A4F917DDF33E CRC64;

 Query Match 37.5%; Score 3; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 5 PIL 7

Db 2 PII 4

RESULT 31

Q35921 PRELIMINARY; PRT; 15 AA.

ID Q35921

AC Q35921

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE TRGGLY protein (Fragment).

GN TRGGLY.

OS Salmo salar (Atlantic salmon).

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.

OX NCBI_TaxID=8030;

RN [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Liver;

RC MEDLINE=95053530; PubMed=8000479;

RX Hardiman G., Byrnes L., Peden J., Wolff J., Cannon F.;

RA "Cloning and sequencing of the Atlantic salmon (Salmo salar)

RT cytochrome c oxidase subunit III gene (coxIII) and analysis of coxIII

RT expression during parr-smolt transformation.";

RL Mol. Mar. Biol. Biotechnol. 3:210-216(1994).

DR EMBL; L04502; AAA62410.1; --

KW Mitochondrion.

XW NON TER 15 15

SQ SEQUENCE 15 AA; 1784 MW; 6BFA79B9E031C4BD CRC64;

Query Match 37.5%; Score 3; DB 8; Length 15;

Best Local Similarity 100.0%; Pred. No. 6.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6

Db 12 FPI 14

RESULT 32

Q98929 PRELIMINARY; PRT; 15 AA.

ID Q98929

AC Q98929

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Pyroline-5-carboxylate reductase, P5CR (Fragment).

OS Glycine max (Soybean).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

OX NCBI_TaxID=3847;

RN [1]

RN SEQUENCE.

RP MEDLINE=91378472; PubMed=1898034;

RX Chilson O.P., Kelly-Chilson A.E., Siegel N.R.;

RA "Pyroline-5-carboxylate reductase in soybean nodules:

RT isolation/partial primary structure/evidence for isozymes.";

RL Arch. Biochem. Biophys. 288:350-357(1991).

FT NON TER 15 15

SQ SEQUENCE 15 AA; 1715 MW; D9821F73DF524 CRC64;

Query Match 37.5%; Score 3; DB 10; Length 15;

Best Local Similarity 100.0%; Pred. No. 6.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6

Db 4 FPI 6

RESULT 33

Q92114 PRELIMINARY; PRT; 15 AA.

ID Q92114

AC Q92114

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE mRNA encoding epitope region of NAP-1 monoclonal antibody

DE (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RN SEQUENCE FROM N.A.

RP Fujii-Nakata T., Ishimi Y., Okuda A., Kikuchi A.;

RA "Functional analysis of nucleosome assembly protein, NAP-1; negatively

RT charged C-terminal region is not necessary for the intrinsic assembly

RT activity.";

RL J. Biol. Chem. 0:0-0(1992).

DR EMBL; D12518; BAA02088.1; --

FT NON TER 1 1

SQ SEQUENCE 15 AA; 1733 MW; 92DEE41983905C20 CRC64;

Query Match 37.5%; Score 3; DB 11; Length 15;

Best Local Similarity 100.0%; Pred. No. 6.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6

Db 13 FPI 15

RESULT 34

Q9PS10 PRELIMINARY; PRT; 15 AA.

ID Q9PS10

AC Q9PS10

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE MG-ATPase 85 kDa glycoprotein component (EC 3.6.1.3) (Fragment).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RN SEQUENCE.

RP MEDLINE=93256569; PubMed=8489264;

RX Cunningham H.B., Yazaki P.J., Domingo R.C., Oades K.V., Bohlen H.,

RA Sabbadini R.A., Dahms A.S.;

RL Arch. Biochem. Biophys. 303:32-43(1993).

SQ SEQUENCE 15 AA; 1646 MW; 411C468010211D52 CRC64;

Query Match 37.5%; Score 3; DB 13; Length 15;

Best Local Similarity 100.0%; Pred. No. 6.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PII 7

Db 6 PII 8

RESULT 35

Q9UCLO PRELIMINARY; PRT; 16 AA.

ID Q9UCLO

AC Q9UCLO

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Serum amyloid A isotype 1 protein (Serum amyloid A protein)

DE (Fragment).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=93099171; PubMed=1463770;
 RA Baba S., Takahashi T., Kasama T., Shirasawa H.;
 RT "Identification of two novel amyloid A protein subsets coexisting in
 an individual patient of AA-amyloidosis.";
 RL Biochim. Biophys. Acta 1180:195-200(1992).
 CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
 CC COMPLEX (BY SIMILARITY).
 CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
 SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
 DR InterPro; IPR000096; Serum_amyloid_A.
 DR Pfam; PF00277; SAA_proteins; 1.
 KW Acute phase; HDL.
 SQ SEQUENCE 16 AA; 1585 MW; 1CBA41E77C839CC1 CRC64;

Query Match 37.5%; Score 3; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
 |||
 Db 1 RGP 3

RESULT 36

O9UCK9 PRELIMINARY; PRT; 16 AA.
 AC Q9UCK9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Serum amyloid A isotype 2 alpha protein (Serum amyloid A protein)
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93099171; PubMed=1463770;
 RA Baba S., Takahashi T., Kasama T., Shirasawa H.;
 RT "Identification of two novel amyloid A protein subsets coexisting in
 an individual patient of AA-amyloidosis.";
 RL Biochim. Biophys. Acta 1180:195-200(1992).
 CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
 CC COMPLEX (BY SIMILARITY).
 CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
 SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
 DR InterPro; IPR000096; Serum_amyloid_A.
 DR Pfam; PF00277; SAA_proteins; 1.
 KW Acute phase; HDL.
 SQ SEQUENCE 16 AA; 1612 MW; 1CBA4F077C9C8CC1 CRC64;

Query Match 37.5%; Score 3; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
 |||
 Db 1 RGP 3

RESULT 37

O9TZR1 PRELIMINARY; PRT; 16 AA.
 AC Q9TZR1;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Fertilization protein (Fragment).
 OS Haliotis fulgens (Green abalone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Vetigastropoda; Haliotidae; Haliotis.
 OX NCBI_TaxID=6456;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98393704; PubMed=9724763;
 RA Metz E.C., Robles-Sikisaka R., Vacquier V.D.;
 RT "Nonsynonymous substitution in abalone sperm fertilization genes
 exceeds substitution in introns and mitochondrial DNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10678-10681(1998).
 DR EMBL; AF076837; AAC33936.1; -.
 FT NON_TER 1 1
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1788 MW; OCAECAB163DA5154 CRC64;

Query Match 37.5%; Score 3; DB 5; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
 |||
 Db 3 RGP 5

RESULT 38

Q28324 PRELIMINARY; PRT; 16 AA.
 AC Q28324;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Beta-x-globin (Fragment).
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80227766; PubMed=6248519;
 RA Haynes J.R., Rosteck P.R.Jr., Schon E.A., Gallagher P.M., Burks D.J.,
 RA Smith K., Lingrel J.B.;
 RT "The isolation of the beta-a-, beta-c-, and gamma-globin genes and a
 presumptive embryonic globin gene from a goat dna recombinant
 library.";
 RL J. Biol. Chem. 255:6355-6367(1980).
 DR EMBL; K00659; AAA30919.1; -.
 FT NON_TER 1 1
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1784 MW; D027A9E223320213 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
 |||
 Db 5 ILV 7

RESULT 39

Q8MC25 PRELIMINARY; PRT; 16 AA.
 ID Q8MC25;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE PeaA (Fragment).

GN PSAA.
 OS Sonneratia apetala.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Lythraceae; Sonneratia.
 OC NCBI_TaxID=122813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S165;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035740; AAL14161.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
 Query Match 37.5%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 ILV 8
 Db 12 ILV 14
 RESULT 40
 Q8MC39 PRELIMINARY; PRT; 16 AA.
 ID Q8MC39;
 AC Q8MC39;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE PSAA (Fragment).
 GN PSAA.
 OS Ammannia baccifera.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Lythraceae; Ammannia.
 OC NCBI_TaxID=162022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A610;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035733; AAL14147.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
 Query Match 37.5%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 ILV 8
 Db 12 ILV 14
 RESULT 41
 Q8LVE1 PRELIMINARY; PRT; 16 AA.
 ID Q8LVE1;
 AC Q8LVE1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE PSAA (Fragment).
 GN PSAA.
 OS Punica granatum (Pomegranate).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Lythraceae; Punica.
 OC NCBI_TaxID=22663;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=P728, and P745;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035724; AAL14129.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
 Query Match 37.5%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 ILV 8
 Db 12 ILV 14
 RESULT 42
 Q8MC53 PRELIMINARY; PRT; 16 AA.
 ID Q8MC53;
 AC Q8MC53;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE PSAA (Fragment).
 GN PSAA.
 OS Woodfordia fruticosa.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Lythraceae; Woodfordia.
 OC NCBI_TaxID=141189;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W493;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035722; AAL14125.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
 Query Match 37.5%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 ILV 8
 Db 12 ILV 14
 RESULT 43
 Q8MC17 PRELIMINARY; PRT; 16 AA.
 ID Q8MC17;
 AC Q8MC17;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)


```

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Ludwigia hyssopifolia.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Onagraceae; Ludwigia.
OX NCBI_TaxID=155013;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=L787;
RC Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035745; AAL14171.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 12 ILV 14

RESULT 44
Q8LVE2
ID Q8LVE2 PRELIMINARY; PRT; 16 AA.
AC Q8LVE2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE PsaA (Fragment).
GN PSAA.
OS Lythrum salicaria (Purple loosestrife).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Lythrum.
OX NCBI_TaxID=13129;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=L758, and 758F;
RC Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035727; AAL14135.1; -.
DR EMBL; AF421495; AAM45853.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 12 ILV 14

RESULT 45
Q8LVE0
ID Q8LVE0 PRELIMINARY; PRT; 16 AA.

```

```

AC Q8LVE0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE PsaA (Fragment).
GN PSAA.
OS Trapa maximowiczii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Trapa.
OX NCBI_TaxID=162053;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=T744, and T010;
RC Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035729; AAL14139.1; -.
DR EMBL; AY035730; AAL14141.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 12 ILV 14

RESULT 46
Q8MET2
ID Q8MET2 PRELIMINARY; PRT; 16 AA.
AC Q8MET2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE PSI P700 apoprotein A1 (Fragment).
GN PSAA.
OS Saxifraga stolonifera.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Saxifragaceae; Saxifraga.
OX NCBI_TaxID=182070;
[1]
RN SEQUENCE FROM N.A.
RP Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.E.;
RT "Phylogeny of the Altingiaceae based on cpDNA matK, PY-IGS and nrDNA
RT ITS sequences.";
RL Plant Syst. Evol. 230:13-24(2001).
DR EMBL; AF377995; AAM45512.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 12 ILV 14

RESULT 47
Q8MC45
ID Q8MC45 PRELIMINARY; PRT; 16 AA.

```

Q8MC45;
 AC 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 PSAA (Fragment).
 GN PSAA.
 OS Decodon verticillatus (Swamp loosestrife).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Lythraceae; Decodon.
 OX NCBI_TaxID=162018;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D212;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035728; AAL14137.1; -.
 KW Chloroplast.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
 Query Match 37.5%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7e+03; 0; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 ILV 8
 Db |||
 12 ILV 14

RESULT 48
 Q8MC21 PRELIMINARY; PRT; 16 AA.
 ID Q8MC21;
 AC Q8MC21;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DE 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 PSAA (Fragment).
 GN PSAA.
 OS Combretum wallichii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Combretaceae; Combretum.
 OX NCBI_TaxID=131243;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C505;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035743; AAL14167.1; -.
 KW Chloroplast.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
 Query Match 37.5%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7e+03; 0; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 ILV 8
 Db |||
 12 ILV 14

RESULT 49
 Q8MC51 PRELIMINARY; PRT; 16 AA.
 ID Q8MC51;
 AC Q8MC51;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DE 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 PSAA (Fragment).
 GN PSAA.
 OS Cuphea lanceolata.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Lythraceae; Cuphea.
 OX NCBI_TaxID=3930;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C490;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035723; AAL14127.1; -.
 KW Chloroplast.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
 Query Match 37.5%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7e+03; 0; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 ILV 8
 Db |||
 12 ILV 14

RESULT 51

Q8MC51 PRELIMINARY; PRT; 16 AA.
 ID Q8MC51;
 AC Q8MC51;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DE 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 PSAA (Fragment).
 GN PSAA.
 OS Cuphea lanceolata.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Lythraceae; Cuphea.
 OX NCBI_TaxID=3930;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C490;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035723; AAL14127.1; -.
 KW Chloroplast.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
 Query Match 37.5%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7e+03; 0; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 ILV 8
 Db |||
 12 ILV 14

RESULT 50
 Q8MC33 PRELIMINARY; PRT; 16 AA.
 ID Q8MC33;
 AC Q8MC33;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DE 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 PSAA (Fragment).
 GN PSAA.
 OS Rotala indica.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Lythraceae; Rotala.
 OX NCBI_TaxID=162024;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R492;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 RT Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035736; AAL14153.1; -.
 KW Chloroplast.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
 Query Match 37.5%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7e+03; 0; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 ILV 8
 Db |||
 12 ILV 14

Q8MC19
ID Q8MC19 PRELIMINARY; PRT; 16 AA.
AC Q8MC19
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Quisqualis indica (Rangoon creeper).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Combretaceae; Quisqualis.
OX NCBI_TaxID=3956;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Q379;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225 (2002).
DR EMBL; AY035744; AAL14169.1; -.
KW Chloroplast.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 12 ILV 14

RESULT 52
Q8MC49
ID Q8MC49 PRELIMINARY; PRT; 16 AA.
AC Q8MC49
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Pemphis acidula.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Pemphis.
OX NCBI_TaxID=126635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P630;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225 (2002).
DR EMBL; AY035725; AAL14131.1; -.
KW Chloroplast.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 12 ILV 14

RESULT 53
Q8MC27
ID Q8MC27 PRELIMINARY; PRT; 16 AA.
AC Q8MC27
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Lagerstroemia villosa.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Lagerstroemia.
OX NCBI_TaxID=162025;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L688;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225 (2002).
DR EMBL; AY035739; AAL14159.1; -.
KW Chloroplast.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 12 ILV 14

RESULT 54
Q8MET0
ID Q8MET0 PRELIMINARY; PRT; 16 AA.
AC Q8MET0
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PSI P700 apoprotein A1 (Fragment).
GN PSAA.
OS Cercidiphyllum japonicum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Cercidiphyllaceae; Cercidiphyllum.
OX NCBI_TaxID=13413;
RN [1]
RP SEQUENCE FROM N.A.
RA Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.E.;
RT "Phylogeny of the Altingiaceae based on cpDNA matK, PY-IGS and nrDNA
ITS sequences.";
RL Plant Syst. Evol. 230:13-24 (2001).
DR EMBL; AF377996; AAM45514.1; -.
KW Chloroplast.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 12 ILV 14

RESULT 55

Q8MC23
ID Q8MC23 PRELIMINARY; PRT; 16 AA.
AC Q8MC23;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Sonneratia alba.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Sonneratia.
OX NCBI_TaxID=122812;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S482;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035741; AAL14163.1; --
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ILV 8
DB 12 ILV 14

RESULT 56
Q8MC41
ID Q8MC41 PRELIMINARY; PRT; 16 AA.
AC Q8MC41;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Nesaea luederitzi.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Nesaea.
OX NCBI_TaxID=162020;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N213;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035732; AAL14145.1; --
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ILV 8
DB 12 ILV 14

RESULT 57
Q8MC15
ID Q8MC15 PRELIMINARY; PRT; 16 AA.
AC Q8MC15;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Fuchsia hybrid cultivar.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Onagraceae; Fuchsia.
OX NCBI_TaxID=113545;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F016;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035746; AAL14173.1; --
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ILV 8
DB 12 ILV 14

RESULT 58
Q8MC43
ID Q8MC43 PRELIMINARY; PRT; 16 AA.
AC Q8MC43;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Sonneratia caseolaris.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Sonneratia.
OX NCBI_TaxID=122814;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S435;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035731; AAL14143.1; --
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;
Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ILV 8
DB 12 ILV 14

RESULT 59

Q8MC47 ID Q8MC47 PRELIMINARY; PRT; 16 AA.
 AC Q8MC47;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Psaa (Fragment).
 GN PSAA.
 OS Peplis portula.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Lythraceae; Peplis.
 OX NCBI_TaxID=162016;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=P220;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035726; AAL14133.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
 |||
 Db 12 ILV 14

RESULT 60

Q8MC37 ID Q8MC37 PRELIMINARY; PRT; 16 AA.
 AC Q8MC37;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Psaa (Fragment).
 GN PSAA.
 OS Lawsonia inermis.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Lythraceae; Lawsonia.
 OX NCBI_TaxID=141191;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L494;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035734; AAL14149.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
 |||
 Db 12 ILV 14

RESULT 61

Q8MC29 ID Q8MC29 PRELIMINARY; PRT; 16 AA.
 AC Q8MC29;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Psaa (Fragment).
 GN PSAA.
 OS Duabanga grandiflora.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Lythraceae; Duabanga.
 OX NCBI_TaxID=122808;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D41;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035738; AAL14157.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
 |||
 Db 12 ILV 14

RESULT 62

Q8MC31 ID Q8MC31 PRELIMINARY; PRT; 16 AA.
 AC Q8MC31;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Psaa (Fragment).
 GN PSAA.
 OS Lagerstroemia speciosa.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Lythraceae; Lagerstroemia.
 OX NCBI_TaxID=122810;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L477;
 RA Huang Y., Shi S.;
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
 on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
 Transcribed Spacer (ITS) Sequences.";
 RL Int. J. Plant Sci. 163:215-225(2002).
 DR EMBL; AY035737; AAL14155.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
 |||

```

Db          12 ILV 14

RESULT 63
Q8MES8
ID Q8MES8      PRELIMINARY;      PRT;      16 AA.
AC Q8MES8;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE PSI_P700 apoprotein A1 (Fragment).
GN PSAA.
OS Daphniophyllum calycinum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Daphniphyllaceae; Daphniphyllum.
OX NCBI_TaxID=182071;
RN [1]
RP SEQUENCE FROM N.A.
RA Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.B.;
RT "Phylogeny of the Atingiaceae based on cpDNA matK, psA-ycf3 and nrDNA
ITS sequences.";
RL Plant Syst. Evol. 230:13-24(2001).
DR EMBL; AF377997; AAM45516.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517F5691B89355B9 CRC64;

Query Match          37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 ILV 8
      |||
Db          12 ILV 14

RESULT 64
Q8MC35
ID Q8MC35      PRELIMINARY;      PRT;      16 AA.
AC Q8MC35;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE PsAA (Fragment).
GN PSAA.
OS Heimia myrtifolia.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Heimia.
OX NCBI_TaxID=133579;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H491;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
on Chloroplast rbcL Gene, psAA-ycf3 Spacer, and Nuclear rDNA Internal
Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035735; AAL1451.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517F5691B89355B9 CRC64;

Query Match          37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 ILV 8
      |||
Db          12 ILV 14

```

```

RESULT 65
Q92727
ID Q92727      PRELIMINARY;      PRT;      17 AA.
AC Q92727; P78498;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Retinoblastoma susceptibility protein (RB1) (Fragment).
GN RB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hogg A., Onadim Z., Baird P.N., Cowell J.K.;
RT "Detection of heterozygous mutations in the RB1 gene in retinoblastoma
patients using single-strand conformation polymorphism analysis and
polymerase chain reaction sequencing.";
RL Oncogene 7:1445-1451(1992).
RN [2]
RP SEQUENCE OF 1-10 FROM N.A.
RX MEDLINE=95187159; PubMed=7881418;
RA Lohmann D.R., Brandt B., Hopping W., Passarge E., Horsthemke B.;
RT "Spectrum of small length germline mutations in the RB1 gene.";
RL Hum. Mol. Genet. 3:2187-2193(1994).
DR EMBL; L41911; AAB59483.1; -.
DR EMBL; L49233; AAB82562.1; -.
FT NON_TER
SQ SEQUENCE 17 AA; 1907 MW; 1E5F711F14D24F18 CRC64;

Query Match          37.5%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 ILV 8
      |||
Db          1 ILV 3

RESULT 66
Q96RT3
ID Q96RT3      PRELIMINARY;      PRT;      17 AA.
AC Q96RT3;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Tuberosus sclerosis 1 (Fragment).
GN TSC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fang L., Wu Z.Y., Wang N., MuRong S.X., Lin M.T., Chao D.R.,
RA Fang Z.M.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF274229; AAK60416.1; -.
FT NON_TER
SQ SEQUENCE 17 AA; 1971 MW; 611013A3EB6826F5 CRC64;

Query Match          37.5%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 RGP 3
      |||

```

Db 1 RGP 3

RESULT 67

Q8M1C8 PRELIMINARY; PRT; 17 AA.

AC Q8M1C8; 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DE Prion protein (Fragment).

GN PRMP.

OS Orycteropus afer (hardvark).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Tubulidentata; Orycteropodidae; Orycteropus.

OX NCBI_TaxID=9818;

RN [1]

RA SEQUENCE FROM N.A.

RP Poux C., van Rheede T., Madsen O., de Jong W.W.;

RT "Sequence gaps join mice and men.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ438206; CAD27291.1; -.

FT NON TER 17

SQ SEQUENCE 17 AA; 1869 MW; 40B52A0CECF40D8 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 7.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8

Db 10 ILV 12

RESULT 68

Q8M1C1 PRELIMINARY; PRT; 17 AA.

AC Q8M1C1; 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DE Prion protein (Fragment).

GN PRMP.

OS Physeter catodon (Sperm whale) (Physeter macrocephalus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;

OC Physeteridae; Physeter.

OX NCBI_TaxID=9755;

RN [1]

RA SEQUENCE FROM N.A.

RP Poux C., van Rheede T., Madsen O., de Jong W.W.;

RT "Sequence gaps join mice and men.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ438193; CAD27278.1; -.

FT NON TER 17

SQ SEQUENCE 17 AA; 1942 MW; B1AB5496B11C40C5 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 7.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8

Db 10 ILV 12

RESULT 69

Q8M1D3 PRELIMINARY; PRT; 17 AA.

AC Q8M1D3; 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DE Prion protein (Fragment).

GN PRMP.

OS Orycteropus afer (hardvark).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Tubulidentata; Orycteropodidae; Orycteropus.

OX NCBI_TaxID=9818;

RN [1]

RA SEQUENCE FROM N.A.

RP Poux C., van Rheede T., Madsen O., de Jong W.W.;

RT "Sequence gaps join mice and men.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ438206; CAD27291.1; -.

FT NON TER 17

SQ SEQUENCE 17 AA; 1869 MW; 40B52A0CECF40D8 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 7.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8

Db 10 ILV 12

RESULT 70

Q8M1G3 PRELIMINARY; PRT; 17 AA.

AC Q8M1G3; 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DE Prion protein (Fragment).

GN PRMP.

OS Dicerops bicornis (Black rhinoceros).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Dicerops.

OX NCBI_TaxID=9805;

RN [1]

RA SEQUENCE FROM N.A.

RP Poux C., van Rheede T., Madsen O., de Jong W.W.;

RT "Sequence gaps join mice and men.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ438195; CAD27280.1; -.

FT NON TER 17

SQ SEQUENCE 17 AA; 1885 MW; B1A03E10121C5FF8 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 7.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8

Db 10 ILV 12

RESULT 71

Q9TRH5 PRELIMINARY; PRT; 17 AA.

AC Q9TRH5; 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DE Alpha-Si-casein homolog (fragment).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RA SEQUENCE.

RL MEDLINE=93231344; PubMed=1299613;

RT "Isolation of a new ligand-carrying casein fragment from bovine

DE Prion protein (Fragment).

GN PRMP.

OS Manis sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Pholidota; Manidae; Manis.

OX NCBI_TaxID=49127;

RN [1]

RA SEQUENCE FROM N.A.

RP Poux C., van Rheede T., Madsen O., de Jong W.W.;

RT "Sequence gaps join mice and men.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ438196; CAD27281.1; -.

FT NON TER 17

SQ SEQUENCE 17 AA; 1859 MW; 5CC03E10121C40D8 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 7.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8

Db 10 ILV 12

RESULT 70

Q8M1G3 PRELIMINARY; PRT; 17 AA.

AC Q8M1G3; 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DE Prion protein (Fragment).

GN PRMP.

OS Dicerops bicornis (Black rhinoceros).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Dicerops.

OX NCBI_TaxID=9805;

RN [1]

RA SEQUENCE FROM N.A.

RP Poux C., van Rheede T., Madsen O., de Jong W.W.;

RT "Sequence gaps join mice and men.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ438195; CAD27280.1; -.

FT NON TER 17

SQ SEQUENCE 17 AA; 1885 MW; B1A03E10121C5FF8 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 7.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8

Db 10 ILV 12

RESULT 71

Q9TRH5 PRELIMINARY; PRT; 17 AA.

AC Q9TRH5; 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DE Alpha-Si-casein homolog (fragment).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RA SEQUENCE.

RL MEDLINE=93231344; PubMed=1299613;

RT "Isolation of a new ligand-carrying casein fragment from bovine

RT mammary gland microsomes.";
 RL FBS Left. 305;189-191(1992).
 SQ SEQUENCE 17 AA; 1950 MW; 8890EF0685A0537F CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFP 5
 ||||
 Db 4 PFP 6

RESULT 72

Q8MIF6 PRELIMINARY; PRT; 17 AA.
 ID Q8MIF6;
 AC Q8MIF6;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Prion protein (Fragment).
 GN PRMP.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Poux C., van Rheede T., Madsen O., de Jong W.W.;
 RT "Sequence gaps join mice and men."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ438194; CAD27279.1; -.
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 1857 MW; BIA03E1012C40C5 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
 ||||
 Db 10 ILV 12

RESULT 73

Q8MI97 PRELIMINARY; PRT; 17 AA.
 ID Q8MI97;
 AC Q8MI97;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Prion protein (Fragment).
 GN PRMP.
 OS Trichechus manatus (Caribbean manatee) (West Indian manatee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Sirenia; Trichechidae; Trichechus.
 OX NCBI_TaxID=9778;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Poux C., van Rheede T., Madsen O., de Jong W.W.;
 RT "Sequence gaps join mice and men."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ438205; CAD27290.1; -.
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 1837 MW; BIA52A0CECF40C5 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
 ||||
 Db 10 ILV 12

RESULT 74

Q8MIG9 PRELIMINARY; PRT; 17 AA.
 ID Q8MIG9;
 AC Q8MIG9;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Prion protein (Fragment).
 GN PRMP.
 OS Cynopterus sphinx (Indian short-nosed fruit bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
 OC Pteropodidae; Cynopterus.
 OX NCBI_TaxID=9400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Poux C., van Rheede T., Madsen O., de Jong W.W.;
 RT "Sequence gaps join mice and men."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ438197; CAD27282.1; -.
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 1867 MW; BIA03E101FRA440C5 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
 ||||
 Db 10 ILV 12

RESULT 75

Q8MIF2 PRELIMINARY; PRT; 17 AA.
 ID Q8MIF2;
 AC Q8MIF2;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Prion protein (Fragment).
 GN PRMP.
 OS Elephas maximus (Indian elephant).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Proboscidea; Elephantidae; Elephas.
 OX NCBI_TaxID=9783;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Poux C., van Rheede T., Madsen O., de Jong W.W.;
 RT "Sequence gaps join mice and men."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ438204; CAD27289.1; -.
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 1867 MW; BIA52A0CFDAB40C5 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
 ||||
 Db 10 ILV 12

Search completed: November 25, 2003, 19:34:10
 Job time : 16.0233 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 20.4186 Seconds
(without alignments)
62.189 Million cell updates/sec

Title: US-09-641-801-29

Perfect score: 8

Sequence: 1 RGPPPIIV 8

Scoring table:

OLIGO 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

```

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	100.0	8	22	Colostrin derive
2	8	100.0	8	22	Colostrin peptid
3	8	100.0	8	22	Colostrin peptid
4	8	100.0	8	22	Ewe colostrin
5	8	100.0	8	23	Colostrin consti
6	8	100.0	8	23	Colostrin consti
7	8	100.0	8	23	Neural cell regula
8	6	75.0	6	20	Non-crosslinked pr
9	6	75.0	6	21	Peptide substrate

10	6	75.0	17	15	AAR58340	Hypotensive polype
11	6	75.0	19	15	AAR58341	Hypotensive polype
12	5	62.5	15	13	AAR28573	DCPase inhibitor p
13	5	62.5	7	15	AAR45831	Aureobasidin type
14	5	62.5	8	15	AAR58333	Aureobasidin type
15	5	62.5	16	24	ABP932258	G protein-coupled
16	5	62.5	18	21	ABP27612	Human secreted pro
17	5	62.5	18	21	ABP27613	Human secreted pro
18	4	50.0	5	18	AAW54333	Bradykinin analogo
19	4	50.0	5	19	AAW65793	Polyprolyl inhibit
20	4	50.0	5	22	ABP86116	Serine proteinase
21	4	50.0	5	22	ABP86117	Serine proteinase
22	4	50.0	6	16	AAR77192	Internal sequence
23	4	50.0	7	19	AAW56422	Amino acid sequenc
24	4	50.0	7	22	AAE09134	Bacteriophage type
25	4	50.0	8	15	AAR45825	Aureobasidin type
26	4	50.0	9	17	AAR89371	Cw6 consensus pept
27	4	50.0	9	19	AAR80249	Active site sequen
28	4	50.0	9	22	ABP14561	Human C35 peptide
29	4	50.0	9	22	AAU28830	DPI tryptic digest
30	4	50.0	9	22	AAU26478	Depression-Associ
31	4	50.0	9	22	AAG89664	p53 epitope B7 sup
32	4	50.0	9	22	AAG89665	p53 epitope B7 sup
33	4	50.0	9	22	ABP76157	Tumour associated
34	4	50.0	9	22	ABP76158	Tumour associated
35	4	50.0	9	23	ABG96732	Human leukocyte an
36	4	50.0	9	23	ABG67743	Human ADP1 tryptic
37	4	50.0	9	24	ABR20445	Human cancer-relat
38	4	50.0	9	24	ABR20847	Human cancer-relat
39	4	50.0	9	24	ABR21656	Human cancer-relat
40	4	50.0	9	24	ABR21837	Human cancer-relat
41	4	50.0	9	24	ABR22240	Human cancer-relat
42	4	50.0	9	24	ABR22262	Human cancer-relat
43	4	50.0	9	24	ABR23247	Human cancer-relat
44	4	50.0	9	24	ABR23645	Human cancer-relat
45	4	50.0	10	17	AAV17845	Backbone cyclised
46	4	50.0	10	17	AAV17846	Backbone cyclised
47	4	50.0	10	17	AAV17847	Backbone cyclised
48	4	50.0	10	18	AAW36625	Thrombopoietin rec
49	4	50.0	10	18	AAW09474	Thrombopoietin rec
50	4	50.0	10	21	AAV17007	TPO-mimetic peptid
51	4	50.0	10	22	AAU25844	Human thrombopoiet
52	4	50.0	10	22	AAU06436	Saccharomyces cere
53	4	50.0	10	22	AAG87057	Human Leukocyte An
54	4	50.0	10	23	ABP72893	TPO mimetic peptid
55	4	50.0	10	24	ABR47211	Staphylococcus aur
56	4	50.0	10	24	ABR47287	Staphylococcus aur
57	4	50.0	10	24	ABR20306	Human cancer-relat
58	4	50.0	10	24	ABR21693	Human cancer-relat
59	4	50.0	10	24	ABR21964	Human cancer-relat
60	4	50.0	10	24	ABR23102	Human cancer-relat
61	4	50.0	11	18	AAW13931	CDR-3 fragment of
62	4	50.0	11	23	ABG68633	Desmocollin 1 pept
63	4	50.0	11	23	ABG68635	Desmocollin 1 pept
64	4	50.0	12	18	AAW36886	HTLV-II protease c
65	4	50.0	12	21	AAW12848	STAT3 binding pept
66	4	50.0	13	18	AAW36390	Antimicrobial pto
67	4	50.0	13	22	AAG73433	Human gene 27-enco
68	4	50.0	13	23	ABG64297	Human albumin fusi
69	4	50.0	14	19	AAW81795	D. viviparus DV17
70	4	50.0	15	17	AAW49166	Human leukocyte an
71	4	50.0	15	18	AAW38927	Peptide resembling
72	4	50.0	15	23	ABB98785	Human ribosomal pr
73	4	50.0	15	23	AAU77172	Transcriptional CO
74	4	50.0	15	24	ABR41125	LRP6 specific poly
75	4	50.0	15	24	ABR34952	Human cancer-relat
76	4	50.0	15	24	ABR34957	Human cancer-relat
77	4	50.0	15	24	ABR35179	Human cancer-relat
78	4	50.0	15	24	ABR35572	Human cancer-relat
79	4	50.0	15	24	ABR35614	Human cancer-relat
80	4	50.0	15	24	ABR35687	Human cancer-relat
81	4	50.0	15	24	ABR35776	Human cancer-relat
82	4	50.0	15	24	ABR35777	Human cancer-relat

83 4 50.0 15 24 ABR35800 Human cancer-relat
 84 4 50.0 15 24 ABR35873 Human cancer-relat
 85 4 50.0 15 24 ABR35928 Human cancer-relat
 86 4 50.0 15 24 ABR35933 Human cancer-relat
 87 4 50.0 15 24 ABR36130 Human cancer-relat
 88 4 50.0 15 24 ABR36482 Human cancer-relat
 89 4 50.0 15 24 ABR36513 Human cancer-relat
 90 4 50.0 15 24 ABR36584 Human cancer-relat
 91 4 50.0 15 24 ABR36654 Human cancer-relat
 92 4 50.0 15 24 ABR36655 Human cancer-relat
 93 4 50.0 15 24 ABR36678 Human cancer-relat
 94 4 50.0 15 24 ABR36743 Human cancer-relat
 95 4 50.0 15 24 ABR36787 Human cancer-relat
 96 4 50.0 15 24 ABR36792 Human cancer-relat
 97 4 50.0 15 24 ABR37021 Human cancer-relat
 98 4 50.0 15 24 ABR37420 Human cancer-relat
 99 4 50.0 15 24 ABR37463 Human cancer-relat
 100 4 50.0 15 24 ABR37534 Human cancer-relat

ALIGNMENTS

RESULT 1
 AAB72274
 ID AAB72274 standard; peptide; 8 AA.
 XX
 AC AAB72274;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Colostrinin derived cytokine inducing peptide SEQ ID 29.
 XX
 KW Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.
 XX
 OS Synthetic.
 XX
 PN WO200111937-A2.
 XX
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22818.
 XX
 PR 17-AUG-1999; 99US-0149311.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REG-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX WPI; 2001-202804/20.
 XX
 XX
 PT Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprising administering colostrinin as an immunological
 PT regulator -
 XX
 PS Claim 1; Page 34; 50pp; English.
 XX
 CC Sequences ABR72246 - AAB72275 represent peptides derived from colostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrinin and its derived peptides are useful for
 CC inducing cytokine production, for modulating an immunological response
 CC and for inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies.

XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 8; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGPFPILV 8
 Db 1 RGPFPILV 8
 |||||
 |||||
 RESULT 2
 AAB72527
 ID AAB72527 standard; Peptide; 8 AA.
 XX
 AC AAB72527;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Colostrinin peptide #28.
 XX
 KW Dermatalogical; oxidative stress regulator; colostrinin.
 XX
 OS Unidentified.
 XX
 PN WO200112650-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22665.
 XX
 PR 17-AUG-1999; 99US-0149310.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX WPI; 2001-218342/22.
 XX
 PT Modulating oxidative stress level in a cell, involves contacting the
 PT cell with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations -
 XX
 PS Claim 6; Page 26; 48pp; English.
 XX
 CC The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 8; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGPFPILV 8
 Db 1 RGPFPILV 8
 |||||
 |||||
 RESULT 3
 AAB72559
 ID AAB72559 standard; Peptide; 8 AA.
 XX
 AC AAB72559;
 XX
 DT 09-MAY-2001 (first entry)
 XX

```

DE Colostrinin peptide #28.
XX
XX Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX
XX Unidentified.
OS
XX WO200112651-A2.
PN
XX 22-FEB-2001.
PD
XX 17-AUG-2000; 2000WO-US22774.
PF
XX 17-AUG-1999; 99US-0149633.
PR
XX (TEXA ) UNIV TEXAS SYSTEM.
PA
XX
XX Boldogh I;
PI
XX WPI; 2001-226545/23.
DR
XX
XX Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating
PT damaged neural cells in a patient .
XX
XX Claim 6; Page 22; 35pp; English.
PS
XX
XX The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
XX
XX Query Match 100.0%; Score 8; DB 22; Length 8;
SQ Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPPFILV 8
Db 1 RGPPFILV 8

RESULT 4
AAB59339
ID AAB59339 standard; Peptide; 8 AA.
XX
XX AAB59339;
AC
XX
XX 21-MAR-2001 (first entry)
DT
XX
XX Ewe colostrinin peptide fragment C-14.
DE
XX
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
KW
XX
XX Ovis sp.
XX
XX WO200075173-A2.
PN
XX
XX 14-DEC-2000.
PD
XX
XX 02-JUN-2000; 2000WO-GB02128.
PF
XX
XX 02-JUN-1999; 99GB-0012852.
PR
XX
XX (REGE-) REGEN THERAPEUTICS PLC.
PA
XX
XX Georgiades JA;
PI
XX
XX WPI; 2001-071058/08.
DR
XX
XX Peptides having an N-terminal amino acid sequence isolated from
PT

PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -
XX
XX Claim 7; Page 27; 63pp; English.
PS
XX
XX The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.
XX
XX
XX Query Match 100.0%; Score 8; DB 22; Length 8;
SQ Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPPFILV 8
Db 1 RGPPFILV 8

RESULT 5
AAE20256
ID AAE20256 standard; peptide; 8 AA.
XX
XX AAE20256;
AC
XX
XX 18-JUN-2002 (first entry)
DT
XX
XX Colostrinin constituent peptide #28.
DE
XX
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulneteray.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH 8
FT Modified-site /note= "Optionally C-terminal amide"
FT
XX
XX WO200213850-A1.
PN
XX
XX 21-FEB-2002.
PD
XX
XX 17-AUG-2000; 2000WO-US22776.
PF
XX
XX 17-AUG-2000; 2000WO-US22776.
PR
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
PA
XX
XX Stanton GJ, Hughes TK, Boldogh I;
PI
XX
XX WPI; 2002-269151/31.
DR
XX
XX Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog -
XX
XX Claim 6; Page 26; 51pp; English.
PS
XX
XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/

```

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.
 XX
 XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPFPILV 8
 |||||
 Db 1 RGPFPILV 8

RESULT 6

AA051063
 ID AA051063 standard; Peptide; 8 AA.

AC AA051063;

XX 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide (casein amino acids 214-222).

XX Colostrinin; colostrum; immunomodulator; cardiovascular;

KW blood cell regulator; cytokine inducer; beta-casein; human.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

PH Modified-site 8

FT /note= "optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA) UNIV TEXAS SYSTEM.

PA (REG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 PI WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.
 PS
 XX

CC The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified
 CC as having a beta-casein homologue precursor, and corresponds to
 CC casein amino acids 214-222. Methods are claimed for: inducing a
 CC cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ
 CC or an organism, and the cell is mammalian, including human;
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a
 CC cytokine; modulating an immune response in a patient by administering
 CC an immunological regulator under conditions effective to induce a
 CC cytokine, where the immunological regulator is administered topically
 CC or as part of a dietary supplement, and where the immune response is
 CC specific or non specific, an interferon response or an antibody
 CC response; modulating blood cell proliferation by contacting blood
 CC cells with a blood cell regulator, where the blood cells are present
 CC in a cell culture or an organism, are mammalian or human, and where
 CC the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent. A
 CC claimed cytokine-inducing composition comprises a pharmaceutical
 CC carrier and an active agent such as the present peptide.
 XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPFPILV 8
 |||||
 Db 1 RGPFPILV 8

RESULT 7

AA014605

ID AA014605 standard; peptide; 8 AA.

AC AA014605;

XX 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 28.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

XX neural cell treatment.

XX Unidentified.

OS

XX Key Location/Qualifiers

PH Modified-site 8

FT /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;
 PI WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -

XX Claim 7; Page 22; 37pp; English.
 PS
 XX

CC The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention.

SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPFPILV 8
|||||

Db 1 RGPFPILV 8

RESULT 8

AAAY30980
ID AAY30980 standard; peptide; 6 AA.

XX AC AAY30980;

XX 21-OCT-1999 (first entry)

DE Non-crosslinked protein particle peptide 29.

XX Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
KW albumin; haemoglobin; nanometer; micrometer; clearance.

XX Synthetic.

XX US5945033-A.

XX 31-AUG-1999.

XX 12-NOV-1996; 96US-0747137.

XX 14-MAR-1994; 94US-0212546.

XX 15-JAN-1991; 91US-0641720.

XX 13-OCT-1992; 92US-0959560.

XX 01-JUN-1993; 93US-0069831.

XX 12-NOV-1996; 96US-0747137.

XX (HEMO-) HEMOSPHERE INC.

XX Yen RCK;

XX WPI; 1999-508153/42.

XX Non-crosslinked protein particles for therapeutic and diagnostic use

XX Example 22; Column 61-62; 65pp; English.

CC This invention describes a novel aqueous suspension of monodisperse
CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which
CC is stable against dissolving upon dilution with an alcohol-free aqueous
CC medium. The method involves (a) forming an aqueous solution containing
CC albumin and hemoglobin and (b) treating the aqueous solution with an
CC alcohol to cause the solution to become turbid. The particles are useful
CC as agents for in vivo administration, either of their own administration
CC or as a vehicle for other therapeutic or diagnostic agents. The method
CC permits the formation of albumin and hemoglobin particles in the
CC nanometer and micrometer size range, in a form closer to their natural
CC form than the forms of the prior art. The particles therefore constitute
CC a more closely controlled agent for in vivo administration, with greater
CC ease of clearance from the body after their period of usefulness.
CC AAY30982-X31135 represent peptides used in the method of the invention.

SQ Sequence 6 AA;

Query Match 75.0%; Score 6; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPFPPI 6
|||||

Db 1 RGPFPPI 6

RESULT 9

AAAB18488
ID AAB18488 standard; peptide; 6 AA.

XX AC AAB18488;

XX 15-JAN-2001 (first entry)

XX Peptide substrate used to test prolyl-tripeptidyl peptidase activity.

XX Prolyl tripeptidyl-peptidase; amidolytic activity; periodontal disease;
KW gingivitis; periodontitis.

XX Synthetic.

XX Key Modified-site 1 Location/Qualifiers
FT /note= "hydrogen attached"

XX WO200052147-A2.

XX 08-SEP-2000.

XX 03-MAR-2000; 2000WO-US05551.

XX 05-MAR-1999; 99US-0123148.

XX (UYGE-) UNIV GEORGIA RES FOUND INC.

XX (TRAV/) TRAVIS J.

XX (POTE/) POTEMPA J.

XX (BANE/) BANBULA A.

XX Travis J, Potempa J, Banbula A;

XX WPI; 2000-594181/56.

XX Prolyl tripeptidyl-peptidase, active analog, fragment or variant useful
PT for identifying its inhibitor which is useful for protecting an animal
PT from a periodontal disease such as gingivitis and periodontitis

XX Claim 3; Page 37; 58pp; English.

XX The present sequence represents a substrate which was used to test
CC the activity of prolyl tripeptidyl-peptidases PTP-A and DPP IV. The
CC prolyl tripeptidyl-peptidase has an amidolytic activity, and cleaves
CC a peptide bond in a target polypeptide having at least 4 amino acids.
CC This bond is between a proline and an amino acid attached to the
CC alpha-carboxyl group end of the proline. The polypeptide is useful for
CC identifying inhibitors. These inhibitors are then useful for reducing
CC the growth of bacterium or for protecting an animal from a periodontal
CC disease such as gingivitis and periodontitis caused by Porphyromonas
CC gingivalis.

SQ Sequence 6 AA;

Query Match 75.0%; Score 6; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPFPPI 6
|||||

Db 1 RGPFPPI 6

RESULT 10

AAAR58340
ID AAR58340 standard; peptide; 17 AA.

XX AC AAR58340;

XX

DT 22-SEP-1994 (first entry)
 XX Hypotensive polypeptide.
 DE Hypotensive; antioxidative; calcium absorption; salt; food;
 XX pharmaceuticals; physiologically active agents.
 KW Lactobacillus helveticus.
 XX JP06041191-A.
 FN 15-FEB-1994.
 XX 03-MAR-1993; 93JP-0043047.
 PF 04-MAR-1992; 92JP-0047340.
 PR (CALV) CALPIS SHOKUHN KOGYO KK.
 XX WPI; 1994-089332/11.
 DR New polypeptide - used in physiologically active agents having
 XX e.g. hypotensive antioxidative and calcium absorption promoting
 PT activity
 PT Claim 1-2; Page 10; 10pp; Japanese.
 PS Sequences (AAR58319-341) are used in conjunction with
 XX physiologically active agents showing a property such as
 CC hypotensive activity, calcium absorption promoting activity and
 CC antioxidative activity. The peptides are non-toxic and can be
 CC used in physiologically active agents.
 XX Sequence 17 AA;
 SQ Query Match 75.0%; Score 6; DB 15; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGPFPPI 6
 DB 10 RGPFPPI 15
 DE RESULT 11
 AAR58341
 ID AAR58341 standard; peptide; 19 AA.
 AC AAR58341;
 XX 22-SEP-1994 (first entry)
 DT Hypotensive polypeptide.
 DE Hypotensive; antioxidative; calcium absorption; salt; food;
 XX pharmaceuticals; physiologically active agents.
 KW Lactobacillus helveticus.
 XX JP06041191-A.
 FN 15-FEB-1994.
 XX 03-MAR-1993; 93JP-0043047.
 PF 04-MAR-1992; 92JP-0047340.
 PR (CALV) CALPIS SHOKUHN KOGYO KK.
 XX WPI; 1994-089332/11.
 DR New polypeptide - used in physiologically active agents having
 XX e.g. hypotensive antioxidative and calcium absorption promoting
 PT activity

PT activity
 XX Claim 1-2; Page 10; 10pp; Japanese.
 XX Sequences (AAR58319-341) are used in conjunction with
 CC physiologically active agents showing a property such as
 CC hypotensive activity, calcium absorption promoting activity and
 CC antioxidative activity. The peptides are non-toxic and can be
 CC used in physiologically active agents.
 XX Sequence 19 AA;
 SQ Query Match 75.0%; Score 6; DB 15; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGPFPPI 6
 DB 12 RGPFPPI 17
 DE RESULT 12
 AAR28573
 ID AAR28573 standard; peptide; 5 AA.
 AC AAR28573;
 XX 22-MAR-1993 (first entry)
 DT DCPase inhibitor peptide.
 DE Dipeptidyl carboxypeptidase; DCPase; inhibitor; vasodepression;
 XX internal blood pressure.
 KW Bacillus sp.
 XX JP04288098-A.
 PN 13-OCT-1992.
 PD 14-MAR-1991; 91JP-0074581.
 PF 14-MAR-1991; 91JP-0074581.
 PR (EZAK) EZAKI GLICO CO.
 XX WPI; 1992-387722/47.
 DR New peptide obtd. from Bacillus sp. strain - inhibits di:peptidyl
 PT carboxy:peptidase and so are blood pressure regulators
 XX Disclosure; Page 2; 3pp; Japanese.
 PS This peptide is a preferred example of the generic sequence given in
 CC AAR28574. Peptides covered by this formula are dipeptidyl
 CC carboxypeptidase (DCPase) inhibitors. They inhibit vasodepressor
 CC activity and keep internal blood pressures normal. These peptides
 CC may be administered orally, eg. daily in food, without side effects.
 XX Sequence 5 AA;
 SQ Query Match 62.5%; Score 5; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GPFPI 6
 DB 1 GPFPI 5
 DE RESULT 13
 AAR45831
 ID AAR45831 standard; Protein; 7 AA.

Query Match	62.5%;	Score 5;	DB 15;	Length 7;	
Best Local Similarity	100.0%;	Pred. No. 9.3e+05;			
Matches	5;	Conservative	0;	Mismatches	0; Indels 0; Gaps
QY	4	FPILV 8			
DB	3	FPILV 7			
RESULT 14					
AAR58333					
ID	AAR58333	standard; peptide; 8 AA.			
AC	AAR58333;				
DT	22-SEP-1994	(first entry)			
DE	Hypotensive polypeptide.				
KW	Hypotensive; antioxidant; calcium absorption; salt; food;				
KW	pharmaceuticals; physiologically active agents.				
OS	Lactobacillus helveticus.				
PN	JP06041191-A.				
PD	15-FEB-1994.				
PF	03-MAR-1993;	93JP-0043047.			
PR	04-MAR-1992;	92JP-0047340.			
FA	(CALV) CALPIS SHOKUHIN KOGYO KK.				
DR	WPI; 1994-089332/11.				
PT	New polypeptide - used in physiologically active agents having				
FT	e.g. hypotensive antioxidant and calcium absorption promoting				
PT	activity				
PS	Claim 1-2; Page 9; 10pp; Japanese.				
CC	Sequences (AAR58319-341) are used in conjunction with				
CC	physiologically active agents showing a property such as				
CC	hypotensive activity, calcium absorption promoting activity and				
CC	antioxidative activity. The peptides are non-toxic and can be				
CC	used in physiologically active agents.				
Sequence	8 AA;				
Query Match	62.5%;	Score 5;	DB 15;	Length 8;	
Best Local Similarity	100.0%;	Pred. No. 9.3e+05;			
Matches	5;	Conservative	0;	Mismatches	0; Indels 0; Gaps
QY	1	RGPPF 5			
DB	4	RGPPF 8			
RESULT 15					
ABP83258					
ID	ABP83258	standard; Peptide; 16 AA.			
AC	ABP83258;				
DT	04-MAR-2003	(first entry)			
DE	G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1931.				
KW	G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;				
KW	G protein-coupled receptor modulator; antibody; immune-related disease;				
KW	growth-related disease; cell regeneration-related disease; AIDS; cancer;				
KW	immunological-related cell proliferative disease; autoimmune disease;				

KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.

OS Homo sapiens.

PN WO200261087-A2.

XX 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US50107.

XX 19-DEC-2000; 2000US-257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burmer GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases -

PS Claim 1; Fig 2; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

XX Sequence 16 AA;

Query Match 62.5%; Score 5; DB 24; Length 16;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFPIL 7

Db 1 PFPIL 5

RESULT 16

AAB27612

ID AAB27612 standard; Peptide; 18 AA.

XX

AC AAB27612;

XX

DT 02-FEB-2001 (first entry)

XX Human secreted protein BLAST search protein SEQ ID NO: 113.

DE

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antitumor;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.

XX Homo sapiens.

XX WO200055175-A1.

XX 21-SEP-2000.

XX 09-MAR-2000; 2000WO-US06049.

XX 12-MAR-1999; 99US-0124144.

XX 11-JUN-1999; 99US-0138574.

XX 03-DEC-1999; 99US-0168667.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

XX Rosen CA, Ruben SM, Komatsoulis G;

XX

XX WPI; 2000-638175/61.

XX

PT Isolated nucleic acid molecule encoding a human secreted protein is
 PT used in preventing, treating or ameliorating a medical condition -

XX

XX Disclosure; Page 399; 428pp; English.

XX

CC The invention relates to the isolation of genes AAC58990-C59039 encoding
 CC the human secreted proteins AAB27560-B27609. This sequence represents a
 CC peptide fragment homologous to the protein encoded by the gene given
 CC in the descriptor line. The sequence is a search result from a BLASTX
 CC homology search. The genes and proteins are useful for preventing,
 CC ameliorating or treating medical conditions, e.g. by protein or gene
 CC therapy. The genes are isolated from a range of human tissues disclosed
 CC in the specification. The nucleic acids, proteins, antibodies and
 CC (ant)agonists are useful in the diagnosis, treatment and prevention of:
 CC (a) cancer, e.g. breast and ovarian cancer, and other cancers of the
 CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
 CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis; (c) cardiovascular disorders such
 CC as myocardial ischaemias; (d) wound healing; (e) neurological diseases
 CC e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such
 CC as viral, bacterial, fungal and parasitic infections.

XX Sequence 18 AA;

Query Match 62.5%; Score 5; DB 21; Length 18;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPFP 5

Db 11 RGPFP 15

RESULT 17

AAB27613

ID AAB27613 standard; Peptide; 18 AA.

XX

AC AAB27613;

XX

DT 02-FEB-2001 (first entry)

XX

DE Human secreted protein BLAST search protein SEQ ID NO: 114.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antitumor;
 KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 XX Homo sapiens.
 OS
 XX WO20005175-A1.
 PN
 XX 21-SEP-2000.
 PD
 XX
 XX 09-MAR-2000; 2000WO-US06049.
 XX
 XX 12-MAR-1999; 99US-0124144.
 PR
 XX 11-JUN-1999; 99US-0138574.
 PR
 XX 03-DEC-1999; 99US-0168667.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Rosen CA, Ruben SM, Komatsoulis G;
 PI
 XX WPI; 2000-638175/61.
 DR
 XX Isolated nucleic acid molecule encoding a human secreted protein is
 PT used in preventing, treating or ameliorating a medical condition -
 PT
 XX Disclosure; Page 399; 428pp; English.
 PS
 XX The invention relates to the isolation of genes AAC58990-C59039 encoding
 CC the human secreted proteins AAB27560-B27609. This sequence represents a
 CC fragment of the protein encoded by the gene given in the descriptor
 CC line. The sequence is used as a query sequence for doing BLASTX searches
 CC to determine homologous sequence to the protein. The genes and proteins
 CC are useful for preventing, ameliorating or treating medical conditions,
 CC e.g. by protein or gene therapy. The genes are isolated from a range of
 CC human tissues disclosed in the specification. The nucleic acids,
 CC proteins, antibodies and (ant)agonists are useful in the diagnosis,
 CC treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer,
 CC and other cancers of the adrenal gland, bone, bone marrow, breast,
 CC gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders
 CC e.g. Addison's disease, allergies, autoimmune haemolytic anaemia,
 CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
 CC sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemia; (d) wound
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and
 CC (f) infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections.
 XX
 XX Sequence 18 AA;
 SQ
 Query Match 62.5%; Score 5; DB 21; Length 18;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGPPF 5
 DB 11 RGPPF 15
 RESULT 18
 AAW54333
 ID AAW54333 standard; peptide; 5 AA.
 XX
 XX AAW54333;
 AC
 XX 30-JUL-1998 (first entry)
 DT
 XX Bradykinin analogous peptide 16.
 DE
 XX Inhibition; thrombin-induced platelet; prevention; platelet aggregation;
 KW ADP-induced activation.
 KW

XX Synthetic.
 OS
 XX WO9641640-A1.
 PN
 XX 27-DEC-1996.
 PD
 XX 07-JUN-1996; 96WO-US09940.
 PF
 XX 09-JUN-1995; 95US-0000096.
 PR
 XX (UNMI) UNIV MICHIGAN.
 PA
 XX Hasan AAK, Schmaier AH;
 PI
 XX WPI; 1997-065304/06.
 DR
 XX Inhibition of platelet activation and aggregation - by admin. of new
 PT or known bradykinin analogues
 PT
 XX Disclosure; Page 42; 73pp; English.
 PS
 XX Administration of a peptide or multimer related to bradykinin or other
 CC disclosed peptides and multimers can be used for the inhibition of
 CC thrombin-induced platelets or other cells. They can also be used for
 CC preventing platelet aggregation, or inhibiting ADP-induced activation.
 CC This is useful to prevent arterial occlusions arising from coronary
 CC thrombosis and stroke.
 XX
 XX Sequence 5 AA;
 SQ
 Query Match 50.0%; Score 4; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GPPF 5
 DB 1 GPPF 4
 RESULT 19
 AAW65793
 ID AAW65793 standard; peptide; 5 AA.
 XX
 XX AAW65793;
 AC
 XX 19-OCT-1998 (first entry)
 DT
 XX Polypolyl inhibitor of cyclophilin.
 DE
 XX polypolyl; cyclophilin; inhibitor; neurotrophic compound; PPI;
 KW ptiptydyl-prolyl isomerase; rotamase; immunophilin protein; degeneration;
 KW neuronal damage.
 KW
 XX Synthetic.
 OS
 XX WO9825950-A1.
 PN
 XX 18-JUN-1998.
 PD
 XX 08-DEC-1997; 97WO-US23102.
 PF
 XX 09-DEC-1996; 96US-0761902.
 PR
 XX (GUIL-) GUILFORD PHARM INC.
 PA
 XX Hamilton GS, Steiner JP, Wei L;
 PI
 XX WPI; 1998-348444/30.
 DR
 XX Effecting neuronal activity in mammals - by administering tetra-
 PT and penta- peptide inhibitors of cyclophilin and rotamase enzyme,
 PT useful in treatment of neuronal damage or degeneration disorders
 PT

XX PS Claim 11; Page 40; 70pp; English.

XX CC The invention relates to a method of effecting a neuronal activity. It

XX CC comprises administering a neurotrophic compound with an affinity for a

XX CC cyclophilin type immunophilin. The immunophilin shows peptidyl-prolyl

XX CC isomerase (rotamase) activity. The neurotrophic compound achieves the

XX CC stimulation of damaged neurons, promotion of neuronal regeneration or

XX CC prevention of neurodegeneration, and treatment of neurological disorder.

XX CC The neurotrophic compounds are potent peptidyl-proline isomerase

XX CC (rotamase) inhibitors. They are of use in disorders which include

XX CC peripheral neuropathy caused by physical injury or disease state, i.e.

XX CC physical injury to the brain or spinal cord, stroke, or neurological

XX CC disorder leading to neurodegeneration, notably Alzheimer's and

XX CC Parkinson's diseases, or amyotrophic lateral sclerosis. The neurotrophic

XX CC compounds avoid the side effects of immunosuppressant drugs, including

XX CC nephrotoxicity, impaired glomerular filtration, interstitial fibrosis,

XX CC involuntary tremors, headaches, and hypertension. They are also free from

XX CC the difficulties in delivery and bioavailability of large molecular

XX CC weight proteins. The present sequence represents a specifically claimed

XX CC neurotrophic compound.

SQ Sequence 5 AA;

Query Match 50.0%; Score 4; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFPI 6
 ||||
 2 PFPI 5

Db

RESULT 20

AAB86116
 ID AAB86116 standard; peptide; 5 AA.

AC AAB86116;

DT 17-JUL-2001 (first entry)

XX Serine proteinase inhibiting pentapeptide.

KW Serine proteinase inhibitor; topical; prophylactic; cosmetic;
 KW dry skin treatment; desmosome-degrading proteinase inhibitor;
 KW desmosome; skin-flaking; desquamation.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1

FT /label= OTHER
 FT /note= "Gly residue modified by N-CBZ
 (N-benzyloxycarbonyl)"

XX DE19950020-A1.

XX 19-APR-2001.

XX 16-OCT-1999; 99DE-1050020.

XX 16-OCT-1999; 99DE-1050020.

XX (HENK) HENKEL KGAA.

XX Saettler A, Weiss A, Schlotmann K, Foerster T;

XX WPI; 2001-336587/36.

XX Use of compositions containing inhibitors of desmosome degradation to
 PT prevent skin-flaking during prophylactic or cosmetic treatment of dry
 PT skin -

XX

PS Claim 6; Page 3; 14pp; German.

XX CC This sequence represents a novel pentapeptide capable of inhibiting

XX CC serine proteinases. The product of the invention can be used in the

XX CC topical prophylactic or cosmetic treatment of dry skin of a composition

XX CC which contains a skin-compatible carrier and an inhibitor for

XX CC desmosome-degrading proteinases. The product can also be used in skin

XX CC treatments to prevent breakdown of desmosome structures, the compositions

XX CC being used as alcohol solutions, gels, emulsions, e.g. in shampoos. A

XX CC wide range of inhibitors prevent skin-flaking (desquamation) caused by

XX CC (preferably serine) proteinases and help to retain the keratinocytes.

SQ Sequence 5 AA;

Query Match 50.0%; Score 4; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPPP 5
 ||||
 1 GPPP 4

Db

RESULT 21

AAB86117

ID AAB86117 standard; peptide; 5 AA.

XX AAB86117;

DT 17-JUL-2001 (first entry)

XX Serine proteinase inhibiting pentapeptide.

XX Serine proteinase inhibitor.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1

FT /label= OTHER
 FT /note= "Gly residue modified by N-CBZ
 (N-benzyloxycarbonyl)"

XX DE19950019-A1.

XX 19-APR-2001.

XX 16-OCT-1999; 99DE-1050019.

XX 16-OCT-1999; 99DE-1050019.

XX (HENK) HENKEL KGAA.

XX Saettler A, Weiss A, Schlotmann K, Foerster T;

XX WPI; 2001-336586/36.

XX Surfactant-containing detergents or cleaning agents for cleaning the
 PT skin or hard surfaces contain inhibitors against proteinase-caused skin
 PT flaking -

XX Claim 2; Page 3; 18pp; German.

XX CC This invention describes a novel serine proteinase inhibitor which can
 CC be used in surfactant-containing detergents or cleaning agents also
 CC contain inhibitors against proteinase-caused desmosome degradation,
 CC where the inhibitors being such that at 0.0005% concentration they show
 CC an at least 5% prevention effect. Claimed uses are: (i) topical
 CC prophylactic or cosmetic treatment of dry skin, especially in cleaning of
 CC the skin with prevention of, or reduction in, dry skin formation; or (ii)
 CC manual cleaning of hard surfaces with similar prevention or reduction on
 CC the hands. A wide range of inhibitors prevent skin-flaking (desquamation)
 CC caused by (preferably serine) proteinases and help to retain the

CC keratinocytes whether being used to wash the skin or being used manually
 CC to clean hard surfaces.

XX Sequence 5 AA;

Query Match 50.0%; Score 4; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPFP 5
 ||||
 Db 1 GPFP 4

RESULT 22

AA77192
 ID AAR77192 standard; Protein; 6 AA.

XX AC

XX AAR77192;

XX 25-MAR-2003 (updated)

DT 24-NOV-1995 (first entry)

XX Internal sequence of cytochrome P-450OX.

DE Cytochrome; P-450ox; monooxygenase.

XX Synthetic.

XX OS

XX Key Location/Qualifiers

FT Misc-difference 1..6

FT /note= "X represents unspecified AA"

XX WO9516041-A1.

XX 15-JUN-1995.

XX 28-NOV-1994; 94WO-EP03938.

XX 08-DEC-1993; 93EP-0810860.

XX (CIBA) CIBA GEIGY AG.

PA (UVRO-) UNIV ROYAL VETERINARY & AGRIC.

PI Halkier BA, Koch BM, Lindberg MLLER B, Sibbesen O;
 PI Lindberg MOLLER B;

XX WPI; 1995-224324/29.

XX DNA encoding cytochrome P-450 mono:oxygenase(s) - for modifying
 PT biosynthetic production of cyanogenic glycoside(s) and
 PT glucosinolate(s) in crop plant(s) for increased pest resistance
 PT or improved nutritive value

XX Example; Page 27; 73pp; English.

XX Cytochrome P-450OX resembles the cytochrome P-450 reported to
 CC convert oximes to nitriles in rat liver microsomes. The mol. wt.
 CC of P-450OX as determined by SDS-PAGE is 51 kD. AA sequences are
 CC obtd. by Edman degradation. The internal polypeptides are obtd.
 CC by trypsin digestion of the purified protein and subsequent sepn.
 CC of peptides using reverse phase HPLC. The N-terminal sequence is
 CC given in AAR77188. A cytochrome with a mol. wt. of 51 kD and this
 CC N-terminal sequence is claimed. Internal peptides are given in
 CC AAR77189-R77192.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 6 AA;

Query Match 50.0%; Score 4; DB 16; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPI 6
 ||||
 Db 3 PPPI 6

RESULT 23

AAW56422

ID AAW56422 standard; peptide; 7 AA.

XX AC

XX 31-JUL-1998 (first entry)

XX Amino acid sequence of a tasty peptide.

XX Tasty peptide; flavour; food; modification; enhance; food taste.

XX Unidentified.

XX EP832972-A2.

XX 01-APR-1998.

XX 17-SEP-1997; 97EP-0116132.

XX 23-SEP-1996; 96EP-0115211.

XX (GIVA) GIVAUDAN-ROURE INT SA.

XX Lerch K, Muheim A, Silke N;

XX WPI; 1998-195226/18.

XX New tasty peptide(s) in homogeneous form - useful for, e.g.

XX preparing foods and masking food taste

XX Claim 3; Page 3; 27pp; English.

XX The present sequence represents a tasty peptide. Tasty peptides

XX contribute, in combination with volatile compounds, to the overall

XX impression of a flavour. The specification describes the production of

XX several tasty peptides in homogeneous form, isolated DNA sequences

XX encoding them and organisms transformed with these sequences. The tasty

XX peptides may be used in preparing food to modify, enhance or mask

XX different food tastes.

XX Sequence 7 AA;

Query Match 50.0%; Score 4; DB 19; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGFP 4

||||

Db 1 RGFP 4

RESULT 24

AAE09134

ID AAE09134 standard; peptide; 7 AA.

XX AC

XX AAE09134;

XX 15-NOV-2001 (first entry)

XX Bacteriophage Type VI peptide, used in the invention.

XX Vaccine; therapy; autoimmune disorder; Epstein-Barr virus; EBV; anaemia;

XX polymyositis; systemic lupus erythematosus; SLE; rheumatoid arthritis;

XX Sjogren's syndrome; diabetes mellitus; adrenalitis; multiple sclerosis;

XX demyelinating disease; Hashimoto's thyroiditis; autoimmune infertility;

XX hypoparathyroidism; primary biliary cirrhosis; ankylosing spondylitis;

XX inflammatory bowel disease; Addison's disease; thyroiditis; filariasis;

KW Graves' disease; ulcerative colitis; dermatomyositis; myasthenia gravis;
 KW Crohn's disease; CREST syndrome; autoimmune cystitis; glomerulonephritis;
 KW polyarteritis nodosa; hepatitis; atopic rhinitis; Goodpasture's syndrome;
 KW sarcoidosis; rheumatic fever; anti-phospholipid syndrome; farmer's lung;
 KW Cushing's syndrome; bird-fancier's lung; alveolitis; erythema nodosum;
 KW pyoderma gangrenosum; fibromyalgia; Kawasaki's disease; cardiomyopathy;
 KW Sampter's syndrome; asthma; polymyalgia rheumatica; psoriasis; arteritis;
 KW erythroblastosis foetalis; cyclophilia; IGA nephropathy; Hodgkin's lymphoma;
 KW renal cell carcinoma; eosinophilia; immunosuppressive; ophthalmological;
 KW thrombocytic; neuroprotective; cytostatic; nephrotropic; antiallergic;
 KW dengue; antiulcer; vasotropic; antipyretic; hepatotropic.
 XX
 OS Bacteriophage.
 XX
 XX
 PN W0200158481-A2.
 XX
 XX 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US04191.
 XX
 XX 09-FEB-2000; 2000US-0500904.
 XX
 XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 PA
 PI Harley JB, James JA, Kaufman KM;
 XX
 XX WPI; 2001-522437/57.
 DR
 XX

XX Bacteriophage.

XX W0200158481-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US04191.

XX 09-FEB-2000; 2000US-0500904.

XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.

PA Harley JB, James JA, Kaufman KM;

XX WPI; 2001-522437/57.

XX Novel vaccine for alleviating or preventing autoimmune disorders
 PT induced Epstein-Barr virus (EBV) infection e.g. systemic lupus
 PT erythematosis, juvenile onset diabetes mellitus, comprises EBV virus or
 PT its component
 XX

PS Example 10; Page 56; 114pp; English.

XX The present invention relates to a vaccine for alleviating or preventing
 CC autoimmune disorders induced by infection with Epstein-Barr virus (EBV),
 CC comprising EBV or its component in a carrier. The vaccine is useful for
 CC preventing or alleviating autoimmune disorders induced by EBV, e.g.
 CC systemic lupus erythematosus (SLE), Sjogren's syndrome, juvenile onset
 CC diabetes mellitus, rheumatoid arthritis, Wegener's granulomatosis,
 CC inflammatory bowel disease, polymyositis, dermatomyositis, multiple
 CC endocrine failure, Schmidt's syndrome, autoimmune uveitis, Addison's
 CC disease, adrenalitis, primary biliary cirrhosis, Graves' disease,
 CC thyroiditis, Hashimoto's thyroiditis, autoimmune thyroid disease,
 CC pernicious and haemolytic anaemia, lupoid hepatitis, demyelinating
 CC disease, multiple sclerosis, subacute cutaneous lupus erythematosus,
 CC hypoparathyroidism, Dressler's syndrome, myasthenia gravis, autoimmune
 CC idiopathic thrombocytopenic purpura, autoimmune pemphigus vulgaris,
 CC pemphigus, bullous pemphigoid, dermatitis herpetiformis, alopecia
 CC areata, autoimmune cystitis, pemphigoid, scleroderma, progressive
 CC systemic sclerosis, CREST syndrome (calcinosis, Raynaud's oesophageal
 CC dysmotility, sclerodactyly and telangiectasia), adult onset diabetes
 CC mellitus (Type II diabetes), male or female autoimmune infertility,
 CC ankylosing spondylitis, ulcerative colitis, Crohn's disease, mixed
 CC connective tissue disease, polyarteritis nodosa, systemic necrotizing
 CC vasculitis, glomerulonephritis, atopic dermatitis, atopic rhinitis,
 CC Goodpasture's syndrome, Chagas' disease, sarcoidosis, rheumatic fever,
 CC asthma, recurrent abortion, anti-phospholipid syndrome, farmer's lung,
 CC erythema multiforme, postcardotomy syndrome, Cushing's syndrome,
 CC autoimmune chronic active hepatitis, bird-fancier's lung, allergic
 CC encephalomyelitis, toxic necrodermal lysis, alopecia, Alport's syndrome,
 CC allergic alveolitis, fibrosing alveolitis, interstitial lung disease,
 CC erythema nodosum, pyoderma gangrenosum, transfusion reaction, chronic
 CC fatigue syndrome, fibromyalgia, Takayasu's arteritis, Kawasaki's disease,
 CC polymyalgia rheumatica, temporal arteritis, giant cell arteritis, dengue,
 CC Sampter's syndrome (triaditis, nasal polyps, eosinophilia) and Behcet's
 CC disease, Caplan's syndrome, encephalomyositis, erythema elevatum et
 CC diutinum, psoriasis, erythroblastosis foetalis, Shulman's syndrome et
 CC nephropathy, Felty's syndrome, fascitis with eosinophilia, filaritis,
 CC chronic cystitis, heterochromic cystitis, Fuch's cyclitis, Hodgkin's and
 CC non-Hodgkin's lymphoma, cardiomyopathy, Henoch-Schonlein purpura, post
 CC vaccination syndromes, renal cell carcinoma, Eaton-Lambert syndrome or

CC relapsing polychondritis. The present sequence is Bacteriophage Type VI
 CC peptide used in the invention.

SQ Sequence 7 AA;

Query Match 50.0%; Score 4; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7

Db 4 FPIL 7

RESULT 25

AAAR45825

ID AAR45825 standard; Protein; 8 AA.

XX AAR45825;

XX 25-MAR-2003 (updated)

DT 20-JUL-1994 (first entry)

XX Aureobasidin type cyclic peptide (cpd. 23).

XX Aureobasidin; alpha-hydroxy acid; N-methyl-alpha-amino acid;
 XX antifungal; synthesis; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT /label= MeVal

FT /note= "MeVal has a D-Hmp (2(R)-hydroxy-
 3(R)-methylpentanoate) substituent
 which is bound to residue 8 to
 form the cyclic peptide"

FT Modified-site 3

FT /label= OTHER

FT /note= "Mephe"

FT Modified-site 5

FT /label= aile

FT Modified-site 6

FT /label= OTHER

FT /note= "MeLeu"

FT Modified-site 8

FT /label= OTHER

FT /note= "betaHOMeVal"

FT Misc-difference 2..5
 FT /note= "two intramolecular hydrogen bonds between
 residues 2 and 5"

FT Misc-difference 7..1

FT /note= "one intramolecular hydrogen bond between
 residues 7 and the D-Hmp substituent of
 residue 1"

PN EP581429-A2.

XX 02-FEB-1994.

XX 10-JUN-1993; 93BP-0304515.

XX 19-JUN-1992; 92JP-0184561.

XX 16-OCT-1992; 92JP-0303177.

XX (TAKI) TAKARA SHUZO CO LTD.

XX Inami K, Kato I, Kurome T, Shiba T, Takesako K;

XX WPI; 1994-036663/05.

XX Synthesis of cyclic peptide(s) of aureobasidin type - and new
 PT cyclic peptide(s) with antifungal activity

XX PS Disclosure; Page 9; 74pp; English.

XX CC Cyclic aureobasidin type peptides (e.g. of generic formula given

CC in AAR45804) may be synthesised by cyclizing an O-protected or

CC unprotected linear peptide (e.g. of generic formula given in

CC AAR45803) or a reactive deriv. of it.

CC Representative cyclic peptides obtained by this method are given

CC in AAR45806-35. Peptides given AAR45820 and AAR45284-26 are new cpds.

CC and can be prep'd. by a fermentation method. Peptides given in

CC AAR45828-35 are new cpds. which are prep'd. by the new method.

CC The cpd. given AAR45834 showed higher activity against Candida

CC albicans TIMM 0171 than the cpd. given in AAR45805.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX CC

XX SQ Sequence 8 AA;

XX Query Match 50.0%; Score 4; DB 15; Length 8;

XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;

XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7

DB |||||

DB 3 FPIL 6

RESULT 26

AAR89371

ID AAR89371 standard; peptide; 9 AA.

XX AC AAR89371;

XX DT 18-SEP-1996 (first entry)

XX DE Cw6 consensus peptide derived immunogenic peptide #3.

XX KW Immunogenic peptide; supermotif; HLA molecule; CTL response;

XX KW therapeutic; diagnostic; cancer; viral infection; hepatitis B;

XX KW hepatitis C.

XX OS Synthetic.

XX PN WO9603140-A1.

XX PD 08-FEB-1996.

XX PF 21-JUL-1995; 95WO-US09234.

XX PR 30-MAY-1995; 95US-0452843.

XX PR 21-JUL-1994; 94US-0278634.

XX PR 23-NOV-1994; 94US-0344824.

XX PA (CYTE-) CYTEL CORP.

XX PI Sette A, Sidney J;

XX DR WPI; 1996-116784/12.

XX PT Compsn. comprising immunogenic peptide with supermotif allowing more

PT than one HLA mol. to bind - used to induce CTL response in patient

PT and for in vivo and ex vivo therapeutic and diagnostic applications

XX PS Claim 2; Page 26; 32pp; English.

XX CC The sequences given in AAR9362-82 are immunogenic peptides which were

CC use in the composition of the invention. The composition comprises

CC an immunogenic peptide of 9-10 residues with a supermotif which

CC allows binding of more than one HLA molecule. It pref. comprises

CC two conserved residues, a first at the 2nd position from the N-

CC terminal is Pro, and a 2nd at the C-terminal is Met. These peptides

CC are used to induce a CTL response in a patient. They are also

CC useful in compositions for in vivo and ex vivo therapeutic and

CC diagnostic applications, e.g. the treatment of cancer and viral

CC infections, e.g. hepatitis B and C.

XX SQ Sequence 9 AA;

XX Query Match 50.0%; Score 4; DB 17; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;

XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPI 6

DB |||||

DB 2 PPPI 5

RESULT 27

AAW80249

ID AAW80249 standard; Peptide; 9 AA.

XX AC AAW80249;

XX DT 06-JAN-1999 (first entry)

XX DE Active site sequence of the beta-lactamase gene in mutant #7.

XX KW plasmid pBR322; tetracycline resistance gene; TetR; mutant;

XX KW Escherichia coli; active site; beta-lactamase gene.

XX OS Synthetic.

XX PN US5824469-A.

XX PD 20-OCT-1998.

XX PF 30-SEP-1994; 94US-0316415.

XX PR 19-JUN-1989; 89US-0368674.

PR 17-JUL-1986; 86US-0887070.

PR 12-MAY-1992; 92US-0881607.

PR 11-AUG-1993; 93US-0105108.

PR 30-SEP-1994; 94US-0316415.

XX PA (UNIW) UNIV WASHINGTON.

XX PI Horwitz MS, Loeb LA;

XX DR WPI; 1998-582545/49.

XX DR N-PSDB; AAV66448.

XX PT Identification of biologically active DNA sequences - by

PT transforming cells with random oligo-nucleotide(s)

XX PS Example 8; Fig 6; 24pp; English.

XX CC AAW80243-49 represent new carbenicillin resistant mutants identified

CC from a screening of tetracycline resistant mutants. The sequences

CC are mutant active site sequences of the beta-lactamase gene, derived

CC from plasmid pBR322. The carbenicillin resistant sequences were produced

CC to exemplify the invention. The specification describes a method for

CC obtaining an oligonucleotide that confers a predetermined biological

CC function, such as regulation of expression or a biological activity of

CC a polypeptide, on a cell. The method comprises cloning a heterogeneous

CC pool of oligonucleotides into an expression vector, where the clones

CC oligonucleotides are transcribed or act as regulatory sequences,

CC introducing a random sample of the cloned oligonucleotides into a

CC population of cells that do not exhibit the predetermined biological

CC function, selecting a subpopulation of cells exhibiting the

CC predetermined biological function, and isolating an oligonucleotide that

CC confers this function from the selected subpopulation of cells. The

CC process is used, for example, for identifying new forms of the

CC Escherichia coli tetracycline resistance gene promoter and the active

XX site of the beta-lactamase gene.

XX SQ Sequence 9 AA;

Query Match 50.0%; Score 4; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPIL 7
 |||||
 Db 2 FPIL 5

RESULT 28
 ABB14561
 ID ABB14561 standard; Peptide; 9 AA.

AC ABB14561;

DT 22-JAN-2002 (first entry)

DE Human C35 peptide epitope #2065.

KW Human; C35; cytostatic; gene therapy; vaccine; tumour antigen;
 KW breast cancer; bladder cancer; tumour immunotherapy; epitope;
 KW major histocompatibility complex binding peptide; MHC.

OS Homo sapiens.

PN WO200174859-A2.

XX 11-OCT-2001.

PF 04-APR-2001; 2001WO-US10855.

PR 04-APR-2000; 2000US-194463P.

PA (UYRP) UNIV ROCHESTER.

PI Zauderer M, Evans EE, Borrello MA;

XX WPI; 2001-626383/72.

XX Novel C35 polypeptides and C35 genes useful in immunogenic compositions
 PT and vaccines, for inducing antibody and cell-mediated immunity against
 PT target cells, such as tumor cells that express C35 gene -

PS Disclosure; Page 171; 331pp; English.

XX The present invention relates to human C35 (see AAG78997). C35 is a novel
 CC tumour antigen that is overexpressed in human breast and bladder
 CC carcinoma. C35 is thought to be a promising candidate for tumour
 CC immunotherapy, in immunogenic compositions and vaccines, to induce
 CC antibody and cell-mediated immunity against target cells such as tumour
 CC cells that express C35 genes. The present sequence is a C35 peptide
 CC epitope. This peptide is predicted to be a major histocompatibility
 CC complex (MHC) binding peptide.

XX Sequence 9 AA;

Query Match 50.0%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPPF 5
 |||||

Db 1 GPPF 4

RESULT 29
 AAU28830

ID AAU28830 standard; Peptide; 9 AA.

XX AAU28830;

XX 03-JAN-2002 (first entry)

XX

DPI tryptic digest peptide #427.

XX Human; depression associated protein isoform; tryptic digest peptide;
 KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
 KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
 KW maniac-depressive illness; schizoaffective disorder.

XX Homo sapiens.

PN WO200162787-A1.

PD 30-AUG-2001.

XX 23-FEB-2001; 2001WO-GS00786.

PF 24-FEB-2000; 2000GB-0004412.

PR 08-DEC-2000; 2000GB-0030050.

PR 12-DEC-2000; 2000US-0254830.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMAc, Parekh RB, Rohlf C, Terratt JA, Tyson KL;

XX WPI; 2001-570626/64.

XX Novel nucleic acid encoding a protein associated with bipolar affective
 PT disorder, which is used for diagnosis, prophylaxis and therapy of
 PT neuropsychiatric disorders, such as bipolar affective disorder -

PS Disclosure; Page 39; 153pp; English.

XX The present invention relates to the identification of depression
 CC associated protein isoforms (DPis), particularly the tryptic digest
 CC peptides of these proteins. Some of the DPis (AAU28404-AAU28625)
 CC described are decreased in the cerebrospinal fluid (CSF) of BAD
 CC (bipolar affective disorder) subjects, whilst other DPis
 CC (AAU28626-AAU28887) are increased in BAD subjects. Also described
 CC are peptide sequences identified from DPI-45 and DPI-213 and the
 CC nucleic acid sequences they are encoded by. The sequences of the
 CC invention are useful for clinical screening, diagnosis, prognosis,
 CC therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also
 CC known as bipolar mood disorder, BP), maniac-depressive illnesses,
 CC attention deficit disorders, schizoaffective disorders, and unipolar
 CC affective disorders. The present sequence represents one of the DPI
 CC tryptic digest peptides of the present invention.

XX Sequence 9 AA;

Query Match 50.0%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPI 6
 |||||

Db 2 PPPI 5

RESULT 30
 AAU26478

ID AAU26478 standard; Peptide; 9 AA.

XX AAU26478;

XX 18-DEC-2001 (first entry)

XX Depression-Associated Protein isoform DPI-255 #2.

XX Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;
 KW DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;
 KW CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;
 KW attention deficient disorder; schizoaffective disorder;
 KW unipolar affective disorder.

XX

OS Homo sapiens.
 XX WO200163294-A2.
 XX
 XX 30-AUG-2001.
 XX
 XX 23-FEB-2001; 2001WO-GB00791.
 XX
 XX 24-FEB-2000; 2000GB-0004412.
 PR 08-DEC-2000; 2000GB-0030050.
 PR 12-DEC-2000; 2000US-0254830.
 XX
 PA (OXFO-) OXFORD GLYSCSCIENCES UK LTD.
 XX
 XX Herath HMAC, Parekh RB, Rohlf C;
 XX WPI; 2001-582081/65.
 XX
 XX Preparation for diagnosing or treating bipolar affected disorder (BAD)
 PT or unipolar depression, or for screening for modulators, comprises a
 PT BAD-associated protein isoform -
 PT
 XX Claim 8; Page 39; 163pp; English.
 XX
 CC The invention relates to a preparation comprising an isolated Bipolar
 CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are
 CC used to screen, diagnose or prognosis of BAD or unipolar depression.
 CC determine the stage or severity of BAD or unipolar depression, identify a
 CC subject at risk of developing BAD or unipolar depression, or monitor the
 CC effect of therapy in a subject. They are also used to screen for or
 CC identify agents that interact with a DPI. These agents, antibodies
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat
 CC or prevent BAD or unipolar depression. Diseases that can be treated are
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a
 CC unipolar affective disorder. The DPIs are used in proteomics. The
 CC proteomic approach of using DPIs for screening, diagnosis or prognosis of
 CC BAD or unipolar depression overcomes the problems of using gene
 CC expression analysis, such as not being able to obtain central nervous
 CC system (CNS) tissue from a living patient under normal circumstances.
 CC The present sequence is a DIP increased in the CSF (cerebro-spinal
 CC fluid) of subjects having BAD.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 50.0%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PFPI 6
 ||||
 Db 2 PFPI 5
 ||||
 RESULT 31
 AAG89664
 ID AAG89664 standard; Peptide; 9 AA.
 XX
 AC AAG89664;
 XX
 DT 11-SEP-2001 (first entry)
 XX
 DE p53 epitope B7 supermotif peptide #29.
 XX
 KW Human; p53; tumour suppressor; human leukocyte antigen; HLA; CTL;
 KW cytotoxic T lymphocyte; T cell; immune response; tumour; cancer;
 KW vaccine; epitope; cytostatic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200141788-A1.
 PN 14-JUN-2001.
 XX
 PD

XX 11-DEC-2000; 2000WO-US33629.
 XX
 PR 10-DEC-1999; 99US-0458297.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis B;
 PI Keogh E;
 XX
 DR WPI; 2001-381493/40.
 XX
 XX Epitope-based vaccines comprising P53 epitope having a specified
 PT sequences, useful for treating and preventing cancer, the epitopic
 PT peptides is useful as diagnostic agents and for evaluating immune
 PT response -
 XX
 XX Claim 1; Page 123; 138pp; English.
 PS
 XX The present invention describes isolated prepared P53 epitopes (I). Also
 CC described are: (1) a cytotoxic T lymphocyte (CTL) that is cultured
 CC in vivo and binds to a complex of (I); (2) a peptide (II) comprising (I)
 CC and a second epitope and has less than 50 contiguous amino acids; (3) a
 CC vaccine composition comprising (II), a unit dose of a peptide with less
 CC than 50 contiguous amino acids with 100% identity to the native peptide
 CC sequence of p53, and a pharmaceutical excipient; (4) an isolated nucleic
 CC acid encoding (I); and (5) an isolated nucleic acid encoding (II). (I)
 CC has cytostatic activity and can be used in vaccines. The vaccine
 CC composition is useful for treating or preventing cancer. (I) and (II)
 CC are useful as diagnostic agents and for evaluating immune responses.
 CC Unlike conventional epitopes, immunosuppressive epitopes that may be
 CC present in whole antigens can be avoided with the use of the vaccine
 CC composition of (I). The ability to combine selected epitopes and
 CC further, to modify the composition of the epitopes enhances the
 CC immunogenicity. The possible pathological side effects caused by
 CC infectious agents or whole protein antigens, which might have their own
 CC intrinsic biological activity, are eliminated. AAG89363 to AAG89747
 CC represent amino acid sequences used in the exemplification of the
 CC present invention.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 50.0%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 FPIL 7
 ||||
 Db 1 FPIL 4
 ||||
 RESULT 32
 AAG89665
 ID AAG89665 standard; Peptide; 9 AA.
 XX
 AC AAG89665;
 XX
 DT 11-SEP-2001 (first entry)
 XX
 DE p53 epitope B7 supermotif peptide #30.
 XX
 KW Human; p53; tumour suppressor; human leukocyte antigen; HLA; CTL;
 KW cytotoxic T lymphocyte; T cell; immune response; tumour; cancer;
 KW vaccine; epitope; cytostatic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200141788-A1.
 PN 14-JUN-2001.
 XX
 PD 11-DEC-2000; 2000WO-US33629.
 PF

```

XX PR 10-DEC-1999; 99US-0458237.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
XX PI Keogh E;
XX WPI: 2001-381493/40.
XX
XX PT Epitope-based vaccines comprising P53 epitope having a specified
XX PT sequences, useful for treating and preventing cancer, the epitopic
XX PT peptides is useful as diagnostic agents and for evaluating immune
XX PT response -
XX PS Claim 1; Page 123; 138pp; English.
XX
XX CC The present invention describes isolated prepared P53 epitopes (I). Also
XX CC described are: (1) a cytotoxic T lymphocyte (CTL) that is cultured
XX CC in vivo and binds to a complex of (I); (2) a peptide (II) comprising (I)
XX CC and a second epitope and has less than 50 contiguous amino acids; (3) a
XX CC vaccine composition comprising (II), a unit dose of a peptide with less
XX CC than 50 contiguous amino acids with 100% identity to the native peptide
XX CC sequence of p53, and a pharmaceutical excipient; (4) an isolated nucleic
XX CC acid encoding (I); and (5) an isolated nucleic acid encoding (II). (I)
XX CC has cytostatic activity and can be used in vaccines. The vaccine
XX CC composition is useful for treating or preventing cancer. (I) and (II)
XX CC are useful as diagnostic agents and for evaluating immune responses.
XX CC Unlike conventional epitopes, immunosuppressive epitopes that may be
XX CC present in whole antigens can be avoided with the use of the vaccine
XX CC composition of (I). The ability to combine selected epitopes and
XX CC further, to modify the composition of the epitopes enhances the
XX CC immunogenicity. The possible pathological side effects caused by
XX CC infectious agents or whole protein antigens, which might have their own
XX CC intrinsic biological activity, are eliminated. AAG89363 to AAG89747
XX CC represent amino acid sequences used in the exemplification of the
XX CC present invention.
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 50.0%; Score 4; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 FPIL 7
XX ||||
XX 1 FPIL 4
XX
XX Db
XX
XX RESULT 33
XX AAB76157
XX ID AAB76157 standard; Peptide; 9 AA.
XX
XX AC AAB76157;
XX
XX DT 10-APR-2001 (first entry)
XX
XX DE Tumour associated antigen p53 immunogenic peptide.
XX
XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
XX KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;
XX KW HLA binding peptide; immune response; glycoprotein; cytostatic;
XX KW virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;
XX KW human immunodeficiency virus; protozoacide; viral infection; cancer;
XX KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;
XX KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;
XX KW renal carcinoma; cervical carcinoma; lymphoma; malaria;
XX KW condyloma acuminatum.
XX
XX OS Homo sapiens.
XX
XX PN WO200100225-A1.
XX
XX PD 04-JAN-2001.
XX
XX PF 28-JUN-2000; 2000WO-US17842.

```

```

PD 04-JAN-2001.
XX
XX PF 28-JUN-2000; 2000WO-US17842.
XX
XX PR 29-JUN-1999; 99US-0141422.
XX
XX PA (EPIM-) EPIMMUNE INC.
XX
XX PI Sette A, Sidney J, Southwood S;
XX PI WPI: 2001-112389/12.
XX
XX PT Composition comprising human leukocyte antigen binding peptide which
XX PT comprises isolated, prepared epitope useful for treating viral
XX PT infections such as acquired immunodeficiency syndrome, and cancer -
XX
XX PS Claim 1; Page 48; 58pp; English.
XX
XX CC The present invention describes a composition (I) which comprises at
XX CC least one human leukocyte antigen (HLA) binding peptide comprising an
XX CC isolated, prepared epitope comprising one of 547 8-11 residue amino acid
XX CC sequences (S1), given in AAB75803 to AAB76349. (I) has cytostatic,
XX CC virucide, hepatotropic, antiinflammatory, anti-HIV (human
XX CC immunodeficiency virus) and protozoacide activities, which can be used
XX CC in vaccine production and is an inducer of cytotoxic T-cell response.
XX CC (I) is useful for inducing a cytotoxic T cell response against a
XX CC histocompatibility complex (MHC) class I allele, by contacting cytotoxic
XX CC T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to
XX CC treat and/or prevent viral infection and cancer such as prostate cancer,
XX CC hepatitis B, hepatitis C, human papilloma virus (HPV) infection,
XX CC cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal
XX CC carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma
XX CC acuminatum.
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 50.0%; Score 4; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 FPIL 7
XX ||||
XX 1 FPIL 4
XX
XX Db
XX
XX RESULT 34
XX AAB76158
XX ID AAB76158 standard; Peptide; 9 AA.
XX
XX AC AAB76158;
XX
XX DT 10-APR-2001 (first entry)
XX
XX DE Tumour associated antigen p53 immunogenic peptide.
XX
XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
XX KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;
XX KW HLA binding peptide; immune response; glycoprotein; cytostatic;
XX KW virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;
XX KW human immunodeficiency virus; protozoacide; viral infection; cancer;
XX KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;
XX KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;
XX KW renal carcinoma; cervical carcinoma; lymphoma; malaria;
XX KW condyloma acuminatum.
XX
XX OS Homo sapiens.
XX
XX PN WO200100225-A1.
XX
XX PD 04-JAN-2001.
XX
XX PF 28-JUN-2000; 2000WO-US17842.

```



```

XX PR 29-JUN-1999; 99US-0141422.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S;
XX XX WPI; 2001-112389/12.
XX PT Composition comprising human leukocyte antigen binding peptide which
XX PT comprises isolated, prepared epitope useful for treating viral
XX PT infections such as acquired immunodeficiency syndrome, and cancer -
XX PS Claim 1; Page 48; 58pp; English.
XX CC The present invention describes a composition (I) which comprises at
XX CC least one human leukocyte antigen (HLA) binding peptide comprising an
XX CC isolated, prepared epitope comprising one of 547 8-11 residue amino acid
XX CC sequences (S1), given in AAB75803 to AAB76349. (I) has cytostatic,
XX CC virucide, hepatotropic, antiinflammatory, anti-HIV (human
XX CC immunodeficiency virus) and protozoacide activities, which can be used
XX CC in vaccine production and is an inducer of cytotoxic T-cell response.
XX CC (I) is useful for inducing a cytotoxic T cell response against a
XX CC preselected antigen in a patient expressing a specific major
XX CC histocompatibility complex (MHC) class I allele, by contacting cytotoxic
XX CC T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to
XX CC treat and/or prevent viral infection and cancer such as prostate cancer,
XX CC hepatitis B, hepatitis C, human papilloma virus (HPV) infection,
XX CC cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal
XX CC carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma
XX CC acuminatum.
XX SQ Sequence 9 AA;
    Query Match 50.0%; Score 4; DB 22; Length 9;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 FPIL 7
Db 1 FPIL 4
    ||||
    ||||

RESULT 35
ABG96732
ID ABG96732 standard; Peptide; 9 AA.
XX AC ABG96732;
XX XX 16-DEC-2002 (first entry)
XX DE Human leukocyte antigen (HLA) B*1501 epitope #6.
XX KW Soluble human leukocyte antigen; HLA; sHLA; cell pharm;
XX KW multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
XX KW viral infection; cancer; autoimmune disease; vaccine development; MHC;
XX KW major histocompatibility complex; diagnostic development;
XX KW HLA class I polymorphism; HLA-B15 allotype.
XX OS Homo sapiens.
XX PN WO200262846-A2.
XX XX 15-AUG-2002.
XX PD 18-DEC-2001; 2001WO-US49744.
XX PF 18-DEC-2000; 2000US-256409P.
XX PR 18-DEC-2000; 2000US-256410P.
XX PR 10-OCT-2001; 2001US-0974366.
XX XX (HILD//) HILDBRAND W H.
XX PA (PRIL/) PRILLMAN K R.

```

```

XX PI Hildebrand WH, Prillman KR;
XX XX WPI; 2002-698563/75.
XX PT Producing soluble human leukocyte antigen (HLA) in cell pharm useful
XX PT for studies of peptide loading for characterizing human immune
XX PT responses involves using HLA allelic cDNA or genomic DNA as starting
XX PT material -
XX XX Disclosure; Page 172; 300pp; English.
XX CC The invention describes a method of producing soluble human leukocyte
XX CC antigen (HLA) molecules (sHLA) in cell pharm involving amplifying HLA
XX CC allelic DNA by PCR using a locus specific primer to produce truncated a
XX CC PCR product (PI), inserting PI into mammalian expression vector;
XX CC electroporating the plasmid into a host cell; inoculating the cell pharm
XX CC with the host cell such that cell pharm produces sHLA. A multimeric HLA
XX CC complex (I) is useful for testing functionality of peptide ligands bound
XX CC by at least two soluble HLA molecules. (I) can be tested for its ability
XX CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune
XX CC responses in humans. (I) is useful for studying T cell responses to
XX CC pathological conditions such as viral infections and cancer, and for
XX CC modulating the human immune system to induce tolerance in autoimmune
XX CC diseases. The individual secreted major histocompatibility complex (MHC)
XX CC molecules produced are useful for studies of peptide loading (i.e., in
XX CC vaccine development) and to the development of diagnostics. With the
XX CC secreted MHC molecules, naturally loaded peptides can be eluted from the
XX CC MHC molecule and characterised. The secreted MHC molecules allow the
XX CC assessment of structural and functional impact of HLA class I
XX CC polymorphism. The molecules are also useful to generate ligands and hence
XX CC ligand maps from the peptide pools extracted from series of distinct yet
XX CC related class I HLA-B15 allotypes; compare the different ligand maps to
XX CC identify potentially shared elements; and characterise the elements
XX CC identified to positively or negatively validate the occurrence of
XX CC overlapping ligands. The truncated version of (MHC) can be produced in
XX CC mammalian or insect/bacterial cells such that milligram or greater
XX CC quantities of an individual class I or class II molecule can be obtained.
XX CC This sequence represents a HLA (human leukocyte antigen) epitope.
XX SQ Sequence 9 AA;
    Query Match 50.0%; Score 4; DB 23; Length 9;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RGPF 4
Db 6 RGPF 9
    ||||
    ||||

RESULT 36
ABG67743
ID ABG67743 standard; Peptide; 9 AA.
XX AC ABG67743;
XX XX 07-OCT-2002 (first entry)
XX DE Human ADPI tryptic digest peptide #452.
XX KW Human; Alzheimer's disease; AD; brain tissue; ADP; ADPI;
XX KW Alzheimer's disease-associated feature; neuroprotective;
XX KW Alzheimer's disease-associated protein isoform; nootropic;
XX KW ADPI tryptic digest peptide.
XX OS Homo sapiens.
XX PN WO200246767-A2.
XX XX 13-JUN-2002.
XX PD 29-NOV-2001; 2001WO-GB05289.
XX PF

```

XX 08-DEC-2000; 2000US-254431P.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX Herath HMAC, Parekh RB, Rohlff C;
 XX WPI; 2002-508575/54.
 XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,
 PT comprises detecting Alzheimer's disease-associated features or
 PT Alzheimer's disease-associated protein isoforms in brain tissue
 PT from the subject -
 XX
 XX Claim 7; Page 63; 427pp; English.
 XX The present invention relates to methods and compositions for the
 CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in
 CC a subject. The method comprises analysing a sample of brain tissue
 CC from a subject by 2D electrophoresis to generate a 2D array of
 CC Alzheimer's disease-associated features (ADFs), whose relative
 CC abundance correlates with the presence, absence, stage or severity of
 CC AD and comparing the abundance of each feature with the abundance of
 CC that chosen feature in brain tissue from persons free from AD. The
 CC invention also describes Alzheimer's disease-associated protein
 CC isoforms (ADPIs) detectable in brain tissue. The methods and
 CC compositions of the invention are useful for the screening, diagnosis
 CC or prognosis of AD in a subject, for determining the stage or severity
 CC of AD in a subject, for identifying a subject at risk of developing AD,
 CC or for monitoring the effect of therapy administered to a subject
 CC having AD. Antibodies capable of binding to ADPIs are useful for
 CC treating or preventing AD, and for determining the efficacy of a given
 CC treatment regime. An agent that modulates the activity of ADPI is
 CC useful in the manufacture of a medicament for the treatment or
 CC prevention of AD in a subject. ABG67292-ABG68038 represent human ADPI
 CC tryptic digest peptides.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 50.0%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PFPI 6
 Db |||||
 2 PFPI 5
 RESULT 37
 ABR20445
 ID ABR20445 standard; Peptide; 9 AA.
 AC ABR20445;
 XX
 XX 19-MAY-2003 (first entry)
 DT
 DE Human cancer-related protein 185P2C9 HLA peptide #280.
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX Homo sapiens.
 OS
 XX WO200283921-A2.
 PN
 XX 24-OCT-2002.
 PD
 XX 10-APR-2002; 2002WO-US11654.
 PF
 XX 10-APR-2001; 2001US-282739P.
 PR
 XX 10-APR-2001; 2001US-283112P.
 PR
 XX 25-APR-2001; 2001US-286630P.
 PR
 XX (AGEN-) AGENSYS INC.
 PA
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX WPI; 2003-075555/07.
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX
 XX Claim 13; Page 323; 1021pp; English.
 PS
 XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 50.0%; Score 4; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GPPF 5
 Db |||||
 5 GPPF 8
 RESULT 38
 ABR20847
 ID ABR20847 standard; Peptide; 9 AA.
 AC ABR20847;
 XX
 XX 19-MAY-2003 (first entry)
 DT
 DE Human cancer-related protein 185P2C9 HLA peptide #682.
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX Homo sapiens.
 OS
 XX WO200283921-A2.
 PN
 XX 24-OCT-2002.
 PD
 XX 10-APR-2002; 2002WO-US11654.
 PF
 XX 10-APR-2001; 2001US-282739P.
 PR
 XX 10-APR-2001; 2001US-283112P.
 PR
 XX 25-APR-2001; 2001US-286630P.
 PR
 XX (AGEN-) AGENSYS INC.
 PA
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX WPI; 2003-075555/07.
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX

PA (AGEN-) AGENSYS INC.
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX WPI; 2003-075555/07.
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX
 XX Claim 13; Page 323; 1021pp; English.
 PS
 XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 50.0%; Score 4; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GPPF 5
 Db |||||
 5 GPPF 8
 RESULT 38
 ABR20847
 ID ABR20847 standard; Peptide; 9 AA.
 AC ABR20847;
 XX
 XX 19-MAY-2003 (first entry)
 DT
 DE Human cancer-related protein 185P2C9 HLA peptide #682.
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX Homo sapiens.
 OS
 XX WO200283921-A2.
 PN
 XX 24-OCT-2002.
 PD
 XX 10-APR-2002; 2002WO-US11654.
 PF
 XX 10-APR-2001; 2001US-282739P.
 PR
 XX 10-APR-2001; 2001US-283112P.
 PR
 XX 25-APR-2001; 2001US-286630P.
 PR
 XX (AGEN-) AGENSYS INC.
 PA
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX WPI; 2003-075555/07.
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX

PT in cancer patients -
 PS Claim 13; Page 327; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 50.0%; Score 4; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GPFP 5
 Db |||||
 3 GPFP 6
 RESULT 39
 ABR21656
 ID ABR21656 standard; Peptide; 9 AA.
 AC ABR21656;
 XX
 XX
 DT 19-MAY-2003 (first entry)
 DE Human cancer-related protein 185P2C9 HLA peptide #1491.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 OS
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US11654.
 XX
 PR 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX
 XX (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX
 XX Claim 13; Page 337; 1021pp; English.
 PS
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 50.0%; Score 4; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GPFP 5
 Db |||||
 3 GPFP 6
 RESULT 40
 ABR21837
 ID ABR21837 standard; Peptide; 9 AA.
 XX
 XX
 AC ABR21837;
 XX
 XX
 DT 19-MAY-2003 (first entry)
 DE Human cancer-related protein 185P2C9 HLA peptide #1672.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 OS
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US11654.
 XX
 PR 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX
 XX (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX
 XX Claim 13; Page 339; 1021pp; English.
 PS
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 50.0%; Score 4; DB 24; Length 9;

CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 50.0%; Score 4; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GPFP 5
 Db |||||
 4 GPFP 7

RESULT 40
 ABR21837
 ID ABR21837 standard; Peptide; 9 AA.
 XX
 XX
 AC ABR21837;
 XX
 XX
 DT 19-MAY-2003 (first entry)
 DE Human cancer-related protein 185P2C9 HLA peptide #1672.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 OS
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US11654.
 XX
 PR 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX
 XX (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX
 XX Claim 13; Page 339; 1021pp; English.
 PS
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 50.0%; Score 4; DB 24; Length 9;

Query Match 50.0%; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPPF 5
Db ||||
5 GPPF 8

RESULT 41

ABR22240
ID ABR22240 standard; Peptide; 9 AA.

XX AC ABR22240;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 185P2C9 HLA peptide #2075.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US11654.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 10-APR-2001; 2001US-283112P.

XX PR 25-APR-2001; 2001US-286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX DR WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients

XX PS Claim 13; Page 344; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.

XX SQ Sequence 9 AA;

Query Match 50.0%; Score 4; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPPF 5
Db ||||
3 GPPF 6

RESULT 42

ABR22262

ID ABR22262 standard; Peptide; 9 AA.

XX AC ABR22262;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 185P2C9 HLA peptide #2097.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US11654.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 10-APR-2001; 2001US-283112P.

XX PR 25-APR-2001; 2001US-286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX DR WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients

XX PS Claim 13; Page 344; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.

XX SQ Sequence 9 AA;

Query Match 50.0%; Score 4; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPPF 5
Db ||||
1 GPPF 4

RESULT 43

ABR23247

ID ABR23247 standard; Peptide; 9 AA.

XX AC ABR23247;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 185P2C9 HLA peptide #3082.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.

XX	Homo sapiens.
OS	WO200283921-A2.
XX	
PN	24-OCT-2002.
XX	
PD	10-APR-2002; 2002WO-US11654.
XX	
FF	10-APR-2001; 2001US-282739P.
XX	
PR	10-APR-2001; 2001US-283112P.
PR	25-APR-2001; 2001US-286630P.
XX	
FA	(AGEN-) AGENSYS INC.
XX	
PI	Jakovovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI	Morrison K, Morrison RK, Raitano AB;
XX	
DR	WPI; 2003-075555/07.
XX	
PT	New composition comprising a substance that modulates the structure of
PT	proteins and polynucleotides, useful for therapeutic, prognostic and
PT	diagnostic reagents for eliciting cellular or humoral immune response
PT	in cancer patients -
XX	
PS	Claim 13; Page 355; 1021pp; English.
XX	
CC	The present invention relates to novel human cancer-related genes and
CC	proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC	proteins are useful for eliciting a humoral or cellular immune response.
CC	The genes are useful as probes and primers for the amplification and/or
CC	detection of genes, mRNAs or their fragments, as reagents for the
CC	diagnosis and/or prognosis of cancer, as coding sequences capable of
CC	directing the expression of the protein, as tools for modulating or
CC	inhibiting the expression of genes and/or translation of transcripts, and
CC	as therapeutic agents. The proteins and peptides are useful as
CC	therapeutic, prognostic and diagnostic reagents for cancer. The present
CC	sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC	from the invention.
XX	
SQ	Sequence 9 AA;
	Query Match 50.0%; Score 4; DB 24; Length 9;
	Best Local Similarity 100.0%; Pred.No. 9.3e+05;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Oy	2 GPPF 5
Dd	5 GPFP 8
	AC AC
	ABR23645;
	RESULT 44
	ABR23645
ID	ABR23645 standard; Peptide; 9 AA.
XX	
AC	ABR23645;
XX	
DT	19-MAY-2003 (first entry)
XX	
DE	Human cancer-related protein 185P2C9 HLA peptide #3480.
XX	
KW	Human; cytostatic; vaccine; cancer; immune response; HLA;
KW	human leukocyte antigen.
XX	
OS	Homo sapiens.
XX	
FN	WO200283921-A2.
XX	
PD	24-OCT-2002.
XX	
PF	10-APR-2002; 2002WO-US11654.
XX	
PR	10-APR-2001; 2001US-282739P.
XX	
PR	10-APR-2001; 2001US-282739P.
XX	

```

FT XX /note= "D-form residue"
XX PN WO9533765-A1.
XX PD 14-DEC-1995.
XX PF 08-JUN-1995; 95WO-IB00455.
XX PR 08-JUN-1994; 94IL-0109943.
XX PA (PEPT-) PEPTOR LTD.
XX PA (YISS ) YISSUM RES & DEV CO.
XX PI Bitan G, Eren D, Gilon C, Muller D, Seri-Levy A;
XX PI Zeltser I;
XX DR WPI; 1996-040184/04.
XX XX
XX XX New backbone-cyclised bradykinin and somatostatin analogues - used
XX PT to treat acute asthma, septic shock, trauma, post-operative pain,
XX PT inflammation, cancer and endocrine and GI disorders.
XX PS Claim 19; Page 123; 143pp; English.
XX CC The present invention describes new backbone-cyclised peptide analogues
XX CC comprising a peptide sequence that incorporates at least two building
XX CC units, each of which contains one N atom of the peptide group connected
XX CC to a bridging group comprising a disulphide, amide, thioether, thioester,
XX CC imine, ether or alkene bridge, where at least two building units are
XX CC joined together to form a cyclic structure. The analogues are used to
XX CC treat acute asthma, septic shock, brain trauma and other traumatic
XX CC injury, post-surgical pain, inflammation, cancers, and endocrine and
XX CC gastrointestinal disorders. The peptides are conformationally stabilised
XX CC without affecting pharmacologically active amino acids.
XX SQ Sequence 10 AA;

Query Match 50.0%; Score 4; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
Db 3 RGPF 6

RESULT 46
AAI17846
ID .AAI17846 standard; peptide; 10 AA.
XX AC
XX AC AAI17846;
XX DT 13-AUG-1999 (first entry)
XX DE
XX DE Backbone cyclised peptide analogue #5.
XX KW Backbone cyclised peptide; bridging group; bradykinin; somatostatin;
XX KW acute asthma; septic shock; brain trauma; traumatic injury;
XX KW post-surgical pain; inflammation; cancer; endocrine disorder;
XX KW gastrointestinal disorder.
XX OS Synthetic.
XX PH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Modified-site 3 /note= "Gly is bonded to Gly at position 6 to form a
FT Modified-site 4 cyclic region"
FT Modified-site 6 /label= 4HYP
FT Modified-site 6 /note= "4-hydroxyproline"

```

```

FT FT /note= "Gly is bonded to Gly at position 3 to form a
FT FT cyclic region"
FT FT Misc-difference 8 /note= "D-form residue"
XX PN WO9533765-A1.
XX PD 14-DEC-1995.
XX PF 08-JUN-1995; 95WO-IB00455.
XX PR 08-JUN-1994; 94IL-0109943.
XX PA (PEPT-) PEPTOR LTD.
XX PA (YISS ) YISSUM RES & DEV CO.
XX PI Bitan G, Eren D, Gilon C, Muller D, Seri-Levy A;
XX PI Zeltser I;
XX DR WPI; 1996-040184/04.
XX XX
XX XX New backbone-cyclised bradykinin and somatostatin analogues - used
XX PT to treat acute asthma, septic shock, trauma, post-operative pain,
XX PT inflammation, cancer and endocrine and GI disorders.
XX PS Claim 19; Page 123; 143pp; English.
XX CC The present invention describes new backbone-cyclised peptide analogues
XX CC comprising a peptide sequence that incorporates at least two building
XX CC units, each of which contains one N atom of the peptide group connected
XX CC to a bridging group comprising a disulphide, amide, thioether, thioester,
XX CC imine, ether or alkene bridge, where at least two building units are
XX CC joined together to form a cyclic structure. The analogues are used to
XX CC treat acute asthma, septic shock, brain trauma and other traumatic
XX CC injury, post-surgical pain, inflammation, cancers, and other traumatic
XX CC gastrointestinal disorders. The peptides are conformationally stabilised
XX CC without affecting pharmacologically active amino acids.
XX SQ Sequence 10 AA;

Query Match 50.0%; Score 4; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
Db 2 RGPF 5

RESULT 47
AAI17847
ID .AAI17847 standard; peptide; 10 AA.
XX AC
XX AC AAI17847;
XX DT 13-AUG-1999 (first entry)
XX DE
XX DE Backbone cyclised peptide analogue #6.
XX KW Backbone cyclised peptide; bridging group; bradykinin; somatostatin;
XX KW acute asthma; septic shock; brain trauma; traumatic injury;
XX KW post-surgical pain; inflammation; cancer; endocrine disorder;
XX KW gastrointestinal disorder.
XX OS Synthetic.
XX PH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Modified-site 3 /note= "Gly is bonded to Phe at position 6 to form a
FT Modified-site 4 cyclic region"

```

```

FT FT /label= 4HP
FT FT /note= "4-hydroxyproline"
FT Modified-site 6
FT FT
FT FT /note= "Phe is bonded to Gly at position 3 to form a
FT FT cyclic region"
FT Misc-difference 8
FT FT /note= "D-form residue"
FT FT
XX XX
PN PN WO9533765-A1.
XX XX
PD PD 14-DEC-1995.
XX XX
PF PF 08-JUN-1995; 95WO-IB00455.
XX XX
PR PR 08-JUN-1994; 94IL-0109943.
XX XX
PA (PEPT-) PEPTOR LTD.
PA (YISS) YISSUM RES & DEV CO.
XX XX
PI Bitan G, Eren D, Gilon C, Muller D, Seri-Levy A;
PI Zeltser I;
XX XX
DR WPI; 1996-040184/04.
XX XX
PT New backbone-cyclised bradykinin and somatostatin analogues - used
PT to treat acute asthma, septic shock, trauma, post-operative pain,
PT inflammation, cancer and endocrine and GI disorders.
XX XX
PS Claim 19; Page 123; 143pp; English.
XX XX
CC The present invention describes new backbone-cyclised peptide analogues
CC comprising a peptide sequence that incorporates at least two building
CC units, each of which contains one N atom of the peptide group connected
CC to a bridging group comprising a disulphide, amide, thioether, thioester,
CC imine, ether or alkene bridge, where at least two building units are
CC joined together to form a cyclic structure. The analogues are used to
CC treat acute asthma, septic shock, brain trauma and other traumatic
CC injury, post-surgical pain, inflammation, cancers, and endocrine and
CC gastrointestinal disorders. The peptides are conformationally stabilised
CC without affecting pharmacologically active amino acids.
XX XX
SQ Sequence 10 AA;

Query Match 50.0%; Score 4; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPF 4
Db ||||
2 RGPF 5

RESULT 48
AAW36625
ID AAW36625 standard; peptide; 10 AA.
XX AC
XX AC AAW36625;
XX DT
XX DT 11-MAR-1998 (first entry)
XX DE
XX DE Thrombopoietin receptor binding peptide.
XX KW
XX KW Thrombopoietin receptor; binding peptide; treatment; agonist;
XX KW haematological disorder; thrombocytopaenia; chemotherapy;
XX KW radiation therapy; bone marrow transfusion; diagnosis;
XX KW signal transduction; receptor activation; cell culture.
XX OS
XX OS Synthetic.
XX PN
XX PN WO9640750-A1.
XX PD
XX PD 19-DEC-1996.

Query Match 50.0%; Score 4; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPF 4
Db ||||
2 RGPF 5

RESULT 49
AAW09474
ID AAW09474 standard; protein; 10 AA.
XX AC
XX AC AAW09474;
XX DT
XX DT 10-SEP-1997 (first entry)
XX DE
XX DE Thrombopoietin receptor binding peptide.
XX KW
XX KW Haematology; thrombocytopaenia; TPO; TR; proliferation;
XX KW bone marrow transfusion; chemotherapy; radiation therapy.
XX OS
XX OS Synthetic.
XX PN
XX PN WO9640189-A1.
XX PD
XX PD 19-DEC-1996.
XX PF
XX PF 05-JUN-1996; 96WO-US08998.
XX XX
XX XX 07-JUN-1995; 95US-0485301.
XX XX 07-JUN-1995; 95US-0472371.
XX XX 07-JUN-1995; 95US-0473604.
XX XX 07-JUN-1995; 95US-0476168.
XX XX 07-JUN-1995; 95US-0478128.
XX XX 07-JUN-1995; 95US-0484090.
XX XX
XX XX (GLAX ) GLAXO GROUP LTD.
XX XX
XX XX Barrett RW, Cwirla SE, Dower WJ, Duffin DJ, Gates CM;
XX XX Johnson SS, Mattheakis LC, Schatz PJ, Wagstrom CR;
XX XX Wrighton NC;

```

```

PF 07-JUN-1996; 96WO-US09623.
XX XX
PR 07-JUN-1995; 95US-0485301.
PR 07-JUN-1995; 95US-0478128.
XX XX
XX (GLAX ) GLAXO GROUP LTD.
XX XX
XX Barrett RW, Cwirla SE, Dower WJ, Duffin DJ, Gates CM;
XX Johnson SS, Mattheakis LC, Schatz PJ, Wagstrom CR;
XX Wrighton NC;
XX XX
XX WPI; 1997-052226/05.
XX XX
XX Peptides and peptide mimetics which bind to and activate the
XX thrombopoietin receptor - useful in treatment of haematological
XX disorders, esp. thrombocytopaenia resulting from chemotherapy, etc.
XX PS
XX Disclosure; Page 26; 106pp; English.
XX XX
XX The present peptide, which binds the thrombopoietin receptor (TR),
XX can be used to treat disorders which are susceptible to treatment
XX with a thrombopoietin agonist, preferably haematological disorders
XX and thrombocytopaenia resulting from chemotherapy, radiation
XX therapy or bone marrow transfusions. It can also be used
XX diagnostically, e.g. to investigate the mechanism of thrombopoietin
XX signal transduction and receptor activation, or to maintain the
XX proliferation and growth of thrombopoietin dependent cell lines.
XX SQ
XX Sequence 10 AA;

Query Match 50.0%; Score 4; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPF 4
Db ||||
2 RGPF 5

RESULT 49
AAW09474
ID AAW09474 standard; protein; 10 AA.
XX AC
XX AC AAW09474;
XX DT
XX DT 10-SEP-1997 (first entry)
XX DE
XX DE Thrombopoietin receptor binding peptide.
XX KW
XX KW Haematology; thrombocytopaenia; TPO; TR; proliferation;
XX KW bone marrow transfusion; chemotherapy; radiation therapy.
XX OS
XX OS Synthetic.
XX PN
XX PN WO9640189-A1.
XX PD
XX PD 19-DEC-1996.
XX PF
XX PF 05-JUN-1996; 96WO-US08998.
XX XX
XX XX 07-JUN-1995; 95US-0485301.
XX XX 07-JUN-1995; 95US-0472371.
XX XX 07-JUN-1995; 95US-0473604.
XX XX 07-JUN-1995; 95US-0476168.
XX XX 07-JUN-1995; 95US-0478128.
XX XX 07-JUN-1995; 95US-0484090.
XX XX
XX XX (GLAX ) GLAXO GROUP LTD.
XX XX
XX XX Barrett RW, Cwirla SE, Dower WJ, Duffin DJ, Gates CM;
XX XX Johnson SS, Mattheakis LC, Schatz PJ, Wagstrom CR;
XX XX Wrighton NC;

```


CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines.

XX SQ Sequence 10 AA;

Query Match 50.0%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
 DB 2 RGPF 5
 ||||
 ||||

RESULT 52

AAU06436
 ID AAU06436 standard; Peptide; 10 AA.

AC AAU06436;

DT 24-OCT-2001 (first entry)

DE Human Leukocyte Antigen-A2 (HLA-A2) supermotif binding peptide #28.

KW Prostate cancer-associated antigen; supermotif; human leukocyte antigen;
 KW HLA; cytotoxic T lymphocyte; helper T lymphocyte; HLA superfamily; CTL;
 KW immunogenicity; immunosuppression; HTL.

OS Homo sapiens.

PN WO200145728-A2.

XX 28-JUN-2001.

PF 20-DEC-2000; 2000WO-US35516.

PR 21-DEC-1999; 99US-0171312.

PR 07-AUG-2000; 2000US-0633364.

XX (EPIM-) EPIMMUNE INC.

PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
 PI Keogh E;

XX WPI; 2001-398311/42.

PT Tumour antigen-associated group-based vaccines useful for vaccinating
 PT against prostate cancer -

XX Example 2; Page 238; 252pp; English.

CC The sequences represent prostate cancer-associated antigens and derived
 CC motif or supermotif epitopes. The peptide epitopes are included in
 CC prostate cancer vaccine compositions. The peptide epitopes are included in
 CC human leukocyte antigen (HLA) molecules, which recognise the motifs.
 CC Peptides with a high binding affinity are further tested for their
 CC ability to induce a cytotoxic T lymphocyte (CTL) or a helper T lymphocyte
 CC (HTL) response. Supermotif-bearing peptides may also be tested for their
 CC binding affinity to multiple alleles within the HLA superfamily. The
 CC vaccine compositions can be modified, for example, to enhance

CC immunogenicity, to avoid the inclusion of immunosuppressive groups, or to
 CC alter the immune response to suit the target disease. These group-based
 CC vaccines allow the focus of an immune response to multiple selected
 CC antigens from the same pathogen. Variability among the immune responses
 CC of patients can therefore be alleviated by the inclusion of groups from
 CC multiple antigens in a vaccine.

XX SQ Sequence 10 AA;

Query Match 50.0%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PILV 8
 DB 7 PILV 10
 ||||
 ||||

RESULT 53

AAG87057
 ID AAG87057 standard; Peptide; 10 AA.

XX AC AAG87057;

DT 11-SEP-2001 (first entry)

DE Saccharomyces cerevisiae peptide, SEQ ID NO: 2006.

KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
 KW drug discovery; drug design.

XX OS Saccharomyces cerevisiae.

PN WO200142276-A1.

XX 14-JUN-2001.

XX PF 13-DEC-2000; 2000WO-GB04773.

PR 13-DEC-1999; 99GB-0029471.

XX (PROT-) PROTEOM LTD.

PI Roberts GW, Heal JR;

XX WPI; 2001-367863/38.

PT Identifying complementary peptides by analysis of protein and
 PT nucleotide sequence databases, useful in drug design -

XX Example 3; Page 306; 488pp; English.

CC The invention relates to the identification of complementary peptides
 CC by analysis of protein and nucleotide sequence databases from higher
 CC eukaryotic genomes, excluding human and plants. The specific
 CC complementary peptides interact with their relevant target proteins
 CC encoded in the eukaryote genome. The peptides may be used as reagents
 CC and drugs for drug discovery and as lead ligands for drug design and
 CC development. The present sequence is a complementary peptide from
 CC Saccharomyces cerevisiae.

XX SQ Sequence 10 AA;

Query Match 50.0%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PILV 8
 DB 2 PILV 5
 ||||
 ||||

RESULT 54

Query Match 50.0%; Score 4; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX
 XX Claim 13; Page 337; 1021pp; English.
 PS
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 50.0%; Score 4; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GPPF 5
 DB |||||
 4 GPPF 7
 RESULT 59
 ABR21964
 ID ABR21964 standard; Peptide; 10 AA.
 AC
 XX ABR21964;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 185P2C9 HLA peptide #1799.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US11654.
 XX
 PR 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX

DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX
 XX Claim 13; Page 340; 1021pp; English.
 PS
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 50.0%; Score 4; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GPPF 5
 DB |||||
 6 GPPF 9
 RESULT 60
 ABR23102
 ID ABR23102 standard; Peptide; 10 AA.
 XX
 AC ABR23102;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 185P2C9 HLA peptide #2937.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US11654.
 XX
 PR 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX
 XX Claim 13; Page 354; 1021pp; English.
 PS
 CC The present invention relates to novel human cancer-related genes and

CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC The genes are useful for eliciting a humoral or cellular immune response.
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 SQ Sequence 10 AA;

Query Match 50.0%; Score 4; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPPP 5
 Db 4 GPPP 7

RESULT 61
 AAW13931
 ID AAW13931 standard; Protein; 11 AA.
 AC AAW13931;
 XX

DT 15-MAY-1997 (first entry)

DE CDR-3 fragment of heavy chain of anti-HB virus antibody #1.

XX Antibody; heavy chain; light chain; variable region; human; monoclonal;
 KW complementarity determining region; human; adr type hepatitis B virus;
 KW HB virus; CDR; virus antigen; anti-HB antibody; vaccine.
 XX

OS Homo sapiens.

FN JP09020798-A.

PD 21-JAN-1997.

PF 11-JUL-1995; 95JP-0174752.

PR 11-JUL-1995; 95JP-0174752.

PA (ASAH) ASAH KASEI KOGYO KK.

DR WPI; 1997-140911/13.

XX N-PSDB; AAT60126.

XX Human anti-Hepatitis B antibody - used in a adr type HB virus
 PT vaccine

PS Example 1; Page 10; 20pp; Japanese.

XX AAW1329-W13943 represent fragments of the complementarity determining
 CC regions of the heavy and light chains of the human monoclonal antibodies
 CC of the invention. The antibody of the invention preferably contains the
 CC sequence represented by AAW13912 in the complementarity determining
 CC region-1 (CDR-1) of the heavy chain variable region. The antibody of
 CC the invention also contains the sequence represented by AAW13913 in the
 CC CDR-3 of the light chain variable region. The antibody is capable of
 CC binding to adr type hepatitis B (HB) virus antigen. A human anti-HB
 CC virus monoclonal antibody preparation which is highly safe and is
 CC effective to adr type HB virus can be provided, using the monoclonal
 CC antibody. It can also be used as a vaccine against HB infection.
 XX

SQ Sequence 11 AA;

Query Match 50.0%; Score 4; DB 18; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 FPIL 7
 Db 6 FPIL 9
 RESULT 62
 ABG68633
 ID ABG68633 standard; Peptide; 11 AA.
 XX
 AC ABG68633;
 XX
 DT 07-OCT-2002 (first entry)
 DE Desmocollin 1 peptide sequence #1.
 XX
 KW Human; secretory leukoprotease inhibitor; SLPI; corneodesmosin; mouse;
 KW stratum corneum chymotryptic enzyme; envoplaikin; desmoplakin; pig; SCCF;
 KW desmocollin 1; adhesion protein; protease; protease inhibitor; eczema;
 KW contact dermatitis; lung atopic asthma; post viral asthma; viral warts;
 KW bronchial hyper-reactivity; chronic obstructive pulmonary disease;
 KW Crohn's disease; ulcerative colitis; coeliac disease; peptic ulceration;
 KW impetigo; meningitis; skin melanoma; squamous cell carcinoma; psoriasis;
 KW basal cell carcinoma; cutaneous lymphoma; skin cancer; lung malignancy;
 KW gastrointestinal tract malignancy; acne vulgaris; psoriasis vulgaris;
 KW antipsoriatic; dermatological; antiinflammatory; antiallergic.
 XX
 OS Unidentified.

XX WO200244736-A2.

FN 06-JUN-2002.

PD 30-NOV-2001; 2001WO-GB05303.

PF 30-NOV-2000; 2000GB-0029225.

PR 07-DEC-2000; 2000GB-0029879.

XX (MOLE-) MOLECULAR SKINCARE LTD.

PA Tazi-Ahmini R, Bavik C, Ward S, Duff G, Cork M;

PI WPI; 2002-557554/59.

DR Diagnosing a disease or susceptibility to a disease associated with

XX abnormal cell-cell adhesion between epithelial cells, by detecting
 PT mutation in nucleic acid encoding adhesion protein, protease or
 PT protease inhibitor

XX Example C4; Page 145; 257pp; English.

PS The invention relates to a method for diagnosis of a disease or
 CC susceptibility to a disease associated with abnormal cell-cell adhesion
 CC between epithelial cells, comprising detecting a mutation in a nucleic
 CC acid encoding an adhesion protein, a protease or a protease inhibitor, or
 CC modulated level of adhesion protein, protease or protease inhibitor, or
 CC its fragment polypeptide. The method is useful for diagnosing a disease
 CC such as eczema, contact dermatitis, lung atopic asthma, post viral
 CC asthma, bronchial hyper-reactivity, chronic obstructive pulmonary
 CC disease, Crohn's disease, ulcerative colitis, coeliac disease, peptic
 CC ulceration, impetigo, viral warts, meningitis, skin melanoma, squamous
 CC cell carcinoma, basal cell carcinoma, cutaneous lymphoma, skin cancer,
 CC malignancy of the gastrointestinal tract, malignancy of the lung,
 CC psoriasis, acne vulgaris and psoriasis vulgaris. This sequence represents
 CC a peptide used in the scope of the invention.
 XX

SQ Sequence 11 AA;

Query Match 50.0%; Score 4; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPPF 5
 Db ||||
 6 GPPF 9

RESULT 63

ABG68635
 ID ABG68635 standard; Peptide; 11 AA.

XX AC AEG68635;
 XX DT 07-OCT-2002 (first entry)
 XX DE Desmocollin 1 peptide sequence #2.

XX KW Human; secretory leukoprotease inhibitor; SLPI; corneodesmosin; mouse;
 KW stratum corneum chymotryptic enzyme; envoplaikin; pig; SCCE;
 KW desmocollin 1; adhesion protein; protease; protease inhibitor; eczema;
 KW contact dermatitis; lung atopic asthma; post viral asthma; viral warts;
 KW bronchial hyper-reactivity; chronic obstructive pulmonary disease;
 KW Crohn's disease; ulcerative colitis; coeliac disease; peptic ulceration;
 KW impetigo; meningitis; skin melanoma; squamous cell carcinoma; psoriasis;
 KW basal cell carcinoma; cutaneous lymphoma; skin cancer; lung malignancy;
 KW gastrointestinal tract malignancy; acne vulgaris; psoriasis vulgaris;
 KW antipsoriatic; dermatological; antiinflammatory; antiallergic.

XX OS Unidentified.

XX PN WO200244736-A2.

XX PD 06-JUN-2002.

XX PF 30-NOV-2001; 2001WO-GB05303.

XX PR 30-NOV-2000; 2000GB-0029225.

XX PR 07-DEC-2000; 2000GB-0029879.

XX PA (MOLE-) MOLECULAR SKINCARE LTD.

XX PI Tazi-Ahmini R, Bavik C, Ward S, Duff G, Cork M;

XX WPI; 2002-557554/59.

XX PT Diagnosing a disease or susceptibility to a disease associated with
 PT abnormal cell-cell adhesion between epithelial cells, by detecting
 PT mutation in nucleic acid encoding adhesion protein, protease or
 PT protease inhibitor

XX PS Example E5; Page 193; 257pp; English.

XX CC The invention relates to a method for diagnosis of a disease or
 CC susceptibility to a disease associated with abnormal cell-cell adhesion
 CC between epithelial cells, comprising detecting a mutation in a nucleic
 CC acid encoding an adhesion protein, a protease or a protease inhibitor, or
 CC modulated level of adhesion protein, protease or protease inhibitor, or
 CC its fragment polypeptide. The method is useful for diagnosing a disease
 CC such as eczema, contact dermatitis, lung atopic asthma, post viral
 CC asthma, bronchial hyper-reactivity, chronic obstructive pulmonary
 CC disease, Crohn's disease, ulcerative colitis, coeliac disease, peptic
 CC ulceration, impetigo, viral warts, meningitis, skin melanoma, squamous
 CC cell carcinoma, basal cell carcinoma, cutaneous lymphoma, skin cancer,
 CC malignancy of the gastrointestinal tract, malignancy of the lung,
 CC psoriasis, acne vulgaris and psoriasis vulgaris. This sequence represents
 CC a peptide used in the scope of the invention.

XX SQ Sequence 11 AA;

Query Match

Best Local Similarity 50.0%; Score 4; DB 23; Length 11;
 ID AAB12848
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPPF 5
 Db ||||

Db

RESULT 64

AAW36886

ID AAW36886 standard; Peptide; 12 AA.

XX AC AAW36886;
 XX DT 11-MAY-1998 (first entry)

XX DE HTLV-II protease cleavage recognition site.
 XX KW Ricin; toxin; antiviral; virucide; retrovirus; protease; HTLV-I;
 KW cancer; infection; therapy; linker.

XX OS Synthetic.

XX PN WO9741233-A1.

XX PD 06-NOV-1997.

XX PF 29-APR-1997; 97WO-CA00288.

XX PR 30-APR-1996; 96US-0016509.

XX PA (CANG-) CANGENE CORP.

XX PI Borgford T;

XX WPI; 1997-549735/50.

XX PT DNAs encoding ricin like toxins A and B - are linked via linker
 PT containing cleavage site for retroviral protease, used to inhibit or
 PT destroy mammalian cells infected with retrovirus

XX PS Claim 5; Page 41; 105pp; English.

XX CC This claimed peptide is a cleavage recognition site for a HTLV-I
 CC protease. It is utilised as a linker between the A and B chains
 CC of a ricin-like protein in a novel recombinant protein. A nucleic
 CC acid (see AAT97919) encoding such a construct is obtained by PCR
 CC mutagenesis of the wild-type ricin linker sequence. The invention
 CC provides novel recombinant proteins which incorporate the A and B
 CC chains of a ricin-like toxin (preferably the A and B chains of
 CC ricin) linked by a heterologous linker sequence containing a
 CC cleavage recognition site for a retroviral protease such as HIV
 CC protease (see AAW36880-82), HTLV-I (see AAW36883-43) or HTLV-II (see
 CC AAW36885-65). The recombinant proteins selectively inhibit or
 CC destroy mammalian cells infected with a retrovirus such as cancer
 CC cells associated with HIV or cells associated with HIV. The
 CC recombinant proteins are non-toxic until the ricin A chain is
 CC liberated from the B chain by a retroviral protease, and thus can
 CC be used to specifically target infected cells without the need
 CC for a cell binding component.

XX SQ Sequence 12 AA;

Query Match

Best Local Similarity 50.0%; Score 4; DB 18; Length 12;
 ID AAB12848
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7
 Db ||||

6 FPIL 9

RESULT 65

AAB12848

ID AAB12848 standard; peptide; 12 AA.

XX AC AAB12848;

XX

DT 06-DEC-2000 (first entry)
 XX STA3 binding peptide #1.
 DE
 XX
 KW STA3; signal transducer and activator of transcription; human; cancer;
 KW cell signalling; cytokine; growth factor; oncogenesis; tumour;
 KW apoptosis; cytostatic; tumourigenesis.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 3
 FT /label= Ser, Pro
 XX
 PN WO200044774-A2.
 XX
 PD 03-AUG-2000.
 XX
 PF 27-JAN-2000; 2000WO-US01845.
 XX
 PR 27-JAN-1999; 99US-0117600.
 XX
 PA (UYSF-) UNIV SOUTH FLORIDA.
 XX
 PI Jove R, Dalton W, Sebt S, Yu H, Heller R, Jaroszeski M;
 PI WPI; 2000-505964/45.
 DR
 XX Administering antagonists of STAT (signal transducer and activator of
 PT transcription) signalling in cells for the treatment of cancers -
 PT
 XX Example 13; Page 54; 92pp; English.
 PS
 XX The present invention describes methods for inhibiting the growth of
 CC (I), inducing apoptosis in (II), inhibiting tumourigenesis in (III),
 CC inhibiting neoplastic transformation in (IV) cancer cells and for
 CC enhancing the effectiveness of chemo-(IV) and radiotherapies (VI) for
 CC the treatment of cancer. The methods comprise administering an antagonist
 CC of STAT (signal transducer and activator of transcription) signalling.
 CC The methods may be used for inhibiting the growth of cancer cells (I),
 CC inducing apoptosis in cancer cells (II), inhibiting tumourigenesis
 CC in cancer cells (III), inhibiting neoplastic transformation in cancer
 CC cells (IV) and for enhancing the effectiveness of chemo-(IV) and
 CC radiotherapies (VI) for the treatment of cancer. The present sequence
 CC represents a STAT3 binding peptide, which is used in an example from the
 CC present invention.
 XX
 SQ Sequence 12 AA;
 Query Match 50.0%; Score 4; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 PILV 8
 Db |||||
 4 PILV 7
 RESULT 66
 AAW36390
 ID AAW36390 standard; peptide; 13 AA.
 XX
 AC AAW36390;
 XX
 DT 13-FEB-1998 (first entry)
 XX
 DE Antimicrobial protegrin peptide (190).
 XX
 KW Antimicrobial protegrin; broad spectrum; gram-positive; bacterium;
 KW gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus;
 KW retrovirus; HIV; human immunodeficiency virus; preservation;
 KW disinfection; prophylaxis; treatment; infection; disease;
 KW conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD;

KW Helicobacter pylori; sexually transmitted disease; oral mucositis;
 KW gram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic;
 KW respiratory infection; urinary tract infection; MRSA; protozoan;
 KW vancomycin resistant Enterococcus; pathogen; multi-drug resistance;
 KW penicillin resistant Streptococcus pneumoniae; pig; porcine;
 KW methicillin resistant Staphylococcus aureus; systemic candidiasis.
 XX
 OS Synthetic.
 OS Sus scrofa.
 XX
 PN WO9718826-A1.
 XX
 PD 29-MAY-1997.
 XX
 PF 22-NOV-1996; 96WO-US18544.
 XX
 PR 21-NOV-1996; 96US-0752852.
 PR 22-NOV-1995; 95US-0562346.
 PR 17-MAY-1996; 96US-0649811.
 PR 01-AUG-1996; 96US-0690921.
 XX
 PA (INTR-) INTRABIOTICS PHARM INC.
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Chang CC, Chen J, Gu CL, Lehrer RI, Steinberg DA;
 PI WPI; 1997-297871/27.
 DR
 XX New antimicrobial protegrin peptide(s) - having activity against
 PT bacteria, yeast, fungi, protozoa and certain strains of viruses
 PT (e.g. HIV)
 XX
 XX Claim 23; Page 109; 130pp; English.
 XX The present sequence is an antimicrobial protegrin peptide, which
 CC has a broad spectrum of activity against microbial targets, which
 CC including gram-positive and gram-negative bacteria, yeast, fungi,
 CC protozoa and certain strains of viruses and retroviruses, e.g. HIV.
 CC It can be used to preserve or disinfect a variety of materials,
 CC including medical equipment, foodstuffs, cosmetics, contact lens
 CC solutions, medicaments or other nutrient containing materials. It
 CC can also be used for the prophylaxis or treatment of microbial
 CC infections or diseases in plants and animals, e.g. conjunctivitis,
 CC keratitis, corneal ulcers, stomach ulcers associated with
 CC Helicobacter pylori, sexually transmitted diseases, gram-negative
 CC sepsis, endocarditis, pneumonia and other respiratory infections.
 CC urinary tract infections, systemic candidiasis and oral mucositis.
 CC It is biostatic or biocidal against clinically relevant pathogens
 CC exhibiting multi-drug resistance, e.g. vancomycin resistant
 CC Enterococcus faecium or faecalis, penicillin resistant
 CC Streptococcus pneumoniae and methicillin resistant Staphylococcus
 CC aureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5
 CC to 1 mg/kg/day, by injection.
 XX
 SQ Sequence 13 AA;
 Query Match 50.0%; Score 4; DB 18; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RGPF 4
 Db |||||
 6 RGPF 9
 RESULT 67
 AAG73433
 ID AAG73433 standard; peptide; 13 AA.
 XX
 AC AAG73433;
 XX
 DT 10-AUG-2001 (first entry)
 XX

DE Human gene 27-encoded secreted protein HJAAJ58, SEQ ID NO:206.
 XX Human; secreted protein; proliferative disorder; cancer;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder; tumour;
 KW endocrine disorder; infection; wound healing; vulnery; cell culture; chemotaxis; food additive; binding partner identification.
 KW
 XX Homo sapiens.
 XX
 XX WO200134628-A1.
 XX
 XX 17-MAY-2001.
 XX
 XX 08-NOV-2000; 2000WO-US30653.
 XX
 XX 12-NOV-1999; 99US-0164735.
 XX
 XX 27-JUL-2000; 2000US-0221193.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM, Komatsoulis GA, Birse CE, Ni J, Moore PA;
 XX WPI; 2001-329066/34.
 XX
 XX N-PSDB; AAH32611.
 XX
 XX Nucleic acids encoding 35 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's
 PT disease and diabetic retinopathy -
 XX
 XX Claim 11; Page 553; 604pp; English.
 XX
 CC AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted
 CC protein genes, and AAG73346-AAG73448 represent the proteins they encode.
 CC AAG73449-AAG73519 represent human secreted protein fragments. The genes
 CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 52 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancer, tumours, foetal and developmental
 CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
 CC cardiovascular disorders, angiogenic disorders, kidney disorders,
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine
 CC disorders, and infections. The proteins can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunosorbent assay (ELISA). The present sequence represents a human
 CC secreted protein of the invention.

XX Sequence 13 AA;

Query Match 50.0%; Score 4; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PILV 8
 Db 8 PILV 11
 RESULT 68
 ABG64297
 ID ABG64297 standard; Protein; 13 AA.
 XX
 AC ABG64297;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 XX Human albumin fusion protein #972.
 XX
 KW Albumin fusion protein; therapeutic protein X; human albumin; HA;
 KW human serum albumin; HSA; cancer; reproductive disorder;
 KW digestive disorder; immune disorder; endocrine disorder;
 KW haematopoietic disorder; neural disorder; connective disorder;
 KW cytostatic; antiinfertility; antiinflammatory; antiulcer;
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
 KW osteopathic; antiarthritic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200171137-A1.
 XX
 PD 18-OCT-2001.
 XX
 XX 12-APR-2001; 2001WO-US11988.
 XX
 XX 12-APR-2000; 2000US-229358P.
 PR
 XX 25-APR-2000; 2000US-199384P.
 PR
 XX 21-DEC-2000; 2000US-256931P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Haseltine WA;
 PI
 XX WPI; 2002-010886/01.
 DR
 XX
 XX New fusion protein for treating disease e.g. diabetes comprises an
 PT albumin fused to a therapeutic protein -
 PT
 XX Claim 1; Page 1119; 2102pp; English.
 XX
 CC The present invention relates to albumin fusion proteins comprising a
 CC therapeutic protein X and human albumin (HA, also known as human serum
 CC albumin, HGA). The proteins are useful for treating a disease or
 CC disorder that may be modulated by therapeutic protein X. The albumin
 CC extends the shelf-life of protein X, and may increase its biological
 CC in vitro/in vivo activity. The protein is useful for treating and
 CC diagnosing disorders such as cancer, reproductive disorders, digestive
 CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders
 CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders
 CC (e.g. diabetes), haematopoietic disorders, neural disorders
 CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,
 CC encephalomyelitis, meningitis, schizophrenia), and connective disorders
 CC (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin
 CC fusion proteins of the invention.
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 50.0%; Score 4; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PILV 8

Db 8 PILV 11


```

RESULT 69
AAW81795
ID AAW81795 standard; peptide; 14 AA.
XX
XX AAW81795;
AC
XX
XX
DT 29-JAN-1999 (first entry)
XX
DE D. viviparus DV17 antigen lys C proteolytic peptide fragment #7.
XX
XX DV17; antigen; lungworm; immunogenic protein; ELISA; antibody; cattle;
XX enzyme linked immunosorbent assay; vaccine; dictyocauliasis.
XX
XX Dictyocaulus viviparus.
OS
XX DE19715586-A1.
XX
XX
PD 22-OCT-1998.
XX
XX
XX 15-APR-1997; 97DE-1015586.
XX
XX 15-APR-1997; 97DE-1015586.
XX (FARH ) HOECHST AG.
XX
XX Hofmann J, Pauli A, Schmid K;
XX
XX WPI; 1998-558238/48.
XX N-PSDB; AAV64653.
XX
XX New Dictyocaulus viviparus lungworm protein (DV17) - used in ELISA
XX assay for DV17-specific antibodies and in vaccines against
XX dictyocauliasis in cattle
XX
XX Claim 2; Page 9; 15pp; German.
XX
XX This sequence represents a fragment of an immunogenic protein (DV17)
XX isolated from adult Dictyocaulus viviparus lungworms and generated by
XX Lys C proteolysis. The protein is used in an ELISA assay for
XX DV17-specific antibodies and fragments of the protein can be used in
XX vaccines against dictyocauliasis in cattle.
XX
XX
SQ Sequence 14 AA;
Query Match 50.0%; Score 4; DB 19; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7
Db 2 FPIL 5

RESULT 70
AAW49166
ID AAW49166 standard; peptide; 15 AA.
XX
XX AAW49166;
AC
XX
XX
DT 05-JUN-1998 (first entry)
XX
DE Human leucocyte antigen DQ4 binding peptide #57.
XX
XX Human leucocyte antigen; HLA-DQ4; combinatorial library;
XX autoimmune disease; chronic articular rheumatism.
XX
XX Synthetic.
OS
XX JP08151396-A.
XX
XX 11-JUN-1996.

```

```

XX
XX 28-NOV-1994; 94JP-0292657.
XX
XX 28-NOV-1994; 94JP-0292657.
XX (TEIJ ) TEIJIN LTD.
XX
XX WPI; 1996-329479/33.
XX
XX HLA-binding oligopeptide and an immuno:regulator contg it - used in
XX the treatment of auto:immune disease
XX
XX Claim 3; Page 15; 61pp; Japanese.
XX
XX This peptide is an example of a peptide which binds to a human leucocyte
XX antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid
XX combinatorial library comprising the sequence AAV05953, by screening
XX with an HLA-DQ4 molecule. The peptide is used for the treatment of
XX autoimmune disease, or especially for treatment of viral diseases.
XX
XX
SQ Sequence 15 AA;
Query Match 50.0%; Score 4; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
Db 9 RGPF 12

RESULT 71
AAW38927
ID AAW38927 standard; peptide; 15 AA.
XX
XX AAW38927;
AC
XX
XX 27-MAR-1998 (first entry)
XX
XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:324.
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
OS
XX WO9730074-A1.
XX
XX 21-AUG-1997.
XX
XX 14-FEB-1997; 97WO-US02298.
XX
XX 16-FEB-1996; 96US-0602999.
XX
XX (CYTO-) CYTOGEN CORP.
XX (UYNC-) UNIV NORTH CAROLINA.
XX
XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
XX Sparks AB, Thorn JM;
XX
XX WPI; 1997-424972/39.
XX
XX Src homology region 3 binding peptide - used to activate Src
XX tyrosine kinase(s) and to stimulate immune response by increasing
XX production of certain lymphokine(s), e.g. interleukin-1
XX
XX Claim 22; Page 90; 131pp; English.
XX
XX The present sequence represents a peptide which resembles a Src homology
XX region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
XX (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
XX bind the middle SH3 domain of Nck; (c) peptides which bind the SH3

```

CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p33bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
 CC binding peptides can be used in the method to identify inhibitors of
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.

XX Src related proteins.

XX Sequence 15 AA;
 Query Match 50.0%; Score 4; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPIL 7
 Db 1 FPIL 4

RESULT 72

ABB98785
 ID ABB98785 standard; Peptide; 15 AA.

XX AC ABB98785;

XX DT 03-FEB-2003 (first entry)

XX DE Human ribosomal protein S4-18.04 peptide fragment.

XX KW Human; ribosomal protein S4-18.04; tumour; haemopathy; HIV infection;
 XX immunological disease; inflammation; cytostatic; anti-HIV.

XX OS Homo sapiens.

XX PN CN1345823-A.

XX PD 24-APR-2002.

XX PF 29-SEP-2000; 2000CN-0125506.

XX PR 29-SEP-2000; 2000CN-0125506.

XX PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX PI Mao Y, Xie Y;

XX PS WPI; 2002-584314/63.

XX PT Novel polypeptide-human ribosomal protein S4-18.04 and polynucleotide
 XX for encoding said polypeptide -

XX PS Example 5; Page 19 (Disclosure); 33pp; Chinese.

XX CC The present invention relates to human ribosomal protein S4-18.04 (see
 CC ABB98784). The protein and its coding sequence can be used for treating
 CC several diseases, such as malignant tumours, haemopathy, HIV infection,
 CC immunological disease and various inflammations. The present sequence is
 CC an N-terminal peptide fragment of the protein, which was used in an
 CC example from the invention.

XX SX Sequence 15 AA;

Query Match 50.0%; Score 4; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PILV 8
 Db 7 PILV 10

RESULT 73

AAU77172
 ID AAU77172 standard; Peptide; 15 AA.

XX AC AAU77172;

XX DT 02-JUL-2002 (first entry)

XX DE Transcriptional control factor ZFM1 isomer 25.63 N-terminal peptide.

XX KW Human; transcriptional control factor ZFM1 isomer 25.63; HIV;
 XX malignant tumour; haemopathy; human immunodeficiency virus; cancer;
 XX immunological disease; inflammation; cytostatic; haemostatic; virucide;
 XX immunomodulatory; antiinflammatory; gene therapy.

XX OS Homo sapiens.

XX PN WO200220588-A1.

XX PD 14-MAR-2002.

XX PF 02-JUL-2001; 2001WO-CN01127.

XX PR 07-JUL-2000; 2000CN-0117050.

XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX PI Mao Y, Xie Y;

XX PS WPI; 2002-339796/37.

XX PT Human transcriptional control factor ZFM1 isomer 25.63 and encoding
 XX polynucleotide, used in diagnosis and treatment of malignant tumours,
 XX haemopathy, human immunodeficiency virus infection, immunological
 XX diseases and inflammation -

XX PS Example 5; Page 14; 38pp; Chinese.

XX CC The invention relates to the human transcriptional control factor ZFM1
 XX isomer 25.63 and the polynucleotide encoding it. The sequences of the
 XX invention are used in diagnosis and treatment of malignant tumours,
 XX haemopathy, human immunodeficiency virus (HIV) infection, immunological
 XX diseases and various inflammations. This sequence represents the human
 XX transcriptional control factor ZFM1 isomer 25.63 N-terminal peptide, used
 XX in ELISA.

XX SX Sequence 15 AA;

Query Match 50.0%; Score 4; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PILV 8
 Db 2 PILV 5

RESULT 74

ABR41125

ID ABR41125 standard; peptide; 15 AA.

XX AC ABR41125;

XX DT 02-JUN-2003 (first entry)

XX DE LRP6 specific polyclonal antibody peptide 7.

XX KW High bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;

KW gene therapy; bone density modulation; bone strength; trabecular number;
 KW bone size; bone tissue connectivity; bone disease; osteoporosis;
 KW osteomalacia; rickets; Paget's disease; neoplasm of the bone.

XX Unidentified.

PN WO200292764-A2.

PD 21-NOV-2002.

XX 13-MAY-2002; 2002WO-US14876.

XX 11-MAY-2001; 2001US-290071P.

PR 17-MAY-2001; 2001US-291311P.

PR 01-FEB-2002; 2002US-353058P.

PR 04-MAR-2002; 2002US-361293P.

XX (GENO-) GENOME THERAPEUTICS CORP.

PA (AMEP) WYETH.

PI Babij P, Bex FJ, Yaworsky PJ, Bodine PV;

XX WPI; 2003-129278/12.

XX New transgenic animals (e.g. mice), useful as models for studying bone
 PT density modulation, developing drugs for treating or preventing bone
 PT diseases (e.g. osteoporosis), or diagnosing diseases characterized by
 PT reduced bone density -

PS Disclosure; Page 131; 603pp; English.

XX The invention relates to novel transgenic animals expressing the high
 CC bone mass (HEM) gene, expressing the corresponding wild type HEM gene,
 CC comprising an alteration of the gene encoding LRP5 or LRP6, or
 CC expressing an LRP5 that is modulated by an altered gene control
 CC sequence introduced by homologous or non-homologous recombination. The
 CC transgenic animals are for the study of bone density modulation or bone
 CC mass modulation. The invention has osteopathic and cytostatic activity.
 CC The polynucleotides of the invention may have a use in gene therapy.
 CC The transgenic animals and nucleic acids are for the study of
 CC bone density modulation, where the bone mass is modulated relative to
 CC non-transgenic animals of the same species in more than one parameter
 CC selected from bone density, bone strength, trabecular number, bone
 CC size, or bone tissue connectivity. The transgenic animals, nucleic
 CC acids and methods are useful for identifying molecules involved in bone
 CC development, and for developing pharmaceutical compositions, which may
 CC be employed for treating or preventing bone diseases, e.g.
 CC osteoporosis, osteomalacia, rickets, Paget's disease, or neoplasms of
 CC the bone. The transgenic animals and nucleic acids are also useful in
 CC methods for diagnosing diseases involved in bone development, or
 CC characterised by reduced bone density or mass. The present sequence is
 CC used in the exemplification of the invention.

XX SQ Sequence 15 AA;

Query Match 50.0%; Score 4; DB 24; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPPF 5
 ||||
 Db 6 GPPF 9

RESULT 75

ABR34952

ID ABR34952 standard; Peptide; 15 AA.

XX ABR34952;

AC ABR34952;

XX 19-MAY-2003 (first entry)

DT Human cancer-related protein 185P2C9 HLA peptide #4208.

DE

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

PN 24-OCT-2002.

XX 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

PR 10-APR-2001; 2001US-283112P.

PR 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -

XX Claim 13; Page 557; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
 CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.

XX SQ Sequence 15 AA;

Query Match 50.0%; Score 4; DB 24; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPPF 5
 ||||
 Db 2 GPPF 5

Search completed: November 25, 2003, 19:27:18
 Job time : 21.4186 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 12.8372 Seconds
(without alignments)
114.943 Million cell updates/sec

Title: US-09-641-801-29

Perfect score: 8

Sequence: 1 RGPFPILV 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	8	100.0	8	15	US-10-281-652-29
2	5	62.5	16	15	US-10-225-567A-1931
3	4	50.0	7	12	US-10-118-708-2
4	4	50.0	9	8	US-08-452-843A-10
5	4	50.0	9	10	US-09-824-787B-137
6	4	50.0	9	11	US-09-791-393-263
7	4	50.0	9	11	US-09-791-389-263
8	4	50.0	9	12	US-10-022-066-178
9	4	50.0	9	12	US-09-132-231-57
10	4	50.0	10	12	US-10-083-768-30
11	4	50.0	11	10	US-09-071-838-138
12	4	50.0	11	15	US-10-213-512-138
13	4	50.0	12	12	US-10-118-708-5
14	4	50.0	14	9	US-09-749-234A-7
15	4	50.0	15	11	US-09-774-639-257
16	4	50.0	15	11	US-09-774-639-257
17	4	50.0	15	11	US-09-774-639-257
18	4	50.0	15	11	US-09-774-639-257
19	4	50.0	15	11	US-09-774-639-257
20	4	50.0	15	11	US-09-774-639-257
21	4	50.0	15	11	US-09-774-639-257
22	4	50.0	15	11	US-09-774-639-257
23	4	50.0	15	11	US-09-774-639-257
24	4	50.0	15	11	US-09-774-639-257
25	4	50.0	15	11	US-09-774-639-257
26	4	50.0	15	11	US-09-774-639-257
27	4	50.0	15	11	US-09-774-639-257
28	4	50.0	15	11	US-09-774-639-257
29	4	50.0	15	11	US-09-774-639-257
30	4	50.0	15	11	US-09-774-639-257
31	4	50.0	15	11	US-09-774-639-257
32	4	50.0	15	11	US-09-774-639-257
33	4	50.0	15	11	US-09-774-639-257
34	4	50.0	15	11	US-09-774-639-257
35	4	50.0	15	11	US-09-774-639-257
36	4	50.0	15	11	US-09-774-639-257
37	4	50.0	15	11	US-09-774-639-257
38	4	50.0	15	11	US-09-774-639-257
39	4	50.0	15	11	US-09-774-639-257
40	4	50.0	15	11	US-09-774-639-257
41	4	50.0	15	11	US-09-774-639-257
42	4	50.0	15	11	US-09-774-639-257
43	4	50.0	15	11	US-09-774-639-257
44	4	50.0	15	11	US-09-774-639-257
45	4	50.0	15	11	US-09-774-639-257
46	4	50.0	15	11	US-09-774-639-257
47	4	50.0	15	11	US-09-774-639-257
48	4	50.0	15	11	US-09-774-639-257
49	4	50.0	15	11	US-09-774-639-257
50	4	50.0	15	11	US-09-774-639-257
51	4	50.0	15	11	US-09-774-639-257
52	4	50.0	15	11	US-09-774-639-257
53	4	50.0	15	11	US-09-774-639-257
54	4	50.0	15	11	US-09-774-639-257
55	4	50.0	15	11	US-09-774-639-257
56	4	50.0	15	11	US-09-774-639-257
57	4	50.0	15	11	US-09-774-639-257
58	4	50.0	15	11	US-09-774-639-257
59	4	50.0	15	11	US-09-774-639-257
60	4	50.0	15	11	US-09-774-639-257
61	4	50.0	15	11	US-09-774-639-257
62	4	50.0	15	11	US-09-774-639-257
63	4	50.0	15	11	US-09-774-639-257
64	4	50.0	15	11	US-09-774-639-257
65	4	50.0	15	11	US-09-774-639-257
66	4	50.0	15	11	US-09-774-639-257
67	4	50.0	15	11	US-09-774-639-257
68	4	50.0	15	11	US-09-774-639-257
69	4	50.0	15	11	US-09-774-639-257
70	4	50.0	15	11	US-09-774-639-257
71	4	50.0	15	11	US-09-774-639-257
72	4	50.0	15	11	US-09-774-639-257
73	4	50.0	15	11	US-09-774-639-257
74	4	50.0	15	11	US-09-774-639-257
75	4	50.0	15	11	US-09-774-639-257
76	4	50.0	15	11	US-09-774-639-257
77	4	50.0	15	11	US-09-774-639-257
78	4	50.0	15	11	US-09-774-639-257
79	4	50.0	15	11	US-09-774-639-257
80	4	50.0	15	11	US-09-774-639-257
81	4	50.0	15	11	US-09-774-639-257
82	4	50.0	15	11	US-09-774-639-257
83	4	50.0	15	11	US-09-774-639-257
84	4	50.0	15	11	US-09-774-639-257
85	4	50.0	15	11	US-09-774-639-257
86	4	50.0	15	11	US-09-774-639-257
87	4	50.0	15	11	US-09-774-639-257
88	4	50.0	15	11	US-09-774-639-257

Sequence 339, App
Sequence 324, App
Sequence 1018, App
Sequence 8, Appli
Sequence 16, Appli
Sequence 8, Appli
Sequence 20, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 19, Appli
Sequence 123, App
Sequence 84, Appli
Sequence 34, Appli
Sequence 44, Appli
Sequence 110, Appli
Sequence 84, Appli
Sequence 19, Appli
Sequence 28, Appli
Sequence 10, Appli
Sequence 8, Appli
Sequence 19, Appli
Sequence 28, Appli
Sequence 81, Appli
Sequence 83, Appli
Sequence 123, App
Sequence 411, App
Sequence 39, Appli
Sequence 411, App
Sequence 17, Appli
Sequence 682, App
Sequence 81, Appli
Sequence 83, Appli
Sequence 123, App
Sequence 411, App
Sequence 682, App
Sequence 242, App
Sequence 9, Appli
Sequence 17, Appli
Sequence 22, Appli
Sequence 700, App
Sequence 701, App
Sequence 702, App
Sequence 4, Appli
Sequence 14, Appli
Sequence 34, Appli
Sequence 80, Appli
Sequence 128, App
Sequence 700, App
Sequence 701, App
Sequence 702, App
Sequence 41, Appli
Sequence 62, Appli
Sequence 700, App
Sequence 701, App
Sequence 702, App
Sequence 189, App
Sequence 16, Appli
Sequence 4, Appli
Sequence 14, Appli
Sequence 15, Appli
Sequence 30, Appli
Sequence 32, Appli
Sequence 40, Appli
Sequence 41, Appli
Sequence 42, Appli
Sequence 55, Appli
Sequence 17, Appli
Sequence 34, Appli
Sequence 80, Appli
Sequence 10, Appli
Sequence 70, Appli

89 3 37.5 7 15 US-10-214-932-118 Sequence 118, App
90 3 37.5 7 15 US-10-039-278-17 Sequence 17, Appl
91 3 37.5 8 9 US-09-839-666-6 Sequence 6, Appli
92 3 37.5 8 10 US-09-954-166-12 Sequence 12, Appl
93 3 37.5 8 10 US-09-761-534A-3 Sequence 3, Appli
94 3 37.5 8 10 US-09-756-875-11 Sequence 11, Appl
95 3 37.5 8 10 US-09-756-875-21 Sequence 21, Appl
96 3 37.5 8 10 US-09-756-875-22 Sequence 22, Appl
97 3 37.5 8 10 US-09-756-875-23 Sequence 23, Appl
98 3 37.5 8 10 US-09-756-875-24 Sequence 24, Appl
99 3 37.5 8 10 US-09-756-875-25 Sequence 25, Appl
100 3 37.5 8 10 US-09-756-875-26 Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-10-281-652-29
; Sequence 29, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-29

Query Match 100.0%; Score 8; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPFPILV 8
 | | | | | | | |
Db 1 RGPFPILV 8

RESULT 2
US-10-225-567A-1931
; Sequence 1931, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1931
; LENGTH: 16

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1931

Query Match 62.5%; Score 5; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFPIL 7
 | | | | |
Db 1 PFPIL 5

RESULT 3
US-10-118-708-2
; Sequence 2, Application US/10118708
; Publication No. US20030165991A1
; GENERAL INFORMATION:
; APPLICANT: Hart, L P
; APPLICANT: Pestka, James J
; APPLICANT: Yuan, Qiaoping
; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: MSU 4.1-447
; CURRENT APPLICATION NUMBER: US/10/118,708
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/146,643
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DONPEP.2
; OTHER INFORMATION: peptide mimotope of deoxynivalenol
US-10-118-708-2

Query Match 50.0%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPFP 5
 | | | |
Db 3 GPFP 6

RESULT 4
US-08-452-843A-10
; Sequence 10, Application US/08452843A
; Publication No. US20020098197A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 399632001321
; CURRENT APPLICATION NUMBER: US/08/452,843A
; CURRENT FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cw6 consensus
US-08-452-843A-10

```

Query Match          50.0%; Score 4; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPI 6
Db 2 PPPI 5

RESULT 5
US-09-824-787B-137
; Sequence 137, Application US/09824787B
; Patent No. US20020155447A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Evans, Elizabeth E.
; APPLICANT: Borrello, Melinda A.
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
; FILE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
; FILE REFERENCE: 1821, 0040001
; CURRENT APPLICATION NUMBER: US/09/824,787B
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/194,463
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 137
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-824-787B-137

Query Match          50.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPFP 5
Db 1 GPFP 4

RESULT 6
US-09-791-393-263
; Sequence 263, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 263
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-263

Query Match          50.0%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPI 6
Db 2 PPPI 5

RESULT 7
US-09-791-389-263
; Sequence 263, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 263
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-263

Query Match          50.0%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPI 6
Db 2 PPPI 5

RESULT 8
US-10-022-066-178
; Sequence 178, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 178
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide

```

US-10-022-066-178

Query Match 50.0%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPF 4
Db 6 RGPF 9

RESULT 9

US-09-132-231-57
Sequence 57, Application US/09132231A
Publication No. US20030198950A1
GENERAL INFORMATION:
APPLICANT: HORWITZ, Marshall S.
APPLICANT: LOEB, Lawrence A.
TITLE OF INVENTION: METHOD FOR PRODUCING NOVEL DNA SEQUENCES WITH
TITLE OF INVENTION: BIOLOGICAL ACTIVITY
FILE REFERENCE: 032425-001
CURRENT APPLICATION NUMBER: US/09/132,231A
PRIOR FILING DATE: 1998-08-11
PRIOR APPLICATION NUMBER: US 08/316,415
PRIOR FILING DATE: 1994-09-30
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57
LENGTH: 9
TYPE: PRT
ORGANISM: Escherichia coli
US-09-132-231-57

Query Match 50.0%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPIL 7
Db 2 FPIL 5

RESULT 10

US-10-083-768-30
Sequence 30, Application US/10083768
Publication No. US20030158116A1
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/083,768
FILING DATE: 27-Feb-2002
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-083-768-30

Query Match 50.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPF 4
Db 2 RGPF 5

RESULT 11

US-09-071-838-138
Sequence 138, Application US/09071838
Patent No. US20020152501A1
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramin
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: Nucleic Acids That Control Seed and
TITLE OF INVENTION: Fruit Development in Plants
NUMBER OF SEQUENCES: 324
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,838
FILING DATE: 01-MAY-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-086100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-071-838-138

Query Match 50.0%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7
|||
Db 5 FPIL 8

RESULT 12

US-10-213-512-138
; Sequence 138, Application US/10213512
; Publication No. US20030110536A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Chad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
; FILE OF INVENTION: Fruit Development in Plants
; FILE REFERENCE: 023070-086110US
; CURRENT APPLICATION NUMBER: US/10/213,512
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US/09/177,206
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: US 09/071,838
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 138
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-10-213-512-138

Query Match 50.0%; Score 4; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7
|||
Db 5 FPIL 8

RESULT 13

US-10-118-708-5
; Sequence 5, Application US/10118708
; Publication No. US20030165991A1
; GENERAL INFORMATION:
; APPLICANT: Hart, L P
; APPLICANT: Pestka, James J
; APPLICANT: Yuan, Qiaoping
; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: MSU 4.1-447
; CURRENT APPLICATION NUMBER: US/10/118,708
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/146,643
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C430, the
; OTHER INFORMATION: DONPEP.2 with a structurally flexible linker and a
; OTHER INFORMATION: cysteine residue

US-10-118-708-5

Query Match 50.0%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPFP 5
|||
Db 3 GPFP 6

RESULT 14

US-09-749-234A-7
; Sequence 7, Application US/09749234A
; Patent No. US20020068817A1
; GENERAL INFORMATION:
; APPLICANT: HOFMANN, Joachim
; APPLICANT: SCHMID, Karlheirrich
; APPLICANT: PAULI, Annette
; TITLE OF INVENTION: DICTYOCALUS VIVIPARUS ANTIGEN FOR THE
; DIAGNOSIS OF LUNGWORM INFESTATION AND FOR VACCINATION
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/749,234A
; FILING DATE: 27-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/403,092
; FILING DATE: 199-10-15
; APPLICATION NUMBER: DE 197 15 586.3
; FILING DATE: 15-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 038311/0103
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Query Match 50.0%; Score 4; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7
|||
Db 2 FPIL 5

RESULT 15

US-09-774-639-257
; Sequence 257, Application US/09774639
; Publication No. US20030003555A1


```
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 257
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-774-639-257

Query Match          50.0%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7
Db 8 FPIL 11

RESULT 16
US-09-730-339
; Sequence 339, Application US/09969730
; Publication No. US2003005443A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2
; CURRENT APPLICATION NUMBER: US/09/969,730
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,367
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,365
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,731
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,557
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,563
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/055,970
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,986
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,311
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,808
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,803
; PRIOR FILING DATE: 1997-08-05
```

```
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 339
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-969-730-339

Query Match          50.0%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7
Db 8 FPIL 11

RESULT 17
US-10-161-791-324
; Sequence 324, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 324:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-324

Query Match          50.0%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7
DB 1 FPIL 4

RESULT 18
US-10-225-567A-1018
; Sequence 1018, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1018
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1018

Query Match          50.0%; Score 4; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
DB 3 RGPF 6

RESULT 19
US-09-736-076-8
; Sequence 8, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:

; OTHER INFORMATION: GRK1
US-09-736-076-8

Query Match          50.0%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
DB 7 RGPF 10

RESULT 20
US-09-759-584-16
; Sequence 16, Application US/09759584
; Patent No. US20010014732A1
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,584
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/377,687
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-759-584-16

Query Match          37.5%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 2 ILV 4

RESULT 21
US-09-040-518-8
; Sequence 8, Application US/09040518
; Patent No. US20010042255A1
```

```
;
; GENERAL INFORMATION:
; APPLICANT: Karatzas, Costas N.
; TITLE OF INVENTION: PRODUCTION OF BIOFILAMENTS IN TRANSGENIC
; TITLE OF INVENTION: ANIMALS
; FILE REFERENCE: 06632/011001
; CURRENT APPLICATION NUMBER: US/09/040,518
; CURRENT FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Designed peptide to act as a recognition site for
; OTHER INFORMATION: an enzyme
US-09-040-518-8

Query Match          37.5%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 1 RGP 3

RESULT 22
US-09-784-810A-20
; Sequence 20, Application US/09784810A
; Patent No. US20020082203A1
; GENERAL INFORMATION:
; APPLICANT: RASTELLI, LUCA
; TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 10716-08
; CURRENT APPLICATION NUMBER: US/09/784,810A
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,360
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/191,261
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: motif
US-09-784-810A-20

Query Match          37.5%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 2 ILV 4

RESULT 23
US-10-237-160-1
; Sequence 1, Application US/10237160
; Publication No. US20030133926A1
; GENERAL INFORMATION:
; APPLICANT: Houston, Devin
; TITLE OF INVENTION: Compositions And Methods Relating To Reduction Of
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Graybeal Jackson Haley
```

```
;
; STREET: 777-108th Ave. NE, Suite 2460
; CITY: Bellevue
; STATE: Washington
; COUNTRY: USA
; ZIP: 98004-5117
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 98
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,160
; FILING DATE: 09-Dec-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: King, Joshua
; REGISTRATION NUMBER: 35,570
; REFERENCE/DOCKET NUMBER: 1776-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (425) 455-5575
; TELEFAX: (425) 455-1046
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; FRAGMENT TYPE: N-terminal
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-237-160-1

Query Match          37.5%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFP 5
Db 2 PFP 4

RESULT 24
US-10-313-338A-1
; Sequence 1, Application US/10313338A
; Publication No. US20030170226A1
; GENERAL INFORMATION:
; APPLICANT: Klair Laboratories, Inc.
; APPLICANT: Houston, Devin B.
; TITLE OF INVENTION: COMPOSITIONS AND MENTHODS RELATING TO REDUCTION OF SYMPTOMS O:
; FILE REFERENCE: 1776-1-7
; CURRENT APPLICATION NUMBER: US/10/313,338A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 09/411,605
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-313-338A-1

Query Match          37.5%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFP 5
Db 2 PFP 4

RESULT 25
```

```
US-10-313-790A-1
; Sequence 1, Application US/10313790A
; Publication No. US20030170227A1
; GENERAL INFORMATION:
; APPLICANT: Klaire Laboratories, Inc.
; APPLICANT: Houston, Devin B.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO REDUCTION OF SYMPTOMS OF AU
; FILE REFERENCE: 1776-1-6
; CURRENT APPLICATION NUMBER: US/10/313,790A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 09/411,605
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-313-790A-1
Query Match 37.5%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PPP 5
Db 2 PPP 4
RESULT 26
US-10-158-742A-19
; Sequence 19, Application US/10158742A
; Publication No. US20030104581A1
; GENERAL INFORMATION:
; APPLICANT: Hoess, Eva
; APPLICANT: Meier, Thomas
; APPLICANT: Pestlin, Gabriele
; APPLICANT: Popp, Friedrich
; APPLICANT: Reichert, Klaus
; APPLICANT: Schmuck, Rainer
; APPLICANT: Schneidinger, Bernd
; APPLICANT: Seidel, Christoph
; APPLICANT: Tischer, Wilhelm
; TITLE OF INVENTION: PROCESS FOR MAKING ANTIFUSOGENIC FUSION PEPTIDES THAT FORM
; FILE REFERENCE: 20904
; CURRENT APPLICATION NUMBER: US/10/158,742A
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: EP 01114497.9
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE:
; SEQ ID NO 19
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cleavage
; OTHER INFORMATION: sequence
US-10-158-742A-19
Query Match 37.5%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGP 3
Db 1 RGP 3
RESULT 27
US-10-028-075B-123
; Sequence 123, Application US/10028075B
```

```
; Publication No. US20030113733A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EP 01203748.7
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: sptrembl/Q9PFW5/Q9PFW5
US-10-028-075B-123
Query Match 37.5%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGP 3
Db 2 RGP 4
RESULT 28
US-10-029-206A-123
; Sequence 123, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: sptrembl/Q9PFW5/Q9PFW5
US-10-029-206A-123
Query Match 37.5%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGP 3
Db 2 RGP 4
RESULT 29
US-09-947-387-84
; Sequence 84, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
```

```
; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecule
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-84

Query Match          37.5%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY      4 FPI 6
      |||
Db      3 FPI 5

RESULT 30
US-10-122-246-34
; Sequence 34, Application US/10122246
; Publication No. US20030176354A1
; GENERAL INFORMATION:
; APPLICANT: Abajian, Henry B.
; Feighner, John P.
; Hlavka, Joseph J.
; TITLE OF INVENTION: NEW THERAPEUTIC USES OF TRI_, TETRA_,
; PENTA_, AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stepan P. Gribok, Esq.
; STREET: Duane Morris, LLP; 1650 Market Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Word Perfect 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/122,246
; FILING DATE: 11-Apr-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Gribok, Stephan P.
; REGISTRATION NUMBER: 29,643
; REFERENCE/DOCKET NUMBER: D4850-00021
; TELEPHONE: (215) 979-1000
; TELEFAX: (215) 979-1020
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 5
; OTHER INFORMATION: /label= Trp_NH2
; /note= "A modified Trp residue; an amine group replaces a
; hydroxyl group at the carboxy terminus."
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-10-122-246-34

Query Match          37.5%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY      4 FPI 6
      |||
Db      1 FPI 3

RESULT 31
US-10-122-246-44
; Sequence 44, Application US/10122246
; Publication No. US20030176354A1
; GENERAL INFORMATION:
; APPLICANT: Abajian, Henry B.
; Feighner, John P.
; Hlavka, Joseph J.
; TITLE OF INVENTION: NEW THERAPEUTIC USES OF TRI_, TETRA_,
; PENTA_, AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stepan P. Gribok, Esq.
; STREET: Duane Morris, LLP; 1650 Market Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Word Perfect 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/122,246
; FILING DATE: 11-Apr-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Gribok, Stephan P.
; REGISTRATION NUMBER: 29,643
; REFERENCE/DOCKET NUMBER: D4850-00021
; TELEPHONE: (215) 979-1000
; TELEFAX: (215) 979-1020
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 5
; OTHER INFORMATION: /label= Trp_NH2
; /note= "A modified Trp residue; an amine group replaces a
; hydroxyl group at the carboxy terminus."
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-122-246-44

Query Match          37.5%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;
```

QY 5 PTL 7
|||
Db 1 PTL 3

RESULT 32

US-10-145-206-110
; Sequence 110, Application US/10145206
; Publication No. US20030195156A1

GENERAL INFORMATION:

; APPLICANT: MIN, HOSUNG

; APPLICANT: HSU, HAILING

; APPLICANT: ZHONG, FEI

; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1

; FILE REFERENCE: A-743

; CURRENT APPLICATION NUMBER: US/10/145,206

; CURRENT FILING DATE: 2002-05-13

; PRIOR APPLICATION NUMBER: US 60/290,196

; PRIOR FILING DATE: 2001-05-11

; NUMBER OF SEQ ID NOS: 197

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 110

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Modulator of TALL-1

US-10-145-206-110

Query Match 37.5%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFP 5
|||
Db 1 PFP 3

RESULT 33

US-10-138-375-84

; Sequence 84, Application US/10138375

; Publication No. US20030208037A1

GENERAL INFORMATION:

; APPLICANT: Zhang, Han-Zhong

; APPLICANT: Cai, Sui Xiong

; APPLICANT: Drewe, John A.

; APPLICANT: Yang, Wu

; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for

; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease

; FILE REFERENCE: 1735.0030001

; CURRENT APPLICATION NUMBER: US/10/138,375

; CURRENT FILING DATE: 2002-05-06

; PRIOR FILING DATE: EARLIER FILING DATE: US/09/357,952

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642

; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998

; NUMBER OF SEQ ID NOS: 139

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 84

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide

US-10-138-375-84

Query Match 37.5%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PFI 6

Db |||
3 PFI 5

RESULT 34

US-10-168-758-19

; Sequence 19, Application US/10168758

; Publication No. US20030207812A1

GENERAL INFORMATION:

; APPLICANT: Chapdelaine, Marc J

; APPLICANT: Katherine, Knappenberger

; APPLICANT: Steelman, Gary

; APPLICANT: Suchard, Suzanne

; APPLICANT: Sygowski, Linda

; TITLE OF INVENTION: CD45

; FILE REFERENCE: Z70624-1P US

; CURRENT APPLICATION NUMBER: US/10/168,758

; CURRENT FILING DATE: 2000-12-18

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 19

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-168-758-19

Query Match 37.5%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
|||
Db 1 RGP 3

RESULT 35

US-10-168-758-28

; Sequence 28, Application US/10168758

; Publication No. US20030207812A1

GENERAL INFORMATION:

; APPLICANT: Chapdelaine, Marc J

; APPLICANT: Katherine, Knappenberger

; APPLICANT: Steelman, Gary

; APPLICANT: Suchard, Suzanne

; APPLICANT: Sygowski, Linda

; TITLE OF INVENTION: CD45

; FILE REFERENCE: Z70624-1P US

; CURRENT APPLICATION NUMBER: US/10/168,758

; CURRENT FILING DATE: 2000-12-18

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 28

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-168-758-28

Query Match 37.5%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
|||
Db 1 RGP 3

RESULT 36

US-10-200-923-10

; Sequence 10, Application US/10200923

```
; Publication No. US20030104976A1
; GENERAL INFORMATION:
; APPLICANT: DAVAR, GUDARZ
; APPLICANT: STRICHARTZ, GARY
; APPLICANT: FAREED, MOIN
; APPLICANT: KHODOROVA, ALLA
; TITLE OF INVENTION: ANALGESIC METHODS USING ENDOTHELIN
; FILE REFERENCE: 50073/010002
; CURRENT APPLICATION NUMBER: US/10/200,923
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/307,228
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-200-923-10

Query Match          37.5%; Score 3; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7
Db 2 PIL 4

RESULT 37
US-08-996-140-8
; Sequence 8, Application US/08996140
; Publication No. US20030190318A1
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: USHIO, Shimei
; APPLICANT: KUNIKATA, Toshio
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,140
; FILING DATE: 22-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 356,426/1996
; FILING DATE: 26-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 52,526/1997
; FILING DATE: 21-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 163,490/1997
; FILING DATE: 6-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 215,490/1997
; FILING DATE: 28-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618

; Publication No. US20030104976A1
; GENERAL INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal fragment
US-08-996-140-8

Query Match          37.5%; Score 3; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db 3 ILV 5

RESULT 38
US-09-729-873-19
; Sequence 19, Application US/09729873
; Patent No. US20010036921A1
; GENERAL INFORMATION:
; APPLICANT: Samy Ashkar
; TITLE OF INVENTION: Osteopontin-Derived Chemotactic and Inhibitory Agents
; TITLE OF INVENTION: and Uses Therefor
; FILE REFERENCE: CMZ-123CP
; CURRENT APPLICATION NUMBER: US/09/729,873
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/129,764
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/US00/10344
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-729-873-19

Query Match          37.5%; Score 3; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db 1 ILV 3

RESULT 39
US-09-767-395-28
; Sequence 28, Application US/09767395
; Patent No. US20020004215A1
; GENERAL INFORMATION:
; APPLICANT: Osbourn, Jane K
; Derbyshire, Elaine J
; McCafferty, John G
; Vaughan, Tristan J
; Johnson, Kevin S
; TITLE OF INVENTION: Labelling and selection of molecules
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
```

```
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA: US/09/767,395
; FILING DATE: 23-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/098,244
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/GB97/01835
; FILING DATE: 08-JUL-1997
; APPLICATION NUMBER: GB 9614292.2
; FILING DATE: 08-JUL-1996
; APPLICATION NUMBER: GB 9624880.2
; FILING DATE: 29-NOV-1996
; APPLICATION NUMBER: GB 9712818.5
; FILING DATE: 18-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/34800
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-767-395-28

Query Match          37.5%; Score 3; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PII 7
      |||
Db      2 PII 4

RESULT 40
US-09-947-387-81
; Sequence 81, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecule
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-83

Query Match          37.5%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 FPI 6
      |||
Db      3 FPI 5

RESULT 42
US-09-947-387-123
; Sequence 123, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecule
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
```


; CURRENT FILING DATE: 2001-09-07,
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 123
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-123

Query Match 37.5%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6
|||
Db 4 FPI 6

RESULT 43

US-09-974-879-411
; Sequence 411, Application US/09974879
; Publication No. US20030028003A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P2
; CURRENT APPLICATION NUMBER: US/09/974,879
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 09/818,683
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,900
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,987
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,908
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,984
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,985
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/066,094
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,100
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,089
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,095
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,090
; PRIOR FILING DATE: 1997-11-17

; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 411
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-879-411

Query Match 37.5%; Score 3; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7
|||
Db 4 PIL 6

RESULT 44

US-09-997-961-39
; Sequence 39, Application US/09997961
; Publication No. US20030060613A1
; GENERAL INFORMATION:
; APPLICANT: DEDHAR, Shoukat
; TITLE OF INVENTION: NOVEL USE OF CALRETICULIN IN MODULATING
; HORMONE RESPONSIVENESS AND NEW PHARMACEUTICALS FOR
; TREATING CANCER, OSTEOPOROSIS AND CHRONIC INFLAMMATORY
; DISEASE
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/997,961
; FILING DATE: 29-No. US20030060613A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,935
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/377,432
; FILING DATE: 24-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mool, Leslie A
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 007315-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-09-997-961-39

Query Match 37.5%; Score 3; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
|||
Db 2 GPF 4

RESULT 45
US-09-305-736-411
; Sequence 411, Application US/09305736
; Publication No. US20030088078A1
; GENERAL INFORMATION:
; APPLICANT: Feng et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: PZ020P1
; CURRENT APPLICATION NUMBER: US/09/305,736
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: PCT/US98/23435
; EARLIER FILING DATE: 1998-11-04
; EARLIER APPLICATION NUMBER: 60/064,911
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,912
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,983
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,900
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,988
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,987
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,908
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,984
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,985
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/066,094
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,100
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,089
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,095
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,090
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 612
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 411
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-305-736-411

Query Match 37.5%; Score 3; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7
DB 4 PIL 6

RESULT 46
US-10-349-023-17
; Sequence 17, Application US/10349023
; Publication No. US20030133919A1
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; OKURA, Takanori
; KURIMOTO, Masashi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSER: BROWDY AND NETMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington

STATE: D. C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/349,023
; FILING DATE: 23-Jan-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/556,972
; FILING DATE: 24-Apr-2000
; APPLICATION NUMBER: US/08/996,338
; FILING DATE: 22-DEC-1997
; APPLICATION NUMBER: JP 74,697/1997
; FILING DATE: 12-MAR-1997
; APPLICATION NUMBER: JP 215,488/1997
; FILING DATE: 28-JUL-1997
; APPLICATION NUMBER: JP 291,837/1997
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal fragment
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-349-023-17

Query Match 37.5%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 3 ILV 5

RESULT 47
US-09-933-767-682
; Sequence 682, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,881

; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,880
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,896
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,020
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,876
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,895
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,884
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,894
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,971
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,882
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,899
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,893
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,900
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,901
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,892
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,915
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,019
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,972
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,916
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,373
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,875
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,374
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,917
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,949
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,883
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,897
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,898
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,962
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,963
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,877
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,878
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18

; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 682
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-933-767-682

Query Match 37.5%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0

QY 5 PIL 7
|||
Db 1 PIL 3

RESULT 48

US-10-138-375-81
; Sequence 81, Application US/10138375
; Publication No. US20030208037A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Application:
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Prot
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/10/138,375
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; US-10-138-375-81

Query Match 37.5%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0

```
Qy      4 FPI 6
      |||
Db      4 FPI 6

RESULT 49
US-10-138-375-83
; Sequence 83, Application US/10138375
; Publication No. US20030208037A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/10/138,375
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-10-138-375-83

Query Match      37.5%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 FPI 6
      |||
Db      3 FPI 5

RESULT 50
US-10-138-375-123
; Sequence 123, Application US/10138375
; Publication No. US20030208037A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/10/138,375
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 123
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-10-138-375-123

Query Match      37.5%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 FPI 6
      |||
Db      3 FPI 5

RESULT 51
US-09-818-683-411
; Sequence 411, Application US/09818683
; Publication No. US20030211472A1
; GENERAL INFORMATION:
; APPLICANT: Feng et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P1
; CURRENT APPLICATION NUMBER: US/09/818,683
; CURRENT FILING DATE: 2001-03-28
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 612
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 411
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-818-683-411

Query Match      37.5%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PII 7
      |||
Db      4 PII 6

RESULT 52
US-10-023-282-682
; Sequence 682, Application US/10023282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/023,282
; CURRENT FILING DATE: 2001-12-20
; EARLIER APPLICATION NUMBER: 09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
```

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 682
LENGTH: 6
TYPE: PRT
ORGANISM: Homo sapiens
US-10-023-282-682

Query Match 37.5%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PIL 7
Db 1 PIL 3

RESULT 53
US-10-211-088-242
Sequence 242, Application US/10211088
Publication No. US20030104479A1
GENERAL INFORMATION:
APPLICANT: Bright, Gary R.
APPLICANT: Premkumar, D. David
APPLICANT: Chen, Yih-Tai
TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular
FILE REFERENCE: 01-1022-US
CURRENT APPLICATION NUMBER: US/10/211,088
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/309,395
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/341,589
PRIOR FILING DATE: 2001-12-13
NUMBER OF SEQ ID NOS: 366
SOFTWARE: PatentIn version 3.1
SEQ ID NO 242
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Nuclear localization signal
US-10-211-088-242

Query Match 37.5%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 3 RGP 5

RESULT 54
US-09-734-002-9
Sequence 9, Application US/09734002
Patent No. US20010016333A1
GENERAL INFORMATION:
APPLICANT: Mochazu SEIKI et al.
TITLE OF INVENTION: NOVEL PROTEIN AND MONOCLONAL ANTIBODY SPECIFIC THERETO
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/734,002
FILING DATE: 12-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/01956
FILING DATE: July 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

```
;
; LENGTH: 7
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-734-002-9

Query Match          37.5%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 ILV 8
      |||
Db      5 ILV 7

RESULT 55
US-09-729-873-17
; Sequence 17, Application US/09729873
; Patent No. US20010036921A1
; GENERAL INFORMATION:
; APPLICANT: Samy Ashkar
; TITLE OF INVENTION: Osteopontin-Derived Chemotactic and Inhibitory Agents
; FILE REFERENCE: CMZ-123CP
; CURRENT APPLICATION NUMBER: US/09/729,873
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/129,764
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/US00/10344
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-729-873-17

Query Match          37.5%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 ILV 8
      |||
Db      1 ILV 3

RESULT 56
US-09-731-242A-22
; Sequence 22, Application US/09731242A
; Patent No. US20020058253A1
; GENERAL INFORMATION:
; APPLICANT: KRANZ, DAVID
; APPLICANT: WITTRUP, K. DANE
; APPLICANT: HOLLER, PHILIP
; TITLE OF INVENTION: HIGH AFFINITY TCR PROTEINS AND METHODS
; FILE REFERENCE: 89-99
; CURRENT APPLICATION NUMBER: US/09/731,242A
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/169,179
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/009,388
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 7
; TYPE: PRT

; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: ()..()
; OTHER INFORMATION: CDR3alpha sequence
US-09-731-242A-22

Query Match          37.5%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PIL 7
      |||
Db      5 PIL 7

RESULT 57
US-09-989-789-700
; Sequence 700, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 700
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-700

Query Match          37.5%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGP 3
      |||
Db      1 RGP 3

RESULT 58
US-09-989-789-701
; Sequence 701, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 701
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-701

Query Match          37.5%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGP 3
      |||
```

```
Db      1 RGP 3

RESULT 59
US-09-989-789-702
; Sequence 702, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 702
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-702

Query Match      37.5%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGP 3
      |||
Db      1 RGP 3

RESULT 60
US-09-832-723-4
; Sequence 4, Application US/09832723
; Patent No. US20020098524A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-09-832-723-4

Query Match      37.5%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PIL 7
      |||
Db      4 PIL 6

RESULT 61
US-09-832-723-14
; Sequence 14, Application US/09832723
; Patent No. US20020098524A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-09-832-723-14

Query Match      37.5%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PIL 7
      |||
Db      2 PIL 4

RESULT 62
US-09-947-387-34
; Sequence 34, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Mole
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-34

Query Match      37.5%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 FPI 6
      |||
Db      4 FPI 6
```

```
RESULT 63
US-09-947-387-80
; Sequence 80, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecule
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-947-387-80

Query Match          37.5%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RPI 6
Db 4 RPI 6

RESULT 64
US-09-931-325A-128
; Sequence 128, Application US/09931325A
; Publication No. US20030054337A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: MALARIA IMMUNOGEN AND VACCINE
; FILE REFERENCE: 4564/G3503 ICC-103.1
; CURRENT APPLICATION NUMBER: US/09/931,325A
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US9N NOT YET ASSIGND
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-931-325A-128

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 2 RGP 4

RESULT 65
US-09-990-186-700
; Sequence 700, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 700
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-990-186-700

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 1 RGP 3

RESULT 66
US-09-990-186-701
; Sequence 701, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 701
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-990-186-701

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 1 RGP 3

RESULT 67
US-09-990-186-702
; Sequence 702, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
```



```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 702
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-990-186-702

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGP 3
      |||
Db      1 RGP 3

RESULT 68
US-09-940-727B-41
; Sequence 41, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-41

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGP 3
      |||
Db      1 RGP 3

RESULT 69
US-09-940-727B-41
; Sequence 41, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-41

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGP 3
      |||
Db      5 RGP 7

RESULT 69
US-09-865-548A-62
; Sequence 62, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-994-701

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGP 3
      |||
Db      1 RGP 3

RESULT 70
US-09-989-994-700
; Sequence 700, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 700
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-994-700

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGP 3
      |||
Db      1 RGP 3

RESULT 71
US-09-989-994-701
; Sequence 701, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 701
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-994-701

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGP 3
      |||
Db      1 RGP 3
```

```
RESULT 72
US-09-989-994-702
; Sequence 702, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 702
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-994-702

Query Match      37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGP 3
      |||
Db      1 RGP 3

RESULT 73
US-09-930-915A-169
; Sequence 169, Application US/09930915A
; Publication No. US20030138769A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
; CURRENT APPLICATION NUMBER: US/09/930,915A
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-930-915A-169

Query Match      37.5%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGP 3
      |||
Db      2 RGP 4

RESULT 74
US-10-146-999-16
; Sequence 16, Application US/10146999
; Publication No. US20030148942A1
; GENERAL INFORMATION:
; APPLICANT: Plotnikoff, Nicholas P.
; TITLE OF INVENTION: Methods for Inducing Sustained Immune Response
; FILE REFERENCE: 01-635-A
; CURRENT APPLICATION NUMBER: US/10/146,999
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 60/291,237
```

```
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-999-16

Query Match      37.5%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPP 5
      |||
Db      2 PPP 4

RESULT 75
US-10-303-331-4
; Sequence 4, Application US/10303331
; Publication No. US20030152976A1
; GENERAL INFORMATION:
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Winetzky, Deborah S.
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-3
; CURRENT APPLICATION NUMBER: US/10/303,331
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 09/832,723
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-10-303-331-4

Query Match      37.5%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PIL 7
      |||
Db      4 PIL 6

Search completed: November 25, 2003, 20:37:06
Job time : 13.8372 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 6.46512 Seconds
(without alignments)
52.356 Million cell updates/sec

Title: US-09-641-801-29

Perfect score: 8

Sequence: 1 RGPFPILV 8

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTUS-COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	100.0	8	4	US-09-641-803-29
2	6	75.0	6	2	US-08-747-137-29
3	4	50.0	5	3	US-08-676-242-9
4	4	50.0	6	2	US-08-656-177A-16
5	4	50.0	6	3	US-09-256-797-16
6	4	50.0	7	3	US-09-365-581A-2
7	4	50.0	7	4	US-09-626-821A-2
8	4	50.0	9	6	5310667-13
9	4	50.0	9	6	5310667-14
10	4	50.0	10	2	US-08-764-640-30
11	4	50.0	10	3	US-08-973-225-30
12	4	50.0	10	3	US-09-244-298A-30
13	4	50.0	10	3	US-09-516-704-30
14	4	50.0	10	4	US-09-549-090-30
15	4	50.0	10	4	US-09-832-230A-30
16	4	50.0	11	3	US-08-451-946B-2
17	4	50.0	11	3	US-08-446-938B-2
18	4	50.0	11	3	US-08-311-703A-2
19	4	50.0	11	3	US-08-446-939B-2
20	4	50.0	11	3	US-09-183-543-2
21	4	50.0	11	3	US-08-446-936A-2
22	4	50.0	11	3	US-09-177-249-138
23	4	50.0	11	5	PCT-US92-09326-6
24	4	50.0	12	3	US-09-365-581A-5
25	4	50.0	12	4	US-09-147-208-58
26	4	50.0	12	4	US-09-550-117A-58
27	4	50.0	12	4	US-09-626-821A-5

28	4	50.0	13	2	US-08-752-852A-191	Sequence 191, Appl
29	4	50.0	13	4	US-09-431-705-30	Sequence 30, Appl
30	4	50.0	15	3	US-08-602-999A-324	Sequence 324, Appl
31	4	50.0	15	4	US-09-500-124-324	Sequence 324, Appl
32	4	50.0	19	4	US-09-441-502B-65	Sequence 65, Appl
33	4	50.0	19	4	US-09-441-502B-66	Sequence 66, Appl
34	4	50.0	19	4	US-09-441-502B-71	Sequence 71, Appl
35	4	50.0	20	3	US-08-861-338-8	Sequence 8, Appl
36	3	37.5	4	1	US-08-149-839B-20	Sequence 20, Appl
37	3	37.5	4	1	US-08-377-687-16	Sequence 16, Appl
38	3	37.5	4	1	US-07-734-434A-30	Sequence 30, Appl
39	3	37.5	4	1	US-07-734-434A-33	Sequence 33, Appl
40	3	37.5	4	1	US-08-206-789-1	Sequence 1, Appl
41	3	37.5	4	1	US-08-206-789-3	Sequence 3, Appl
42	3	37.5	4	1	US-08-451-568-20	Sequence 20, Appl
43	3	37.5	4	1	US-08-494-763-4	Sequence 4, Appl
44	3	37.5	4	1	US-08-294-434-4	Sequence 4, Appl
45	3	37.5	4	1	US-08-457-166-4	Sequence 4, Appl
46	3	37.5	4	1	US-08-358-160-175	Sequence 175, Appl
47	3	37.5	4	1	US-08-451-566-20	Sequence 20, Appl
48	3	37.5	4	1	US-08-213-124-22	Sequence 22, Appl
49	3	37.5	4	1	US-08-224-868-4	Sequence 4, Appl
50	3	37.5	4	2	US-08-777-192-16	Sequence 16, Appl
51	3	37.5	4	2	US-08-249-830-3	Sequence 3, Appl
52	3	37.5	4	2	US-08-777-113-20	Sequence 20, Appl
53	3	37.5	4	3	US-09-198-209-3	Sequence 3, Appl
54	3	37.5	4	3	US-08-927-128-10	Sequence 10, Appl
55	3	37.5	4	3	US-09-219-849-16	Sequence 16, Appl
56	3	37.5	4	3	US-08-971-982-16	Sequence 16, Appl
57	3	37.5	4	3	US-09-411-531A-1	Sequence 1, Appl
58	3	37.5	4	3	US-07-901-713A-23	Sequence 23, Appl
59	3	37.5	4	4	US-09-411-605A-1	Sequence 1, Appl
60	3	37.5	4	4	US-09-298-574-20	Sequence 20, Appl
61	3	37.5	4	5	PCT-US93-06591-4	Sequence 4, Appl
62	3	37.5	4	6	5215966-12	Patent No. 5215966
63	3	37.5	5	1	US-08-238-089-34	Sequence 34, Appl
64	3	37.5	5	1	US-08-238-089-44	Sequence 44, Appl
65	3	37.5	5	1	US-08-494-763-2	Sequence 2, Appl
66	3	37.5	5	1	US-08-494-763-5	Sequence 5, Appl
67	3	37.5	5	1	US-08-432-651A-34	Sequence 34, Appl
68	3	37.5	5	1	US-08-432-651A-44	Sequence 44, Appl
69	3	37.5	5	2	US-08-347-335A-4	Sequence 4, Appl
70	3	37.5	5	2	US-08-640-847C-33	Sequence 33, Appl
71	3	37.5	5	3	US-08-962-962C-34	Sequence 34, Appl
72	3	37.5	5	3	US-08-962-962C-44	Sequence 44, Appl
73	3	37.5	5	3	US-09-357-952-84	Sequence 84, Appl
74	3	37.5	5	4	US-09-521-650-84	Sequence 84, Appl
75	3	37.5	5	4	US-09-168-888-84	Sequence 84, Appl
76	3	37.5	5	4	US-09-295-998B-47	Sequence 47, Appl
77	3	37.5	5	4	US-09-209-676-41	Sequence 41, Appl
78	3	37.5	5	4	US-09-295-846B-50	Sequence 50, Appl
79	3	37.5	5	4	US-09-551-737C-50	Sequence 50, Appl
80	3	37.5	5	5	PCT-US95-05560-34	Sequence 34, Appl
81	3	37.5	5	5	PCT-US95-05560-44	Sequence 44, Appl
82	3	37.5	6	1	US-07-943-709-63	Sequence 63, Appl
83	3	37.5	6	1	US-08-179-481-24	Sequence 24, Appl
84	3	37.5	6	1	US-08-584-579-1	Sequence 1, Appl
85	3	37.5	6	1	US-08-456-424-141	Sequence 141, Appl
86	3	37.5	6	2	US-08-672-805-2	Sequence 2, Appl
87	3	37.5	6	2	US-08-672-805-4	Sequence 4, Appl
88	3	37.5	6	2	US-08-672-805-6	Sequence 6, Appl
89	3	37.5	6	2	US-08-377-432-39	Sequence 39, Appl
90	3	37.5	6	2	US-08-540-118-5	Sequence 5, Appl
91	3	37.5	6	2	US-08-889-291-28	Sequence 28, Appl
92	3	37.5	6	3	US-08-947-965-10	Sequence 10, Appl
93	3	37.5	6	3	US-08-860-248C-118	Sequence 118, Appl
94	3	37.5	6	3	US-08-996-338-17	Sequence 17, Appl
95	3	37.5	6	3	US-08-817-177-11	Sequence 11, Appl
96	3	37.5	6	3	US-09-098-244-28	Sequence 28, Appl
97	3	37.5	6	3	US-09-357-952-81	Sequence 81, Appl
98	3	37.5	6	3	US-09-357-952-83	Sequence 83, Appl
99	3	37.5	6	3	US-09-357-952-123	Sequence 123, Appl
100	3	37.5	6	4	US-09-521-650-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-09-641-803-29
; Sequence 29, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-29

Query Match 100.0%; Score 8; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPFPILV 8
Db 1 RGPFPILV 8

RESULT 2
US-08-747-137-29
; Sequence 29, Application US/08747137
; Patent No. 5945033
; GENERAL INFORMATION:
; APPLICANT: YEN, Richard C.K.
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,137
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,546
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,831
; FILING DATE: 01-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,560

; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/641,720
; FILING DATE: 15-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016197-000840US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
US-08-747-137-29

Query Match 75.0%; Score 6; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPFPPI 6
Db 1 RGPFPPI 6

RESULT 3
US-08-676-242-9
; Sequence 9, Application US/08676242C
; Patent No. 6143719
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of Michigan
; APPLICANT: Schmaier, Alvin H.
; APPLICANT: Hasan, Ahmed A.K.
; TITLE OF INVENTION: Bradykinin Analogs As Selective Thrombin Inhibitors
; FILE REFERENCE: 8820-2 US
; CURRENT APPLICATION NUMBER: US/08/676,242C
; CURRENT FILING DATE: 2000-07-16
; EARLIER APPLICATION NUMBER: 60/000,096
; EARLIER FILING DATE: 1995-06-09
; EARLIER APPLICATION NUMBER: PCT/US96/09940
; EARLIER FILING DATE: 1996-06-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Scrambled
US-08-676-242-9

Query Match 50.0%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPFPP 5
Db 1 GPFPP 4

RESULT 4
US-08-656-177A-16
; Sequence 16, Application US/08656177A
; Patent No. 5882851
; GENERAL INFORMATION:
; APPLICANT: Koch, Birgit M.
; APPLICANT: Sibbesen, Ole
; APPLICANT: Haikier, Barbara Ann
; APPLICANT: Moeller, Birger L.
; TITLE OF INVENTION: Cytochrome P-450 Monooxygenases

```
;
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5882851artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,177A
; FILING DATE: 08-AUG-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-19783/A/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8689
; TELEFAX: 919-541-8587
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-656-177A-16

Query Match 50.0%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPI 6
Db 3 PPPI 6

RESULT 5
US-09-256-797-16
; Sequence 16, Application US/09256797
; Patent No. 6133417
; GENERAL INFORMATION:
; APPLICANT: Koch, Birgit M.
; APPLICANT: Sibbesen, Ole
; APPLICANT: Halkier, Barbara Ann
; APPLICANT: Moller, Birger L.
; TITLE OF INVENTION: Cytochrome P-450 Monooxygenases
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSES: No. 6133417artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/256,797
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

Query Match 50.0%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPFP 5
Db 3 GPFP 6

RESULT 7
US-09-626-821A-2
; Sequence 2, Application US/09626821A
; Patent No. 6537762
; GENERAL INFORMATION:
; APPLICANT: Hart, L P
; APPLICANT: Pestka, James J
; APPLICANT: Yuan, Qiaoping

; APPLICATION NUMBER: 08/656,177
; FILING DATE: 08-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-19783/A/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-09-256-797-16

Query Match 50.0%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPI 6
Db 3 PPPI 6

RESULT 6
US-09-365-581A-2
; Sequence 2, Application US/09365581A
; Patent No. 6287776
; GENERAL INFORMATION:
; APPLICANT: Hart, L P
; APPLICANT: Pestka, James J
; APPLICANT: Yuan, Qiaoping
; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES
; TITLE OF INVENTION: THEROF
; FILE REFERENCE: MSU 4.1-447
; CURRENT APPLICATION NUMBER: US/09/365,581A
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,643
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DONPEP.2
; OTHER INFORMATION: peptide mimotope of deoxynivalenol
; US-09-365-581A-2

Query Match 50.0%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPFP 5
Db 3 GPFP 6

RESULT 7
US-09-626-821A-2
; Sequence 2, Application US/09626821A
; Patent No. 6537762
; GENERAL INFORMATION:
; APPLICANT: Hart, L P
; APPLICANT: Pestka, James J
; APPLICANT: Yuan, Qiaoping
```

```
; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: MSU 4.1-447
; CURRENT APPLICATION NUMBER: US/09/626,821A
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,643
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DONPEP.2
; OTHER INFORMATION: peptide mimotope of deoxynivalenol
US-09-626-821A-2

Query Match          50.0%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPFP 5
Db 3 GPFP 6

RESULT 8
5310667-13
; Patent No. 5310667
; APPLICANT: EICHHOLTZ, DAVID A.; GASSER, CHARLES S.; KISHORE,
; GANESH M.
; TITLE OF INVENTION: GLYPHOSATE-TOLERANT 5-ENOLPYRUVYL
; -3-PHOSPHOSHIMKIMATE SYNTHASES
; NUMBER OF SEQUENCES: 37
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/380,963
; FILING DATE: 17-JUL-1989
; SEQ ID NO:13:
; LENGTH: 9
5310667-13

Query Match          50.0%; Score 4; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PILV 8
Db 3 PILV 6

RESULT 9
5310667-14
; Patent No. 5310667
; APPLICANT: EICHHOLTZ, DAVID A.; GASSER, CHARLES S.; KISHORE,
; GANESH M.
; TITLE OF INVENTION: GLYPHOSATE-TOLERANT 5-ENOLPYRUVYL
; -3-PHOSPHOSHIMKIMATE SYNTHASES
; NUMBER OF SEQUENCES: 37
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/380,963
; FILING DATE: 17-JUL-1989
; SEQ ID NO:14:
; LENGTH: 9
5310667-14

Query Match          50.0%; Score 4; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PILV 8
Db 3 PILV 6

US-08-764-640-30
; Sequence 30, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Gates, Christian
; APPLICANT: Schatz, Peter J.
; APPLICANT: Balasubramanian, Palaniappan
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Hendren, Richard W.
; APPLICANT: Depreince, Randolph B.
; APPLICANT: Podduturi, Surekha
; APPLICANT: Yin, Qun
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/764,640
; FILING DATE: 11-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrudiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-764-640-30

Query Match          50.0%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPF 4
Db 2 RGPF 5

RESULT 11
US-08-973-225-30
; Sequence 30, Application US/08973225A
; Patent No. 6083913
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Duffin, David J.
; APPLICANT: Gates, Christian
; APPLICANT: Haselden, Sherril S.
```

Matheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-08-973-225-30

Query Match 50.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
|||
Db 2 RGPF 5

RESULT 12
US-09-244-298A-30
; Sequence 30, Application US/09244298A
; Patent No. 6121238
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Gates, Christian
; APPLICANT: Schatz, Peter J.
; APPLICANT: Balasubramanian, Palaniappan
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Hendren, Richard W.
; APPLICANT: Deprince, Randolph B.
; APPLICANT: Podduturi, Surekha
; APPLICANT: Yin, Qun
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-Dec-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-244-298A-30

Query Match 50.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
|||
Db 2 RGPF 5

RESULT 13
US-09-516-704-30
; Sequence 30, Application US/09516704
; Patent No. 6251864
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Gates, Christian
; APPLICANT: Schatz, Peter J.
; APPLICANT: Balasubramanian, Palaniappan
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Hendren, Richard W.
; APPLICANT: Deprince, Randolph B.
; APPLICANT: Podduturi, Surekha
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000

```
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-516-704-30

Query Match          50.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGPF 4
Db      2 RGPF 5

RESULT 14
US-09-549-090-30
; Sequence 30, Application US/09549090
; Patent No. 6465430
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barlett, Ronald W.
; Cwiria, Steven B.
; Duffin, David J.
; Gates, Christian
; Haselden, Sherril S.
; Mattheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/549,090
; FILING DATE: 13-Apr-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/973,225
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-549-090-30

Query Match          50.0%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGPF 4
Db      2 RGPF 5

RESULT 15
US-09-832-230A-30
; Sequence 30, Application US/09832230A
; Patent No. 6506362
; GENERAL INFORMATION:
; APPLICANT: Dower, William J. et al
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/832,230A
; FILING DATE: 10-Apr-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-832-230A-30

Query Match          50.0%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGPF 4
Db      2 RGPF 5

RESULT 16
US-08-451-946B-2
; Sequence 2, Application US/08451946B
; Patent No. 6001969
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
; PRODUCTS AND USES THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
```


STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,946B
FILING DATE: 26-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/311,703
FILING DATE: 23-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/786,063
FILING DATE: 31-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI91-09V
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-451-946B-2

Query Match 50.0%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPI 6
Db 3 PPPI 6

RESULT 17
US-08-446-938B-2
Sequence 2, Application US/08446938B
Patent No. 6008011
GENERAL INFORMATION:
APPLICANT: Lin, Herbert Y.
APPLICANT: Wang, Xiao-Fan
APPLICANT: Weinberg, Robert A.
TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
TITLE OF INVENTION: Products and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,938B
FILING DATE: 23-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/311,703
FILING DATE: 23-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/786,063
FILING DATE: 31-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI91-09FZ
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-446-938B-2

Query Match 50.0%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPI 6
Db 3 PPPI 6

RESULT 18
US-08-311-703A-2
Sequence 2, Application US/08311703A
Patent No. 6010872
GENERAL INFORMATION:
APPLICANT: Lin, Herbert Y.
APPLICANT: Wang, Xiao-Fan
APPLICANT: Weinberg, Robert A.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
TITLE OF INVENTION: Products and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,703A
FILING DATE: 23-SEP-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/786,063
FILING DATE: 31-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hogle, Doreen
REGISTRATION NUMBER: 36,361
REFERENCE/DOCKET NUMBER: WHI91-09F
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-311-703A-2

Query Match 50.0%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFPI 6
Db 3 PFPI 6

RESULT 19
US-08-446-939B-2
; Sequence 2, Application US/08446939B
; Patent No. 6046157
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,939B
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/311,703
; FILING DATE: 23-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/786,063
; FILING DATE: 23-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH191-09FX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear

US-08-446-939B-2
Query Match 50.0%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFPI 6
Db 3 PFPI 6

RESULT 20
US-09-183-543-2
; Sequence 2, Application US/09183543A
; Patent No. 6086867
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.

; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Modulation of TGF-Beta Type III Receptor Polypept
; FILE REFERENCE: WH191-09FXA
; CURRENT APPLICATION NUMBER: US/09/183,543A
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: US 08/446,939
; EARLIER FILING DATE: 1995-05-23
; EARLIER APPLICATION NUMBER: US 08/311,703
; EARLIER FILING DATE: 1994-09-23
; EARLIER APPLICATION NUMBER: US 07/786,063
; EARLIER FILING DATE: 1991-10-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligopeptide sequence
US-09-183-543-2

Query Match 50.0%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFPI 6
Db 3 PFPI 6

RESULT 21
US-08-446-936A-2
; Sequence 2, Application US/08446936A
; Patent No. 6201108
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
; TITLE OF INVENTION: Products and Uses Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,936A
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/311,703
; FILING DATE: 23-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/786,063
; FILING DATE: 31-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH191-09FY
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540

```
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
US-08-446-936A-2

Query Match          50.0%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPI 6
DB 3 PPPI 6

RESULT 22
US-09-177-249-138
; Sequence 138, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomchiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; FILE REFERENCE: Development in Plants
; CURRENT APPLICATION NUMBER: US/09/177,249
; EARLIER FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 138
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-138

Query Match          50.0%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7
DB 5 FPIL 8

RESULT 23
PCT-US92-09326-6
; Sequence 6, Application PC/TUS9209326
; GENERAL INFORMATION:
; APPLICANT: Whitehead Institute for Biomedical Research
; TITLE OF INVENTION: TGF-BETA TYPE RECEPTOR CDNAS ENCODED
; TITLE OF INVENTION: PRODUCTS AND USES THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
US-09-641-801-29.oligo.ra1

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09326
FILING DATE: 19921030
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/786,063
FILING DATE: 31-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI91-09 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-09326-6

Query Match          50.0%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPI 6
DB 3 PPPI 6

RESULT 24
US-09-365-581A-5
; Sequence 5, Application US/09365581A
; Patent No. 6287776
; GENERAL INFORMATION:
; APPLICANT: Hart, L P
; APPLICANT: Pestka, James J
; APPLICANT: Yuan, Qiaoping
; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES
; FILE REFERENCE: MSU 4.1-447
; CURRENT APPLICATION NUMBER: US/09/365,581A
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,643
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C430, the
; OTHER INFORMATION: DONPEP.2 with a structurally flexible linker and a
; OTHER INFORMATION: cysteine residue
US-09-365-581A-5

Query Match          50.0%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPFP 5
DB 3 GPFP 6

RESULT 25
US-09-147-208-58
; Sequence 58, Application US/09147208
; Patent No. 633303
; GENERAL INFORMATION:
```

APPLICANT: ;
TITLE OF INVENTION: Antiviral Ricin-Like Proteins ;
NUMBER OF SEQUENCES: 71 ;
CORRESPONDENCE ADDRESS: ;
ADDRESSEE: BRESKIN & PARR ;
STREET: 40 King Street West ;
CITY: Toronto ;
STATE: Ontario ;
COUNTRY: Canada ;
ZIP: M5H 3Y2 ;
COMPUTER READABLE FORM: ;
MEDIUM TYPE: Floppy disk ;
COMPUTER: IBM PC compatible ;
OPERATING SYSTEM: PC-DOS/MS-DOS ;
SOFTWARE: Patent In Release #1.0, Version #1.30 ;
CURRENT APPLICATION DATA: ;
APPLICATION NUMBER: US/09/147,208 ;
FILING DATE: 02-MAR-1999 ;
CLASSIFICATION: 514 ;
ATTORNEY/AGENT INFORMATION: ;
NAME: Rudolph, John R. ;
REGISTRATION NUMBER: 38,003 ;
REFERENCE/DOCKET NUMBER: 7841-76 ;
TELECOMMUNICATION INFORMATION: ;
TELEPHONE: (416) 364-7311 ;
TELEFAX: (416) 361-1398 ;
INFORMATION FOR SEQ ID NO: 58: ;
SEQUENCE CHARACTERISTICS: ;
LENGTH: 12 amino acids ;
TYPE: amino acid ;
STRANDEDNESS: single ;
TOPOLOGY: linear ;
MOLECULE TYPE: peptide ;
US-09-147-208-58

Query Match 50.0%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPIL 7
Db 6 FPIL 9

RESULT 26
US-09-550-117A-58
Sequence 58, Application US/09550117A
Patent No. 6531125
GENERAL INFORMATION:
APPLICANT: Borgford, Thor
TITLE OF INVENTION: Antiviral Ricin-Like Proteins
FILE REFERENCE: 10447-10
CURRENT APPLICATION NUMBER: US/09/550,117A
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/147,208
PRIOR FILING DATE: 1999-03-02
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patent In version 3.1
SEQ ID NO 58
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PAP-211/pAP-212
US-09-550-117A-58

Query Match 50.0%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPIL 7
Db 6 FPIL 9

RESULT 27
US-09-626-821A-5
Sequence 5, Application US/09626821A
Patent No. 6537762
GENERAL INFORMATION:
APPLICANT: Hart, L P
APPLICANT: Pestka, James J
APPLICANT: Yuan, Qiaoping
TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: MSU 4.1-447
CURRENT APPLICATION NUMBER: US/09/626,821A
CURRENT FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/146,643
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 5
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: C430, the
OTHER INFORMATION: DONPEP.2 with a structurally flexible linker and a
OTHER INFORMATION: cysteine residue
US-09-626-821A-5

Query Match 50.0%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPPP 5
Db 3 GPPP 6

RESULT 28
US-08-752-852A-191
Sequence 191, Application US/08752852A
Patent No. 5994306
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Chee-Liang
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrner, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742

```

; REFERENCE/DOCKET NUMBER: 8067-034-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-752-852A-191

Query Match 50.0%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
Db 6 RGPF 9

RESULT 29
US-09-431-705-30
; Sequence 30, Application US/09431705
; Patent No. 6585975
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Londono-Arcila, Patricia
; APPLICANT: Freeman, Donna
; TITLE OF INVENTION: Use of salmonella vectors for
; TITLE OF INVENTION: vaccination against helicobacter infection
; FILE REFERENCE: 06132/060001
; CURRENT APPLICATION NUMBER: US/09/431,705
; CURRENT FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-09-431-705-30

Query Match 50.0%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
Db 8 RGPF 11

RESULT 30
US-08-602-999A-324
; Sequence 324, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York

```

```

; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 324:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-324

Query Match 50.0%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FFIL 7
Db 1 FFIL 4

RESULT 31
US-09-500-124-324
; Sequence 324, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872

```

```
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 324:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-324

Query Match 50.0%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPIL 7
Db 1 FPIL 4

RESULT 32
US-09-441-502B-65
; Sequence 65, Application US/09441502B
; Patent No. 6455041
; GENERAL INFORMATION:
; APPLICANT: Dunbar, Bonita S.
; TITLE OF INVENTION: IMMUNOGENIC EPITOPES OF THE HUMAN ZONA PELLUCIDA PROTEIN
; FILE REFERENCE: 12231.2USU1
; CURRENT APPLICATION NUMBER: US/09/441,502B
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-441-502B-65

Query Match 50.0%; Score 4; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPFP 5
Db 4 GPFP 7

RESULT 35
US-08-861-338-8
; Sequence 8, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-861-338-8

Query Match 50.0%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Qy 5 PILV 8
Db 14 PILV 17

RESULT 33
US-09-441-502B-66
; Sequence 66, Application US/09441502B
; Patent No. 6455041
; GENERAL INFORMATION:
; APPLICANT: Dunbar, Bonita S.
; TITLE OF INVENTION: IMMUNOGENIC EPITOPES OF THE HUMAN ZONA PELLUCIDA PROTEIN
; FILE REFERENCE: 12231.2USU1
; CURRENT APPLICATION NUMBER: US/09/441,502B
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-441-502B-66

Query Match 50.0%; Score 4; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PILV 8
Db 14 PILV 17

RESULT 34
US-09-441-502B-71
; Sequence 71, Application US/09441502B
; Patent No. 6455041
; GENERAL INFORMATION:
; APPLICANT: Dunbar, Bonita S.
; TITLE OF INVENTION: IMMUNOGENIC EPITOPES OF THE HUMAN ZONA PELLUCIDA PROTEIN
; FILE REFERENCE: 12231.2USU1
; CURRENT APPLICATION NUMBER: US/09/441,502B
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-441-502B-71

Query Match 50.0%; Score 4; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPFP 5
Db 4 GPFP 7
```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
Db 7 RGPF 10

RESULT 36
US-08-149-839B-20
; Sequence 20, Application US/08149839B
; Patent No. 5514779
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,839B
; FILING DATE: 10-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9112300.0
; FILING DATE: 07-JUN-1991
; PRIOR APPLICATION DATA: PCT/GB92/00999
; FILING DATE: 03-JUN-1992
; APPLICATION NUMBER: GB 9223708.0
; FILING DATE: 12-NOV-1992
; APPLICATION DATA: US 08/002842
; FILING DATE: 14-JAN-1993
; APPLICATION NUMBER: GB 9303564.0
; FILING DATE: 23-FEB-1993
; APPLICATION DATA: PCT/GB93/02179
; FILING DATE: 22-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 3893/99204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-149-839B-20

Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db 2 ILV 4

RESULT 37
US-08-377-687-16
; Sequence 16, Application US/08377687
; Patent No. 5538525
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKI R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,687
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-377-687-16

Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db 2 ILV 4

RESULT 38
US-07-734-434A-30
; Sequence 30, Application US/07734434A
; Patent No. 5554728
; GENERAL INFORMATION:
; APPLICANT: Basava, Channa
; APPLICANT: Hosteler, Karl Y.
; TITLE OF INVENTION: LIPID CONJUGATES OF THERAPEUTIC
; TITLE OF INVENTION: PEPTIDES AND PROTEASE INHIBITORS
; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: VICAL, INC.
; STREET: 9373 Towne Centre Drive
; CITY: San Diego,
; STATE: California
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/734,434A
; FILING DATE: 19910723
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kirkpatrick, Anita M.
; REGISTRATION NUMBER: 32,617
; REFERENCE/DOCKET NUMBER: VICAL.019A
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Misc. differences
; LOCATION: 1-2, 4
; OTHER INFORMATION: Phe-1 is joined to Phe-2 by an
; OTHER INFORMATION: isosteric linkage having the structure -CHOH-CH2-N-; carboxy
; OTHER INFORMATION: terminal Val-4 is an amide.
US-07-734-434A-30

Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6
|||
Db 1 FPI 3

RESULT 39
US-07-734-434A-33
; Sequence 33, Application US/07734434A
; Patent No. 554728
; GENERAL INFORMATION:
; APPLICANT: Basava, Channa
; APPLICANT: Hosteler, Karl Y.
; TITLE OF INVENTION: LIPID CONJUGATES OF THERAPEUTIC
; TITLE OF INVENTION: PEPTIDES AND PROTEASE INHIBITORS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: VICAL, INC.
; STREET: 9373 Towne Centre Drive
; CITY: San Diego,
; STATE: California
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/734,434A
; FILING DATE: 19910723
; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:
; NAME: Kirkpatrick, Anita M.
; REGISTRATION NUMBER: 32,617
; REFERENCE/DOCKET NUMBER: VICAL.019A
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Unusual amino acids; misc. differences
; LOCATION: 1, 1-2, 4
; OTHER INFORMATION: amino terminal Ala-1 residue is a
; OTHER INFORMATION: t-butyloxycarbonyl derivative; Phe-1 and Pro-2 are joined
; OTHER INFORMATION: isosteric link having the structure -CHOH-CH2-N-; carboxy
; OTHER INFORMATION: Val-4 is an amide.
US-07-734-434A-33

Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6
|||
Db 1 FPI 3

RESULT 40
US-08-206-789-1
; Sequence 1, Application US/08206789
; Patent No. 5580854
; GENERAL INFORMATION:
; APPLICANT: Orlewski, Marian
; APPLICANT: Cardozo, Christopher
; APPLICANT: Vinitzky, Alexander
; TITLE OF INVENTION: SUBSTRATE-RELATED
; TITLE OF INVENTION: PEPTIDYL-ALDEHYDE
; TITLE OF INVENTION: INHIBITORS OF THE PROTEOLYTIC ACTIVITY OF THE
; TITLE OF INVENTION: MULTICATALYTIC PROTEINASE COMPLEX
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BRUMBAUGH, GRAVES, DONOHUE &
; ADDRESSEE: RAYMOND
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112-2500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,789
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Seide, Rochelle K.
; REGISTRATION NUMBER: 32,300
; REFERENCE/DOCKET NUMBER: A29525 - 165/25989
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2626
; TELEFAX: 212-765-2519
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
US-08-206-789-1
Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
|||
Db 1 GPF 3

RESULT 41
US-08-206-789-3
; Sequence 3, Application US/08206789
; Patent No. 5580854
; GENERAL INFORMATION:
; APPLICANT: Orłowski, Marian
; APPLICANT: Cardoso, Christopher
; APPLICANT: Vinitsky, Alexander
; TITLE OF INVENTION: SUBSTRATE-RELATED
; TITLE OF INVENTION: PEPTIDYL-ALDEHYDE
; TITLE OF INVENTION: INHIBITORS OF THE PROTEOLYTIC ACTIVITY OF THE
; TITLE OF INVENTION: MULTICATALYTIC PROTEINASE COMPLEX
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BRUNBAUGH, GRAVES, DONOHUE &
; ADDRESSEE: RAYMOND
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112-2500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,789
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Seide, Rochelle K.
; REGISTRATION NUMBER: 32,300
; REFERENCE/DOCKET NUMBER: A29525 - 165/25989
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2626
; TELEFAX: 212-765-2519
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
US-08-206-789-3

Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
|||
Db 1 GPF 3

RESULT 42
US-08-451-568-20
; Sequence 20, Application US/08451568
; Patent No. 5597801
; GENERAL INFORMATION:
; APPLICANT: BROEKERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: VANDERLEVDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,568
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,839
; FILING DATE: 10-NOV-1993
; APPLICATION NUMBER: GB 9112300.0
; FILING DATE: 07-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00999
; FILING DATE: 03-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9223708.0
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002842
; FILING DATE: 14-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9303564.0
; FILING DATE: 23-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02179
; FILING DATE: 22-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 3893/99204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-451-568-20

Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
|||
Db 2 ILV 4

```
RESULT 43
US-08-494-763-4
; Sequence 4, Application US/08494763
; Patent No. 5627035
; GENERAL INFORMATION:
; APPLICANT: Vahlne, Anders
; APPLICANT: Svennerholm, Bo
; APPLICANT: Rymo, Lars
; APPLICANT: Jeansson, Stig
; APPLICANT: Horal, Peter
; TITLE OF INVENTION: Peptides That Block Human
; TITLE OF INVENTION: Immunodeficiency Virus Infections and Methods of Use Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue &
; ADDRESSEE: Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3-1/2 inch 1.44 MB diskette
; COMPUTER: IBM OR COMPATIBLE
; OPERATING SYSTEM: DOS VER. 5.0
; SOFTWARE: WP 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,763
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/988,127
; FILING DATE: 12-FEB-1993
; REFERENCE/DOCKET NUMBER: 28391A
; APPLICATION NUMBER: 07/571,080
; FILING DATE: 22-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Kay-Ellen
; REGISTRATION NUMBER: 36,364
; REFERENCE/DOCKET NUMBER: 28391A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2500
; TELEFAX: (212) 765-2519
; TELEX: 238555
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: peptide
US-08-494-763-4
Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 1 RGP 3
|||
|||

RESULT 44
US-08-294-434-4
; Sequence 4, Application US/08294434
; Patent No. 5635371
; GENERAL INFORMATION:
; APPLICANT: Stout, Jay
; APPLICANT: Wagner, Fred W.
; APPLICANT: Coolidge, Thomas R.
; APPLICANT: Holmquist, Barton
; TITLE OF INVENTION: CHEMICAL METHOD FOR SELECTIVE
; TITLE OF INVENTION: MODIFICATION OF THE N- AND/OR C-TERMINAL AMINO ACID
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5656456west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

```
; TITLE OF INVENTION: ALPHA-CARBON REACTIVE GROUP OF A RECOMBINANT
; TITLE OF INVENTION: POLYPEPTIDE OR A PORTION THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5635371west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,434
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,798
; FILING DATE: 13-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, Albin J.
; REGISTRATION NUMBER: 28,650
; REFERENCE/DOCKET NUMBER: 8648.29-US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-294-434-4
Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 1 RGP 3
|||
|||

RESULT 45
US-08-457-166-4
; Sequence 4, Application US/08457166
; Patent No. 5656456
; GENERAL INFORMATION:
; APPLICANT: Stout, Jay
; APPLICANT: Wagner, Fred W.
; APPLICANT: Coolidge, Thomas R.
; APPLICANT: Holmquist, Barton
; TITLE OF INVENTION: CHEMICAL METHOD FOR SELECTIVE
; TITLE OF INVENTION: MODIFICATION OF THE N- AND/OR C-TERMINAL AMINO ACID
; TITLE OF INVENTION: ALPHA-CARBON REACTIVE GROUP OF A RECOMBINANT
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5656456west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,166
; FILING DATE: 13-JUL-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/091,751
; FILING DATE: 13-JUL-1992
; APPLICATION NUMBER: US/07/912,798
; FILING DATE: 13-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, Albin J.
; REGISTRATION NUMBER: 28,650
; REFERENCE/DOCKET NUMBER: 8648.35-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-457-166-4

Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 1 RGP 3

RESULT 46
US-08-358-160-175
; Sequence 175, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 175:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-175

Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 2 RGP 4

RESULT 47
US-08-451-566-20
; Sequence 20, Application US/08451566
; Patent No. 5691199
; GENERAL INFORMATION:
; APPLICANT: BROEKERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: VANDERLEVDEN JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,566
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149839
; FILING DATE: 10-NOV-1993
; APPLICATION NUMBER: GB 9112300.0
; FILING DATE: 07-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00999
; FILING DATE: 03-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9223708.0
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002842

Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FILING DATE: 14-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9303564.0
FILING DATE: 23-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02179
FILING DATE: 22-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 3893/99204
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-451-566-20

Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 2 ILV 4

RESULT 48
US-08-213-124-22
Sequence 22, Application US/08213124
Patent No. 5693325
GENERAL INFORMATION:
APPLICANT: Kahn, Michael
TITLE OF INVENTION: PEPTIDE VACCINES AND METHODS RELATING
TO THE INVENTION: THERETO
NUMBER OF SEQUENCES: 27
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/213,124
FILING DATE: 15-MAR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Hermanns, Karl R.
REGISTRATION NUMBER: 33,507
REFERENCE/DOCKET NUMBER: 670063.411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANDBERRY
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-213-124-22

Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 1 RGP 3

RESULT 49
US-08-224-868-4
Sequence 4, Application US/08224868
Patent No. 5698448
GENERAL INFORMATION:
APPLICANT: Soldin, Steven J.
TITLE OF INVENTION: IMMUNOSUPPRESSIVE DRUG BINDING PROTEINS
TO THE INVENTION: AND USE
NUMBER OF SEQUENCES: 14
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/224,868
FILING DATE: 08-APR-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/200,404
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/782,761
FILING DATE: 22-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,115
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/279,176
FILING DATE: 02-DEC-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/841,792
FILING DATE: 26-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/521,074
FILING DATE: 09-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 64688/125/CHRE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-224-868-4

Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
|||
Db 2 GPF 4

RESULT 50

US-08-777-192-16
; Sequence 16, Application US/08777192
; Patent No. 5824869
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,192
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-777-192-16

Query Match 37.5%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 6 ILV 8
|||
Db 2 ILV 4

RESULT 51

US-08-249-830-3
; Sequence 3, Application US/08249830
; Patent No. 5840485
; GENERAL INFORMATION:
; APPLICANT: Lebl, Michal
; APPLICANT: Lam, Kit S.
; APPLICANT: Salmon, Sydney E.
; APPLICANT: Krchnak, Victor
; APPLICANT: Sepetov, Nikolai

; APPLICANT: Kocis, Peter
; TITLE OF INVENTION: TOPOLOGICALLY SEGREGATED, ENCODED
; TITLE OF INVENTION: SOLID PHASE LIBRARIES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,830
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Baldwin, Geraldine F.
; REGISTRATION NUMBER: 31,232
; REFERENCE/DOCKET NUMBER: 7156-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-249-830-3

Query Match 37.5%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 2 GPF 4
|||
Db 2 GPF 4

RESULT 52

US-08-777-113-20
; Sequence 20, Application US/08777113
; Patent No. 5986176
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,113
; FILING DATE: 30-DEC-1996

CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/451,566
FILING DATE: 26-MAY-1995
APPLICATION NUMBER: US 08/149839
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: GB 9112300.0
FILING DATE: 07-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00999
FILING DATE: 03-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9223708.0
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002842
FILING DATE: 14-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9303564.0
FILING DATE: 23-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02179
FILING DATE: 22-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 3893/99204
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-777-113-20

Query Match 37.5%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 2 ILV 4

RESULT 53
US-09-198-209-3
Sequence 3, Application US/09198209A
Patent No. 6090912
GENERAL INFORMATION:
APPLICANT: Lebl, Michal
APPLICANT: Lam, Kit S.
APPLICANT: Salmon, Sydney E.
APPLICANT: Krchnak, Victor
APPLICANT: Sepetov, Nikolai
APPLICANT: Kocis, Peter
TITLE OF INVENTION: TOPOLOGICALLY SEGREGATED, ENCODED SOLID PHASE LIBRARIES
CURRENT APPLICATION NUMBER: US/09/198,209A
CURRENT FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: 08/249,830
EARLIER FILING DATE: 1994-05-26
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 4
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-198-209-3

Query Match 37.5%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPF 4
Db 2 GPF 4

RESULT 54
US-08-927-128-10
Sequence 10, Application US/08927128
Patent No. 6127150
GENERAL INFORMATION:
APPLICANT: Coolidge, Thomas
APPLICANT: Wagner, Fred
APPLICANT: ven Heeke, Gino
APPLICANT: Schuster, Sheldon
APPLICANT: Stout, Jay
APPLICANT: Wylie, Dwane
TITLE OF INVENTION: PURIFICATION DIRECTED CLOSING OF PEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 6127150west Center, 90 S. 7th Street
CITY: Minneapolis
STATE: MN
COUNTRY: U.S.A.
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,128
FILING DATE: 05-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/680,004
FILING DATE: 15-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.2USD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/332-5300
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-927-128-10

Query Match 37.5%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 1 RGP 3

```
RESULT 55
US-09-219-849-16
; Sequence 16, Application US/09219849
; Patent No. 6150081
; GENERAL INFORMATION:
; APPLICANT: VAN HEERDE, GEORGE V.
; APPLICANT: VAN RIJN, ALEXIS C.
; APPLICANT: BOWMSTRA, JAN B.
; APPLICANT: DE WOLF, FREDERIK A.
; APPLICANT: MOOBROEK, ANDREAS
; APPLICANT: WERTEN, MARC W.T.
; APPLICANT: WIND, RICHELE D.
; APPLICANT: VAN DEN BOSCH, TANJA J.
; TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
; TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
; FILE REFERENCE: 2728-2
; CURRENT APPLICATION NUMBER: US/09/219,849
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-219-849-16

Query Match          37.5%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGP 3
Db      1 RGP 3

RESULT 56
US-08-971-982-16
; Sequence 16, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSER: CUSHMAN DARBAY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,982
; FILING DATE: 17-No. 6187904-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

US-09-641-801-29.oligo.ra1

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-08-971-982-16

Query Match          37.5%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 ILV 8
Db      2 ILV 4

RESULT 57
US-09-411-531A-1
; Sequence 1, Application US/09411531A
; Patent No. 6251391
; GENERAL INFORMATION:
; APPLICANT: Wilkinson, Randall
; APPLICANT: Houston, Devin
; TITLE OF INVENTION: Compositions and methods relating to the
; inhibition of casomorphin and glutuomorphin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Graybeal Jackson Haley
; STREET: 777-108th Ave. NE, Suite 2460
; CITY: Bellevue
; STATE: Washington
; COUNTRY: USA
; ZIP: 98004-5117
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/411,531A
; FILING DATE: 01-Oct-1999
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: King, Joshua
; REGISTRATION NUMBER: 35,570
; REFERENCE/DOCKET NUMBER: 1776-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (425) 455-5575
; TELEFAX: (425) 455-1046
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-411-531A-1

Query Match          37.5%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PFP 5
Db      1 PFP 5
```

Db 2 PFP 4

RESULT 58
US-07-901-713A-23
; Sequence 23, Application US/07901713A
; Patent No. 6291205
; GENERAL INFORMATION:
; APPLICANT: Tuite, Michael F.
; APPLICANT: Freedman, Robert B.
; APPLICANT: Markus, Henry Z.
; APPLICANT: Schultz, Loren D.
; APPLICANT: Montgomery, Donna L.
; APPLICANT: Ellis, Ronald W.
; TITLE OF INVENTION: METHOD FOR INCREASING PRODUCTION OF
; TITLE OF INVENTION: DISULFIDE BONDED RECOMBINANT PROTEINS BY SACCAROMYCES
; TITLE OF INVENTION: CEREBISIAE
; FILE REFERENCE: 18469
; CURRENT APPLICATION NUMBER: US/07/901,713A
; CURRENT FILING DATE: 1992-08-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: portion of antistasin coding sequence (Figure 8)
US-07-901-713A-23

Query Match 37.5%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPF 4
Db 2 GPF 4

RESULT 59
US-09-411-605A-1
; Sequence 1, Application US/09411605A
; Patent No. 6447772
; GENERAL INFORMATION:
; APPLICANT: Houston, Devin
; TITLE OF INVENTION: Compositions And Methods Relating To Reduction Of Symptoms Of Au
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/411,605A
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-411-605A-1

Query Match 37.5%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFP 5
Db 2 PFP 4

RESULT 60
US-09-298-574-20
; Sequence 20, Application US/09298574
; Patent No. 6521590
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.

APPLICANT: REES, SARAH B.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,574
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/149,839
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00999
FILING DATE: 03-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9223708.0
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002842
FILING DATE: 14-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9303564.0
FILING DATE: 23-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02179
FILING DATE: 22-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 3893/99204
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-298-574-20

Query Match 37.5%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 2 ILV 4

RESULT 61
PCT-US93-06591-4
; Sequence 4, Application PC/TUS9306591
; GENERAL INFORMATION:
; APPLICANT: Stout, Jay
; APPLICANT: Wagner, Fred W.
; APPLICANT: Coolidge, Thomas R.
; APPLICANT: Holmquist, Barton
; TITLE OF INVENTION: METHOD FOR MODIFICATION OF

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,089
FILING DATE: 04-MAY-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gould, Jr., Lewis F.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 3297-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6020
TELEFAX: (215) 575-6015
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label= Trp-NH2
OTHER INFORMATION: /note= "A modified Trp residue: an amine group
OTHER INFORMATION: replaces a hydroxyl group at the carboxy terminus."
US-08-238-089-44

Query Match 37.5%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PIL 7
Db 1 PIL 3

RESULT 65
US-08-494-763-2
Sequence 2, Application US/08494763
Patent No. 5627035
GENERAL INFORMATION:
APPLICANT: Vahlne, Anders
APPLICANT: Svennerholm, Bo
APPLICANT: Rymo, Lars
APPLICANT: Jeansson, Stig
APPLICANT: Horal, Peter
TITLE OF INVENTION: Peptides That Block Human
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue &
ADDRESSEE: Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2 inch 1.44 MB diskette
COMPUTER: IBM OR COMPATIBLE
OPERATING SYSTEM: DOS VER. 5.0
SOFTWARE: WP 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,763
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/988,127
FILING DATE: 12-FEB-1993
APPLICATION NUMBER: 07/571,080
FILING DATE: 22-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Kay-Ellen
REGISTRATION NUMBER: 36,364
REFERENCE/DOCKET NUMBER: 28391A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEFAX: (212) 765-2519
TELEX: 238555
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5
TYPE: amino acid

ATTORNEY/AGENT INFORMATION:
NAME: Smith, Kay-Ellen
REGISTRATION NUMBER: 36,364
REFERENCE/DOCKET NUMBER: 28391A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEFAX: (212) 765-2519
TELEX: 238555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: peptide
US-08-494-763-2
Query Match 37.5%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 2 RGP 4

RESULT 66
US-08-494-763-5
Sequence 5, Application US/08494763
Patent No. 5627035
GENERAL INFORMATION:
APPLICANT: Vahlne, Anders
APPLICANT: Svennerholm, Bo
APPLICANT: Rymo, Lars
APPLICANT: Jeansson, Stig
APPLICANT: Horal, Peter
TITLE OF INVENTION: Peptides That Block Human
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue &
ADDRESSEE: Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2 inch 1.44 MB diskette
COMPUTER: IBM OR COMPATIBLE
OPERATING SYSTEM: DOS VER. 5.0
SOFTWARE: WP 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,763
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/988,127
FILING DATE: 12-FEB-1993
APPLICATION NUMBER: 07/571,080
FILING DATE: 22-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Kay-Ellen
REGISTRATION NUMBER: 36,364
REFERENCE/DOCKET NUMBER: 28391A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEFAX: (212) 765-2519
TELEX: 238555
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5
TYPE: amino acid

```
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: peptide
US-08-494-763-5

Query Match      37.5%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
   |||
Db 1 RGP 3

RESULT 67
US-08-432-651A-34
; Sequence 34, Application US/08432651A
; Patent No. 5767083
; GENERAL INFORMATION:
; APPLICANT: Abajian, Henry B.
; APPLICANT: No. 5767083le, John F.
; APPLICANT: Hlavka, Joseph J.
; TITLE OF INVENTION: TRI-, TETRA-, PENTA-, AND POLYPEPTIDES
; TITLE OF INVENTION: AND THEIR THERAPEUTIC USE AS AN ANTIDEPRESSANT AGENT
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lewis F. Gould, Jr.
; STREET: 1700 Market Street, Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,651A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gould, Jr., Lewis F.
; REGISTRATION NUMBER: 25,057
; REFERENCE/DOCKET NUMBER: 3297-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 575-6020
; TELEFAX: (215) 575-6015
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= Trp-NH2
; OTHER INFORMATION: /note= "A modified Trp residue: an amine group
; OTHER INFORMATION: replaces a hydroxyl group at the carboxy
; OTHER INFORMATION: terminus."
US-08-432-651A-44

Query Match      37.5%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7
   |||
Db 1 PIL 3

RESULT 69
US-08-347-335A-4
; Sequence 4, Application US/08347335A
; Patent No. 5856163
; GENERAL INFORMATION:
; APPLICANT: Hashida, Miyoko
; APPLICANT: Abo, Masanobu
; APPLICANT: Takamura, Yukiko
; APPLICANT: Kirk, Ole
; APPLICANT: Halkier, Torben
; APPLICANT: Pedersen, Sven
; APPLICANT: Patkar, Shankant A.
; APPLICANT: Hansen, Mogens T.
; TITLE OF INVENTION: NOVEL ENZYMES
```

; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 58561630 No. 5856163disk of No. 5856163th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,335A
; FILING DATE: 22-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3706.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-347-335A-4

Query Match 37.5%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 3 PFP 5
|||
Db 3 PFP 5

RESULT 70
US-08-640-847C-33
; Sequence 33, Application US/08640847C
; Patent No. 5993865
; GENERAL INFORMATION:
; APPLICANT: BECH, Lene M.
; APPLICANT: SORENSEN, Steen B.
; APPLICANT: VAAG, Pia
; APPLICANT: MULDERG, Marianne
; APPLICANT: BENFELDT, Thorild
; APPLICANT: LEAH, Robert
; APPLICANT: BREDDAM, Klaus
; TITLE OF INVENTION: BEVERAGE AND A METHOD OF PREPARING IT
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LADAS & PARRY
; STREET: 26 WEST 61 STREET
; CITY: NEW YORK
; STATE: NY
; ZIP: 10023
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3-1/4" Disk 1.44 MB
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
; SOFTWARE: WordPerfect 8 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,847C
; FILING DATE: 26-JUN-1996
; CLASSIFICATION: 426
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK94/00420

; FILING DATE: 08-NOV-1994
; APPLICATION NUMBER: DK001266/93
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MASS, Clifford J.
; REGISTRATION NUMBER: 30,086
; REFERENCE/DOCKET NUMBER: U-010781-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1890
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 Amino Acids
; TYPE: Amino Acids
; TOPOLOGY: Linear
US-08-640-847C-33

Query Match 37.5%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 RGP 3
|||
Db 3 RGP 5

RESULT 71
US-08-962-962C-34
; Sequence 34, Application US/08962962C
; Patent No. 6093797
; GENERAL INFORMATION:
; APPLICANT: Abajian, Henry B.
; APPLICANT: No. 6093797le, John P.
; APPLICANT: Hlavka, Joseph J.
; TITLE OF INVENTION: TRI-, TETRA-, PENTA-, AND POLYPEPTIDES
; TITLE OF INVENTION: AND THEIR THERAPEUTIC USE AS AN ANTIDEPRESSANT AGENT
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lewis F. Gould, Jr.
; STREET: 1700 Market Street, Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/962,962C
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gould, Jr., Lewis F.
; REGISTRATION NUMBER: 25,057
; REFERENCE/DOCKET NUMBER: 3297-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 575-6020
; TELEFAX: (215) 575-6015
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= Ttp-NH2
; OTHER INFORMATION: /note= "A modified Ttp residue: an amine group replaces a

OTHER INFORMATION: hydroxyl group at the carboxy terminus."

US-08-962-962C-34

Query Match 37.5%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6
|||
Db 1 FPI 3

RESULT 72

US-08-962-962C-44
Sequence 44, Application US/08962962C

Patent No. 6093797

GENERAL INFORMATION:

APPLICANT: Abajian, Henry B.

APPLICANT: No. 6093797le, John F.

APPLICANT: Hlavka, Joseph J.

TITLE OF INVENTION: TRI-, TETRA-, PENTA-, AND POLYPEPTIDES

TITLE OF INVENTION: AND THEIR THERAPEUTIC USE AS AN ANTIDEPRESSANT AGENT

NUMBER OF SEQUENCES: 128

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lewis F. Gould, Jr.

STREET: 1700 Market Street, Suite 3232

CITY: Philadelphia

STATE: PA

COUNTRY: US

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/962,962C

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Gould, Jr., Lewis F.

REGISTRATION NUMBER: 25,057

REFERENCE/DOCKET NUMBER: 3297-5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 575-6020

TELEFAX: (215) 575-6015

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 5

OTHER INFORMATION: /label= Trp-NH2

OTHER INFORMATION: /note= "A modified Trp residue: an amine group replaces a

hydroxyl group at the carboxy terminus."

US-08-962-962C-44

Query Match 37.5%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7
|||
Db 1 PIL 3

RESULT 73

US-09-357-952-84

Sequence 84, Application US/09357952

Patent No. 6248904
GENERAL INFORMATION:
APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Who
TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protea
TITLE OF INVENTION: Other Enzymes and the Use Thereof
FILE REFERENCE: 1735.0030001
CURRENT APPLICATION NUMBER: US/09/357,952
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: US 60/093,642
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 84
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-357-952-84

Query Match 37.5%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6
|||
Db 3 FPI 5

RESULT 74

US-09-521-650-84

Sequence 84, Application US/09521650

Patent No. 6335429

GENERAL INFORMATION:

APPLICANT: Weber, Eckard

APPLICANT: Cai, Sui Xiong

APPLICANT: Keana, John F.W.

APPLICANT: Drewe, John A.

APPLICANT: Zhang, Han-Zhong

TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules an

TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence

TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the

TITLE OF INVENTION: Use Thereof

FILE REFERENCE: 1735.0290002

CURRENT APPLICATION NUMBER: US/09/521,650

CURRENT FILING DATE: 2000-03-08

EARLIER APPLICATION NUMBER: 09/168,888

EARLIER FILING DATE: 1998-10-09

EARLIER APPLICATION NUMBER: US 60/061,582

EARLIER FILING DATE: 1997-10-10

EARLIER APPLICATION NUMBER: US 09/033,661

EARLIER FILING DATE: 1998-03-03

NUMBER OF SEQ ID NOS: 142

SOFTWARE: Patent in Ver. 2.0

SEQ ID NO 84

LENGTH: 5

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide

US-09-521-650-84

Query Match 37.5%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6

Db 3 FPI 5
|||

RESULT 75
US-09-168-888-84
; Sequence 84, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-84

Query Match 37.5%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPI 6
|||
Db 3 FPI 5

Search completed: November 25, 2003, 20:30:05
Job time : 7.46512 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 : Search time 12.3488 Seconds
(without alignments)
140.178 Million cell updates/sec

Title: US-09-641-801-30
Perfect score: 18
Sequence: 1 ATFNRYYQDDHGEILKSL 18

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	16.7	7	2 S45648	Na+-transporting A
2	3	16.7	8	2 S66296	Na+-transporting A
3	3	16.7	9	2 B20569	serum amyloid P-co
4	3	16.7	9	2 PH0108	late G1-69 protein
5	3	16.7	10	2 XGHUE	erythrocyte membra
6	3	16.7	10	2 C61440	polygalacturonase
7	3	16.7	11	2 S65395	chemical-sense-rel
8	3	16.7	11	2 D45900	complement C3b rec
9	3	16.7	11	2 S65377	cytochrome-c oxida
10	3	16.7	11	4 I52708	ELAV-like neuronal
11	3	16.7	12	2 B58503	outer membrane por
12	3	16.7	12	2 T46794	hypothetical prote
13	3	16.7	12	2 S27023	Na+/K+-exchanging
14	3	16.7	13	2 JQ2309	hypothetical 1.6K
15	3	16.7	13	2 JQ2319	hypothetical 1.6K
16	3	16.7	13	2 E60396	antigen 7H8/2 - ma
17	3	16.7	13	2 A23694	myosin heavy chain
18	3	16.7	13	2 A57789	gallbladder stone
19	3	16.7	13	2 E53275	Ig kappa-1 chain J
20	3	16.7	14	1 LFEBWC	trp operon leader
21	3	16.7	14	1 LFEBWC	trp operon leader
22	3	16.7	14	2 PS0249	porin - rice (stra
23	3	16.7	14	2 A39239	actin 8 - slime mo
24	3	16.7	14	2 B61308	hemocyanin chain 3
25	3	16.7	14	2 S14336	mastoparan B - hor
26	3	16.7	14	2 PT0259	Ig heavy chain CRD
27	3	16.7	15	2 S49409	H+-transporting tw
28	3	16.7	15	2 PC2374	unidentified 22K p
29	3	16.7	15	2 S36897	ribosomal protein

30	16.7	15	2	E56819	PS I complex subun
31	16.7	15	2	PA0025	protein QA300026 -
32	16.7	15	2	PS0450	23K protein 4307 -
33	16.7	15	2	A60221	apolipoprotein A-I
34	16.7	15	2	A43839	beta-tubulin germ-
35	16.7	15	2	S66215	cartilage oligomer
36	16.7	15	2	PN0562	dystrophin-associa
37	16.7	15	2	A31902	bone acidic glycop
38	16.7	15	2	S66443	NAD(P) transhydrog
39	16.7	16	2	S35627	uvrX protein - pha
40	16.7	16	2	S29631	beta-glucosidase (
41	16.7	16	2	A47393	neuropeptide calla
42	16.7	16	2	PH1778	T cell receptor al
43	16.7	16	2	S10808	protein kinase C 1
44	16.7	16	2	B89821	hypothetical prote
45	16.7	17	1	A05168	conantokin G [vali
46	16.7	17	1	A44896	heat shock protein
47	16.7	18	2	S74195	epoxide hydrolase
48	16.7	18	2	S48863	cyclin C - mouse
49	16.7	18	2	S48241	NAD(P)H-flavin oxi
50	16.7	18	2	S54272	CTC 75 protein - h
51	16.7	18	2	PH1815	T cell receptor al
52	16.7	18	2	S66627	tau protein - huma
53	16.7	18	2	S78767	ribosomal protein
54	16.7	19	2	S28396	T-complex protein
55	16.7	19	2	C40634	orf21 5' of eryK -
56	16.7	19	2	S43624	cytochrome-c oxida
57	16.7	19	2	A49192	transhyretin - bu
58	16.7	19	2	I52721	gene hMLH1 protein
59	16.7	19	2	S68394	H+-transporting tw
60	16.7	20	2	B60894	crystallin - pacif
61	16.7	20	2	A33160	H+-transporting tw
62	16.7	20	2	D49164	chromogranin-B - r
63	16.7	20	2	S00492	hemocyanin chain I
64	16.7	20	2	PN0154	groEL-like protein
65	16.7	20	2	I65242	homotetic protein H
66	16.7	20	2	PL0039	outer membrane pro
67	16.7	20	2	S65746	hypothetical prote
68	16.7	20	2	S71017	hypothetical prote
69	16.7	20	2	PS0188	superoxide dismuta
70	16.7	20	2	B30208	hypothetical prote
71	16.7	20	2	S38763	S-adenosyl-L-methi
72	16.7	20	2	PC1151	equinatoxin 1C - s
73	16.7	20	2	B34016	tenabrosin B - sea
74	16.7	20	2	S78760	ribosomal protein
75	16.7	20	2	S56005	ribosomal protein
76	16.7	20	2	JP0056	ribosomal protein
77	11.1	3	3	A60898	bursin - chicken
78	11.1	3	3	PT0636	T-cell receptor be
79	11.1	4	2	I40697	biotin A - Citroba
80	11.1	4	2	A61300	22K superhelical D
81	11.1	4	2	S53508	starvation-induced
82	11.1	4	2	I61883	profamine p1 - ora
83	11.1	4	2	PT0645	T-cell receptor be
84	11.1	4	2	PT0677	T-cell receptor be
85	11.1	4	2	S52338	pallidipin - assas
86	11.1	4	2	I37013	profamine p1 - Cer
87	11.1	4	2	I84439	profamine p1 - sav
88	11.1	5	1	HOHOHA	proctolin - Americ
89	11.1	5	2	A32014	tram protein - Esc
90	11.1	5	2	I39664	ribosomal protein
91	11.1	5	2	I39966	ribosomal protein
92	11.1	5	2	I39965	ribosomal protein
93	11.1	5	2	I40469	dnazX-like protein
94	11.1	5	2	S70615	endo-1,4-beta-xyla
95	11.1	5	2	B45525	actin 1 - malaria
96	11.1	5	2	A60803	neuropeptide - sea
97	11.1	5	2	A44692	fulicin - giant Af
98	11.1	5	2	A60411	proctolin - Atlant
99	11.1	5	2	S11075	alcohol dehydrogen
100	11.1	5	2	PT0624	T-cell receptor be

PS I complex subun
protein QA300026 -
23K protein 4307 -
apolipoprotein A-I
beta-tubulin germ-
cartilage oligomer
dystrophin-associ
bone acidic glycop
NAD(P) transhydrog
uvrX protein - pha
beta-glucosidase (
neuropeptide calla
T cell receptor al
protein kinase C 1
hypothetical prote
conantokin G [vali
heat shock protein
epoxide hydrolase
cyclin C - mouse
NAD(P)H-flavin oxi
CTC 75 protein - h
T cell receptor al
tau protein - huma
ribosomal protein
T-complex protein
orf21 5' of eryK -
cytochrome-c oxida
transhyretin - bu
gene hMLH1 protein
H+-transporting tw
crystallin - pacif
H+-transporting tw
chromogranin-B - r
hemocyanin chain I
groEL-like protein
homotetic protein H
outer membrane pro
hypothetical prote
hypothetical prote
superoxide dismuta
hypothetical prote
S-adenosyl-L-methi
equinatoxin 1C - s
tenabrosin B - sea
ribosomal protein
ribosomal protein
ribosomal protein
bursin - chicken
T-cell receptor be
biotin A - Citroba
22K superhelical D
starvation-induced
profamine p1 - ora
T-cell receptor be
T-cell receptor be
pallidipin - assas
profamine p1 - Cer
profamine p1 - sav
proctolin - Americ
tram protein - Esc
ribosomal protein
ribosomal protein
ribosomal protein
dnazX-like protein
endo-1,4-beta-xyla
actin 1 - malaria
neuropeptide - sea
fulicin - giant Af
proctolin - Atlant
alcohol dehydrogen
T-cell receptor be

ALIGNMENTS

RESULT 1
S45648
Na+-transporting ATP synthase (EC 3.6.1.1-) alpha chain - Acetobacterium woodii (fragment)
N:Alternate names: ATPase alpha chain
C:Species: Acetobacterium woodii
C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
C:Accession: S45648
R:Reidlinger, J.; Mueller, V.
Eur. J. Biochem. 223, 275-283, 1994
A:Title: Purification of ATP synthase from Acetobacterium woodii and identification as a
A:Reference number: S45648; MUID:94307271; PMID:8033902
A:Accession: S45648
A:Molecule type: protein
A:Residues: 1-3;4-7 <REI>
A:Experimental source: DSM 1030
C:Keywords: hydrolase

Query Match 16.7%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EEI 14
|||
Db 5 EEI 7

RESULT 2
S66296
Na+-transporting ATP synthase (EC 3.6.1.1-) chain c - Acetobacterium woodii (fragment)
N:Alternate names: ATPase chain c
C:Species: Acetobacterium woodii
C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
C:Accession: S66296
R:Reidlinger, J.; Mueller, V.
Eur. J. Biochem. 223, 275-283, 1994
A:Title: Purification of ATP synthase from Acetobacterium woodii and identification as a
A:Reference number: S45648; MUID:94307271; PMID:8033902
A:Accession: S66296
A:Molecule type: protein
A:Residues: 1-8 <REI>
A:Experimental source: DSM 1030
C:Keywords: hydrolase

Query Match 16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EIL 15
|||
Db 2 EIL 4

RESULT 3
B20569
serum amyloid P-component - smooth dogfish (fragment)
C:Species: Mustelus canis (smooth dogfish)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Jun-1993
C:Accession: B20569; A05074
R:Rebey, P.A.; Tanaka, T.; Liu, T.Y.
J. Biol. Chem. 258, 3889-3894, 1983
A:Title: Isolation and characterization of two major serum proteins from the dogfish, Mu
A:Reference number: A92419; MUID:83160932; PMID:6403520
A:Accession: B20569
A:Molecule type: protein
A:Residues: 1-9 <ROB>
C:Keywords: amyloid

Query Match 16.7%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18
|||
Db 5 KSL 7

RESULT 4
PH0108
late G1-69 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH0108
R:Nikaido, T.; Bradley, D.W.; Pardee, A.B.
Exp. Cell Res. 192, 102-109, 1991
A:Title: Molecular cloning of transcripts that accumulate during the late G1 phase i:
A:Reference number: PH0108; MUID:91078351; PMID:1984406
A:Accession: PH0108
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-9 <NIK>

Query Match 16.7%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GEE 13
|||
Db 6 GEE 8

RESULT 5
XGHUE
erythrocyte membrane glycopeptide - human
C:Species: Homo sapiens (man)
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: A03187
R:Weiss, J.B.; Lote, C.J.; Bobinski, H.
Nature New Biol. 234, 25-26, 1971
A:Title: New low molecular weight glycopeptide containing triglucoylcysteine in hum.
A:Reference number: A03187; MUID:72034940; PMID:5286858
A:Accession: A03187
A:Molecule type: protein
A:Residues: 1-10 <WEI>
C:Comment: The identity of the glycoprotein from which this peptide is derived is un
found (see PIR:XGHUEU).
C:Superfamily: unassigned animal peptides
C:Keywords: Glycoprotein
F:1/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DHG 11
|||
Db 7 DHG 9

RESULT 6
C61440
polygalacturonase (EC 3.2.1.15) II b - Aspergillus sp. (fragment)
C:Species: Aspergillus sp.
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 06-Dec-1996
C:Accession: C61440
R:Stratilova, E.; Markovic, O.; Skrovinova, D.; Rexova-Benkova, L.; Jorvall, H.
J. Protein Chem. 12, 15-22, 1993
A:Title: Pectinase Aspergillus sp. polygalacturonase: multiplicity, divergence, and
A:Reference number: A61440; MUID:93151962; PMID:8427629
A:Accession: C61440
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <STP>
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 16.7%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFN 4
 |||
 Db 6 TFN 8

RESULT 7

S65395
 Chemical-sense-related lipophilic-ligand-binding protein - fruit fly (*Drosophila melanogaster*)
 C;Species: *Drosophila melanogaster*
 C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
 C;Accession: S65395
 R;Ozaki, M.; Morisaki, K.; Idei, W.; Ozaki, K.; Tokunaga, F.
 Eur. J. Biochem. 230, 298-308, 1995
 A;Title: A putative lipophilic stimulant carrier protein commonly found in the taste and
 A;Reference number: S65394; MUID:95324537; PMID:7601113
 A;Accession: S65395
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-11 <OZA>

Query Match 16.7%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EEI 14
 |||
 Db 2 EEI 4

RESULT 8

D45900
 complement C3b receptor type 2 - mouse (clone 12) (fragment)
 C;Species: *Mus musculus* (house mouse)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: D45900
 R;Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.
 J. Immunol. 144, 3581-3591, 1990
 A;Title: The murine complement receptor gene family. IV. Alternative splicing of Cr2 gene
 A;Reference number: A45900; MUID:90229754; PMID:2139460
 A;Accession: D45900
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A;Molecule type: mRNA
 A;Residues: 1-11 <KUR>

Query Match 16.7%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EEI 14
 |||
 Db 3 EEI 5

RESULT 9

S65377
 cytochrome-c oxidase (EC 1.9.3.1) chain via-H, cardiac - rat (fragment)
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
 C;Accession: S65377
 R;Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
 Eur. J. Biochem. 230, 235-241, 1995
 A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term
 A;Reference number: S65372; MUID:95324529; PMID:7601105
 A;Accession: S65377
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-11 <SCH>

C;Keywords: cardiac muscle; heart; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DHG 11
 |||
 Db 6 DHG 8

RESULT 10

I52708
 ELAV-like neuronal protein 1, truncated splice form - human
 N;Alternate names: *Drosophila* ELAV(embryonic lethal, abnormal vision)-like 4; Hu anti
 C;Species: *Homo sapiens* (man)
 C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
 C;Accession: I52708
 R;Sekido, Y.; Bader, S.A.; Carbone, D.P.; Johnson, B.E.; Minna, J.D.
 Cancer Res. 54, 4988-4992, 1994
 A;Title: Molecular analysis of the HuD gene encoding a paraneoplastic encephalomyelit
 A;Reference number: I52708; MUID:94349312; PMID:8069866
 A;Accession: I52708
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-11 <SEK>

A;Cross-references: GB:S73887; NID:G688242; PIDN:AD14142.1; PID:G4261842
 C;Comment: This abnormal peptide is expressed. For the long splice form, see PIR:I38;
 C;Genetics:
 A;Gene: GDB:ELAVL4; HUD; PNEU
 A;Cross-references: GDB:141875; OMIM:168360
 A;Map position: lp36-lp36
 C;Keywords: alternative splicing

Query Match 16.7%; Score 3; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILK 16
 |||
 Db 7 ILK 9

RESULT 11

B58503
 outer membrane porin protein OprD homolog - unidentified bacterium (fragment)
 N;Alternate names: 43K bile stone protein
 C;Species: unidentified bacterium
 C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
 C;Accession: B58503
 R;Binette, J.P.; Binette, M.B.
 submitted to the Protein Sequence Database, October 1996
 A;Description: The proteins of kidney and gallbladder stones.
 A;Reference number: A58501
 A;Accession: B58503
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-12 <BIN>

A;Experimental source: human bile with stones
 A;Note: sequenced along with secondary sequence MXIGVNEXL

Query Match 16.7%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QDD 9
 |||
 Db 3 QDD 5

RESULT 12

T46794
 hypothetical protein [imported] - *Haloarcula marismortui* (fragment)
 C;Species: *Haloarcula marismortui*

C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
C;Accession: T46794

R;Arndt, E.

PBS Lett. 267, 193-198, 1990

A;Title: Nucleotide sequence of four genes encoding ribosomal proteins from the 'S10 and A;Reference number: S10731; MUID:90336772; PMID:2143141

A;Accession: T46794

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-12 <ARN>

A;Cross-references: EMBL:X55311; NID:g43610; PIDN:CAA39015.1; PID:g43611

Query Match 16.7%; Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 4.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEE 13

|||

3 GEE 5

RESULT 13

S27023

N⁺/K⁺-exchanging ATPase (EC 3.6.3.9) alpha chain - monarch butterfly (fragment)

N;Alternate names: Na⁺/K⁺-transporting ATPase

C;Species: Danaus plexippus (monarch butterfly)

C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 19-Apr-2002

A;Accession: S27023

R;Holzinger, F.; Frick, C.; Wink, M.

PBS Lett. 314, 477-480, 1992

A;Title: Molecular basis for the insensitivity of the Monarch (Danaus plexippus) to card

A;Reference number: S27023; MUID:93106209; PMID:1334851

A;Accession: S27023

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-12 <HOL>

C;Keywords: hydrolase

Query Match

Best Local Similarity 16.7%; Score 3; DB 2; Length 12;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DDH 10

|||

10 DDH 12

RESULT 14

JQ2309

hypothetical 1.6K protein - tomato chloroplast (strain Toko)

C;Species: chloroplast Lycopersicon esculentum (tomato)

C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 23-Mar-1995

A;Accession: JQ2309

R;Kawagoe, Y.; Kikuta, Y.

Theor. Appl. Genet. 81, 13-20, 1991

A;Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).

A;Reference number: JQ2306

A;Accession: JQ2309

A;Molecule type: DNA

A;Residues: 1-13 <KAW>

A;Experimental source: strain Toko

C;Genetics:

A;Genome: chloroplast

C;Keywords: chloroplast

Query Match

Best Local Similarity 16.7%; Score 3; DB 2; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NRY 6

|||

11 NRY 13

RESULT 15

JQ2319

hypothetical 1.6K protein - potato chloroplast

C;Species: chloroplast Solanum tuberosum (potato)

C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 05-Jan-1996

A;Accession: JQ2319; JQ2314

R;Kawagoe, Y.; Kikuta, Y.

Theor. Appl. Genet. 81, 13-20, 1991

A;Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).

A;Reference number: JQ2306

A;Accession: JQ2319

A;Molecule type: DNA

A;Residues: 1-13 <KWL>

A;Experimental source: cv. W553-4

A;Accession: JQ2314

A;Molecule type: DNA

A;Residues: 1-13 <KW2>

A;Experimental source: cv. 150

C;Genetics:

A;Genome: chloroplast

C;Keywords: chloroplast

Query Match

Best Local Similarity 16.7%; Score 3; DB 2; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NRY 6

|||

11 NRY 13

RESULT 16

E60396

antigen 7H8/2 - malaria parasite (Plasmodium falciparum) (fragments)

C;Species: Plasmodium falciparum

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jun-2000

A;Accession: E60396

R;Limpaiboon, T.; Taylor, D.W.; Jones, G.; Geysen, H.M.; Saul, A.

Southeast Asian J. Trop. Med. Public Health 21, 388-396, 1990

A;Title: Characterization of a Plasmodium falciparum epitope recognized by a monoclo

A;Reference number: A60396; MUID:91164876; PMID:1706114

A;Accession: E60396

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-13 <LIM>

A;Cross-references: GB:M31305

Query Match

Best Local Similarity 16.7%; Score 3; DB 2; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKS 17

|||

2 LKS 4

RESULT 17

A23694

myosin heavy chain, smooth muscle - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 07-Feb-1997

A;Accession: A23694

R;Cole, D.G.; Yount, R.G.

J. Biol. Chem. 265, 22537-22546, 1990

A;Title: Photolabeling of the 6 and 10 S conformations of gizzard myosin with 3' (2')

A;Reference number: A23694; MUID:91093105; PMID:2266144

A;Accession: A23694

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <COL>

C;Keywords: smooth muscle

Query Match 16.7%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.5e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QDD 9
 ||||
 Db 11 QDD 13

RESULT 18
 A57789
 gallbladder stone matrix protein 1, 41K - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 03-May-1996
 C:Accession: A57789
 R:Binette, J.P.; Binette, M.B.
 A:Submitted to the Protein Sequence Database, February 1996
 A:Description: The proteins of gallbladder stones.
 A:Reference number: A57789
 A:Accession: A57789
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13 <BIN>
 A:Experimental source: two gallbladder, one bladder, one kidney stone of different patients
 A>Note: 9-Leu and 12-Lys were also found

Query Match 16.7%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.5e+03; Indels 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QDD 9
 ||||
 Db 3 QDD 5

RESULT 19
 E53275
 Ig kappa-1 chain J5 region (b95 allotype) - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 02-May-1994 #sequence_revision 01-Mar-1996 #text_change 20-Sep-1999
 C:Accession: E53275; E20907
 R:Ayadi, H.; Marche, P.N.; Cazenave, P.A.
 A:Immunogenetics 34, 201-207, 1991
 A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.
 A:Reference number: A53275; MUID:91372868; PMID:1509995
 A:Accession: E53275
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-13 <AYA>
 A>Note: sequence extracted from NCBI backbone (NCBIN:56069, NCBI:P:56169)
 R:Emorine, L.; Max, E.E.
 A:Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multiple
 A:Reference number: A20907; MUID:84169523; PMID:6324107
 A:Accession: E20907
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-12 <EMO>
 C:Comment: This J5 segment may not be functional because of substitutions in the 7 mer
 C:Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.5e+03; Indels 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEE 13
 ||||
 Db 4 GEE 6

RESULT 20
 LFEBWC
 trp operon leader peptide - Citrobacter freundii

C:Species: Citrobacter freundii
 C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 13-Nov-1998
 C:Accession: A03592
 R:Blumenberg, M.; Yanofsky, C.
 J. Bacteriol. 152, 57-62, 1982
 A:Title: Evolutionary divergence of the Citrobacter freundii tryptophan operon regulatory
 A:Reference number: A91792; MUID:83007061; PMID:6749821
 A:Accession: A03592
 A:Molecule type: DNA
 A:Residues: 1-14 <BLU>
 C:Genetics:
 A:Gene: trpL
 C:Function:
 A:Description: involved in control of tryptophan operon transcription by attenuation
 C:Superfamily: trp leader peptide

Query Match 16.7%; Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATF 3
 ||||
 Db 3 ATF 5

RESULT 21
 LFEBWT
 trp operon leader peptide - Salmonella typhimurium
 C:Species: Salmonella typhimurium
 C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 13-Nov-1998
 C:Accession: A03590
 R:Lee, F.; Bertrand, K.; Bennett, G.; Yanofsky, C.
 J. Mol. Biol. 121, 193-217, 1978
 A:Title: Comparison of the nucleotide sequences of the initial transcribed regions of
 A:Reference number: A92850; MUID:78196931; PMID:351195
 A:Accession: A03590
 A:Molecule type: DNA
 A:Residues: 1-14 <LEE>
 C:Genetics:
 A:Gene: trpL; trpE
 C:Function:
 A:Description: involved in control of tryptophan operon transcription by attenuation
 C:Superfamily: trp leader peptide

Query Match 16.7%; Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATF 3
 ||||
 Db 3 ATF 5

RESULT 22
 PS0249
 porin - rice (strain Nihonbare) (fragment)
 C:Species: Oryza sativa (rice)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
 C:Accession: PS0249
 R:Tsugita, A.
 A:Submitted to JIPID, April 1993
 A:Reference number: PS0206
 A:Accession: PS0249
 A:Molecule type: protein
 A:Residues: 1-14 <TSU>
 A:Experimental source: callus

Query Match 16.7%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DDH 10
 ||||

Db 6 DDH 8

RESULT 23
A39239
actin 8 - slime mold (Dictyostelium discoideum) (fragment)
C;Species: Dictyostelium discoideum
C;Date: 20-Sep-1991 #sequence_revision 20-Sep-1991 #text_change 18-Jun-1993
C;Accession: A39239
R;Frankel, S.; Condeelis, J.; Leinwand, L.
J. Biol. Chem. 265, 17980-17987, 1990
A;Title: Expression of actin in Escherichia coli. Aggregation, solubilization, and function
A;Reference number: A39239; MUID:91003269; PMID:2211676
A;Accession: A39239
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <FRA>

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.8e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TFN 4
|||
Db 8 TFN 10

RESULT 24
B61308
hemocyanin chain 3B - Sahara scorpion (fragment)
C;Species: Androctonus australis (Sahara scorpion)
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C;Accession: B61308
R;Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.
FEBS Lett. 106, 289-291, 1979
A;Title: Structural characterization of seven different subunits in Androctonus australis
A;Reference number: A61308; MUID:80047238; PMID:499512
A;Accession: B61308
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <JOL>

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.8e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ILK 16
|||
Db 9 ILK 11

RESULT 25
S14336
mastoparan B - hornet (Vespa basalis)
C;Species: Vespa basalis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Apr-1999
C;Accession: S14336
R;Ho, C.L.; Hwang, L.L.
Biochem. J. 274, 453-456, 1991
A;Title: Structure and biological activities of a new mastoparan isolated from the venom
A;Reference number: S14336; MUID:91174755; PMID:2006909
A;Accession: S14336
A;Molecule type: protein
A;Residues: 1-14 <HOC>
A;Experimental source: venom
C;Function:
A;Description: possesses a potent hemolytic activity which acts in synergy with the lethal
C;Keywords: amidated carboxyl end; mast cell; venom
F;14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.8e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKS 17
|||
Db 3 LKS 5

RESULT 26
PT0259
Ig heavy chain CDR3 region (clone 2-118C) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0259
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity at
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0259
A;Molecule type: DNA
A;Residues: 1-14 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotrimer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.8e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DHG 11
|||
Db 12 DHG 14

RESULT 27
S49409
H+-transporting two-sector ATPase (EC 3.6.3.14) chain a - Streptococcus oralis (frag
C;Species: Streptococcus oralis
C;Date: 29-Nov-1995 #sequence_revision 01-Aug-1997 #text_change 03-Jun-2002
C;Accession: S49409; S38211
R;Penoll, A.; Munoz, R.; Garcia, E.; de la Campa, A.G.
Mol. Microbiol. 12, 587-598, 1994
A;Title: Molecular basis of the optochin-sensitive phenotype of pneumococcus: charac
ases.
A;Reference number: S49398; MUID:95020593; PMID:7934882
A;Accession: S49409
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-15 <FEN>
A;Cross-references: EMBL:Z26853; NID:g407180; PIDN:CAA81457.1; PID:g809112
C;Superfamily: H+-transporting ATP synthase protein 6
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GEE 13
|||
Db 13 GEE 15

RESULT 28
PC2374
unidentified 22K protein [imported] - Bacillus cereus (strain ts-4) (fragment)
C;Species: Bacillus cereus
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: PC2374
R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwar, T.; Hatan, S.
Biosci. Biotechnol. Biochem. 59, 231-235, 1995
A;Title: Identification of DNA-binding proteins changed after induction of sporulati
A;Reference number: PC2369; MUID:95218265; PMID:7766022
A;Accession: PC2374
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <MAS>

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKS 17
 ||||
 Db 5 LKS 7

RESULT 29

S36897
 ribosomal protein S15 - Mycobacterium bovis (fragment)
 C;Species: Mycobacterium bovis
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
 C;Accession: S36897
 R;Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
 FEBS Lett. 331, 9-14, 1993
 A;Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobacterium bovis
 A;Reference number: S36887; MUID:94003653; PMID:8405418
 A;Accession: S36897
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-15 <OHA>
 C;Keywords: protein biosynthesis; ribosome

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EIL 15
 ||||
 Db 9 EIL 11

RESULT 30

E56819
 PS I complex subunit 8 - cucumber (fragment)
 C;Species: Cucumis sativus (cucumber)
 C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
 C;Accession: E56819
 R;Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.
 Biochim. Biophys. Acta 1059, 141-148, 1991
 A;Title: Characterization of genes that encode subunits of cucumber PS I complex by N-terminal amino acid sequence
 A;Reference number: A56819; MUID:9135209; PMID:1883835
 A;Accession: E56819
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-15 <IWA>
 A;Note: sequence extracted from NCBI backbone (NCBIP:58606)

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ODD 9
 ||||
 Db 12 ODD 14

RESULT 31

PA0025
 Protein Q300026 - Arabidopsis thaliana (fragment)
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C;Accession: PA0025
 R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPID, July 1994
 A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis
 A;Reference number: PA0001
 A;Accession: PA0025
 A;Molecule type: protein
 A;Residues: 1-15 <KAM>

A;Experimental source: leaf

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EEI 14
 ||||
 Db 4 EEI 6

RESULT 32

PS0450
 23K protein 4307 - rice (strain Nihonbare) (fragment)
 C;Species: Oryza sativa (rice)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
 C;Accession: PS0450
 R;Tsugita, A.; Miyatake, N.
 submitted to JIPID, April 1993
 A;Reference number: PS0208
 A;Accession: PS0450
 A;Molecule type: protein
 A;Residues: 1-15 <TSU>
 A;Experimental source: germ, strain Nihonbare
 C;Comment: molecular weight 23K, pI 5.3.

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YQD 8
 ||||
 Db 2 YQD 4

RESULT 33

A60221
 apolipoprotein A-I - common carp (fragment)
 C;Species: Cyprinus carpio (common carp)
 C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 31-Dec-1993
 C;Accession: A60221
 R;Harel, A.; Paimaru, M.; Rubinstein, M.; Tal, N.; Schwartz, M.
 J. Neurochem. 55, 1237-1243, 1990
 A;Title: Fish apolipoprotein A-I has heparin binding activity: implication for nerve conduction
 A;Reference number: A60221; MUID:90376100; PMID:2118944
 A;Accession: A60221
 A;Molecule type: protein
 A;Residues: 1-15 <HAR>
 A;Note: protein from plasma and from optic nerve yielded the same sequence
 C;Keywords: lipid binding; lipoprotein

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKS 17
 ||||
 Db 10 LKS 12

RESULT 34

A43839
 beta-tubulin germ-cell isotype - African clawed frog (fragment)
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
 C;Accession: A43839
 R;Bieker, J.J.; Yazdani-Buicky, M.
 Differentiation 50, 15-23, 1992
 A;Title: The multiple beta-tubulin genes of Xenopus: isolation and developmental expression
 A;Reference number: A43839; MUID:92347627; PMID:1379202
 A;Accession: A43839
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid

A;Residues: 1-15 <BIE>
 A;Experimental source: oocyte
 A;Note: sequence extracted from NCBI backbone (NCBIP:110252)

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEE 13
 |||
 Db 9 GEE 11

RESULT 35

S66215
 cartilage oligomeric matrix protein - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C;Accession: S66215
 R;Hauser, N.; Paulsson, M.; Kale, A.A.; DiCesare, P.E.
 FEBS Lett. 368, 307-310, 1995
 A;Title: Tendon extracellular matrix contains pentameric thrombospondin-4 (TSP-4).
 A;Reference number: S66214; MUID:95354859; PMID:7628627
 A;Accession: S66215
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-15 <HAU>

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FNR 5
 |||
 Db 12 FNR 14

RESULT 36

PN0662
 dystrophin-associated glycoprotein A3a-I - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
 C;Accession: PN0662
 R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
 J. Biochem. 114, 634-639, 1993
 A;Title: A dystrophin-associated glycoprotein, A3a (one of 430AG doublets), is retained
 A;Reference number: PN0662; MUID:94156881; PMID:8113213
 A;Accession: PN0662

A;Molecule type: protein
 A;Residues: 1-15 <YOS>
 C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
 C;Keywords: glycoprotein; skeletal muscle

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATF 3
 |||
 Db 3 ATF 5

RESULT 37

A31902
 bone acidic glycoprotein-75 - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 31-Dec-1993
 C;Accession: A31902
 R;Gorski, J.P.; Shimizu, K.
 J. Biol. Chem. 263, 15938-15945, 1988
 A;Title: Isolation of new phosphorylated glycoprotein from mineralized phase of bone
 A;Reference number: A31902; MUID:89034045; PMID:2846530
 A;Accession: A31902

A;Molecule type: protein
 A;Residues: 1-15 <GOR>
 A;Note: 14-Glu and 15-Glu were also found
 C;Keywords: glycoprotein

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RYQ 7
 |||
 Db 5 RYQ 7

RESULT 38

S66443
 NAD(P) transhydrogenase (B-specific) (EC 1.6.1.1) - Rhodospirillum rubrum (fragments)
 N;Alternate names: proton-translocating transhydrogenase
 C;Species: Rhodospirillum rubrum
 C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 03-Jun-2002
 C;Accession: S66443
 R;Diggle, C.; Cotton, N.P.J.; Grimley, R.L.; Quirk, P.G.; Thomas, C.M.; Jackson, J.B.
 Eur. J. Biochem. 232, 315-326, 1995
 A;Title: Conformational dynamics of a mobile loop in the NAD(H)-binding subunit of P
 A;Reference number: S66443; MUID:96048062; PMID:7556167
 A;Accession: S66443
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-5;6-10;11-15 <DIG>
 C;Keywords: oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEE 13
 |||
 Db 12 GEE 14

RESULT 39

uvxX protein - phase T6 (fragment)
 C;Species: phase T6
 C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 08-Oct-1999
 C;Accession: S35627
 R;Winkler, M.; Rueger, W.
 Nucleic Acids Res. 21, 1500, 1993
 A;Title: Cloning and sequencing of the genes of beta-glucosyl-HMC-alpha-glucosyl-tra
 A;Reference number: S35622; MUID:93219141; PMID:8464751
 A;Accession: S35627
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-16 <WIN>
 A;Cross-references: EMBL:X68725; NID:9296439; PIDN:CAA48668.1; PID:g296441
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992

Query Match 16.7%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKS 17
 |||
 Db 6 LKS 8

RESULT 40

S29631
 beta-glucosidase (EC 3.2.1.21) - Thermotoga sp. (strain FJSS3-B.1) (fragment)
 C;Species: Thermotoga sp.
 A;Variety: FJSS3-B.1
 C;Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 07-May-1999
 C;Accession: S29631

R;Ruttersmith, L.D.; Daniel, R.M.
 Biochim. Biophys. Acta 1156, 167-172, 1993
 A;Title: Thermostable beta-glucosidase and beta-xylosidase from *Thermotoga* sp. strain Fj
 A;Reference number: S29631; MUID:93152594; PMID:8427876
 A;Accession: S29631
 A;Molecule type: protein
 A;Residues: 1-16 <RUT>
 A;Experimental source: strain FjSS3-B.1
 C;Function:
 A;Description: catalyzes the hydrolysis of terminal, nonreducing 1,4-linked beta-D-glucose
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 16.7%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EIL 15
 |||
 Db 6 EIL 8

RESULT 41
 A47393
 neuropeptide callatostatin 1 - bluebottle fly (*Calliphora vomitoria*)
 N;Contains: neuropeptide callatostatin 2
 C;Species: *Calliphora vomitoria*
 C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
 C;Accession: A47393; B47393; G47393
 R;Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.
 Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
 A;Title: Callatostatins: neuropeptides from the blowfly *Calliphora vomitoria* with sequen
 A;Reference number: A47393; MUID:93211980; PMID:8460157
 A;Accession: A47393
 A;Molecule type: protein
 A;Residues: 1-16 <DUV>
 A;Experimental source: thoracic ganglia, brains, heads
 A;Note: sequence extracted from NCBI backbone (NCBIP:128476)
 A;Accession: B47393
 A;Molecule type: protein
 A;Residues: 3-16 <DU2>
 A;Experimental source: head
 A;Note: sequence extracted from NCBI backbone (NCBIP:128477)
 A;Accession: C47393
 A;Molecule type: protein
 A;Residues: 1-8 <DU3>
 A;Experimental source: thoracic ganglia
 A;Note: sequence extracted from NCBI backbone (NCBIP:128478)
 C;Function:
 A;Description: inhibits juvenile hormone production
 C;Keywords: amidated carboxyl end; neuropeptide
 F;1-16/Product: callatostatin 1 #status experimental <MAL>
 F;3-16/Product: callatostatin 2 #status experimental <MA2>
 F;9-16/Product: callatostatin 3 #status experimental <MA3>
 F;16/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NRY 6
 |||
 Db 10 NRY 12

RESULT 42
 PH1778
 T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (fragment)
 C;Species: *Homo sapiens* (man)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C;Accession: PH1778
 R;Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
 J. Exp. Med. 178, 1-16, 1993
 A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A;Reference number: PH1754; MUID:93301585; PMID:8391057
 A;Accession: PH1778
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-16 <POR>

Query Match 16.7%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFN 4
 |||
 Db 8 TFN 10

RESULT 43
 S10808
 protein kinase C inhibitor KCIP-1 isoform e - sheep (fragment)
 N;Alternate names: probable lipocortin
 C;Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)
 C;Date: 19-Mar-1997 #sequence_revision 13-Sep-1998 #text_change 13-Sep-1998
 C;Accession: S10808
 R;Toker, A.; Ellis, C.A.; Sellers, L.A.; Aitken, A.
 Eur. J. Biochem. 191, 421-429, 1990
 A;Title: Protein kinase C inhibitor proteins. Purification from sheep brain and sequen
 A;Reference number: S10804; MUID:90345949; PMID:2143472
 A;Accession: S10808
 A;Molecule type: protein
 A;Residues: 1-16 <TOK>
 A;Experimental source: brain

Query Match 16.7%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QDD 9
 |||
 Db 14 QDD 16

RESULT 44
 B83821
 hypothetical protein [imported] - *Staphylococcus aureus* (strain N315)
 C;Species: *Staphylococcus aureus*
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C;Accession: B83821
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; C
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A;Reference number: A89758; MUID:21311952; PMID:11418146
 A;Accession: B89821
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-16 <KUR>
 A;Cross-references: GB:BA000018; PID:gl3700427; PIDN:BA841725.1; GSPDB:GN00149
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: SAS015

Query Match 16.7%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RYQ 7
 |||
 Db 8 RYQ 10

RESULT 45
 A05166

conantokin G [validated] - cone shell (Conus geographus)
N:Alternate names: conotoxin GV; sleeper peptide
C:Species: Conus geographus (geography cone)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 15-Sep-2000
C:Accession: A05168

R:McIntosh, J.M.; Olivera, B.M.; Cruz, L.J.; Gray, W.R.
J. Biol. Chem. 259, 14343-14346, 1984
A:Title: gamma-Carboxylglutamate in a neuroactive toxin.
A:Reference number: A05168, MUID:85054897; PMID:6501296
A:Accession: A05168
A:Molecule type: protein

A:Residues: 1-17 <MC1>
R:Rigby, A.C.; Baleja, J.D.; Furie, B.C.; Furie, B.
submitted to the Brookhaven Protein Data Bank, February 1997
A:Reference number: A67471; PDB:1AD7
A:Contents: annotation; conformation by (1)H-NMR, residues 1-17
R:Rigby, A.C.; Baleja, J.D.; Furie, B.C.; Furie, B.
Biochemistry 36, 6906-6914, 1997

A:Title: Three-dimensional structure of a gamma-carboxylglutamic acid-containing conotoxin
A:Reference number: A58650; MUID:97332451; PMID:9188685
A:Contents: annotation; conformation by (1)H-NMR
C:Superfamily: conantokin

C:Keywords: amidated carboxyl end; carboxylglutamic acid; neurotoxin; venom
F:3,4,7,10,14/Modified site: gamma-carboxylglutamic acid (Glu) #status experimental
F:17/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 16.7%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GEE 13
|||
Db 1 GEE 3

RESULT 46

A44896

heat shock protein 18 - Streptomyces albus (fragment)

C:Species: Streptomyces albus
C>Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 12-Sep-1997
C:Accession: A44896

R:Guglielmi, G.; Mazodier, P.; Thompson, C.J.; Davies, J.
J. Bacteriol. 173, 7374-7381, 1991

A:Title: A survey of the heat shock response in four Streptomyces species reveals two genes
A:Reference number: A44896; MUID:92041638; PMID:1682303

A:Accession: A44896

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-17 <GUG>

A>Note: sequence extracted from NCBI backbone (NCBIP:65105)

C:Superfamily: chaparonin groEL

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ILK 16
|||
Db 3 ILK 5

RESULT 47

S74195

epoxide hydrolase (EC 3.3.2.3), microsomal - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 17-Mar-1999

C:Accession: S74195

R:Araya, Z.; Hellman, U.; Hansson, R.
Eur. J. Biochem. 231, 855-861, 1995

A:Title: Characterisation of taurochenodeoxycholic acid 6-alpha-hydroxylase from pig liver

A:Reference number: S66455; MUID:95377322; PMID:7649186

A:Accession: S74195

A:Molecule type: protein

A:Residues: 1-18 <ARA>
A:Experimental source: liver
C:Superfamily: epoxide hydrolase
C:Keywords: ether hydrolase

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EIL 15
|||
Db 4 EIL 6

RESULT 48

S48863

cyclin C - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999

C:Accession: S48863

R:Wu, L.; Hall, F.L.

submitted to the EMBL Data Library, October 1994

A:Reference number: S48863

A:Accession: S48863

A:Molecule type: mRNA

A:Residues: 1-18 <WUL>

A:Cross-references: EMBL:X82403; NID:G563901; PIDN:CAA57797.1; PID:G563902

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKS 17
|||
Db 5 LKS 7

RESULT 49

S46241

NAD(P)H-flavin oxidoreductase (EC 1.-.-.-) - Vibrio fischeri

C:Species: Vibrio fischeri

C>Date: 10-Dec-1994 #sequence_revision 12-May-1995 #text_change 16-Oct-1998

C:Accession: S46241

R:Inouye, S.

FEBS Lett. 347, 163-168, 1994

A:Title: NAD(P)H-flavin oxidoreductase from the bioluminescent bacterium, Vibrio fischeri

A:Reference number: S46241; MUID:94307374; PMID:8033996

A:Accession: S46241

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 <INO>

C:Keywords: NAD; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NRY 6
|||
Db 10 NRY 12

RESULT 50

S54272

CTC 75 protein - human

C:Species: Homo sapiens (man)

C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999

C:Accession: S54272

R:Genersch, E.; Eckerskorn, C.; Lottspeich, F.; Herzog, C.; Kuehn, K.; Poeschl, E.

EMBO J. 14, 791-800, 1995

A:Title: Purification of the sequence-specific transcription factor CTCBP, involved

A:Reference number: S54272; MUID:95188883; PMID:7882982

A:Accession: S54272

A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <GEN>

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFN 4
|||
Db 2 TFN 4

RESULT 51

PH1815
T cell receptor alpha chain V region (clone 4PBL V alpha 24-7) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1815
R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993

A>Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; MUID:93301585; PMID:8391057

A:Accession: PH1815

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-18 <FOR>

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NRY 6
|||
Db 7 NRY 9

RESULT 52

S66627
tau protein - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S66627
R:Moreno, F.J.; Medina, M.; Perez, M.; Montejo de Garcini, E.; Avila, J.
FEBS Lett. 372, 65-68, 1995

A>Title: Glycogen synthase kinase 3 phosphorylates recombinant human tau protein at ser1

A:Reference number: S66627; MUID:96032547; PMID:7556645

A:Accession: S66627

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8;9-18 <WOR>

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFN 4
|||
Db 4 TFN 6

RESULT 53

S78767
ribosomal protein MRP-S29, mitochondrial - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: S78767
R:Grack, H.R.

submitted to the Protein Sequence Database, July 1999

A:Reference number: S78760

A:Accession: S78767

A:Molecule type: protein

A:Residues: 1-18 <GRA>
C:Keywords: mitochondrial
F:1-18/Product: ribosomal protein MRP-S29 (fragment) #status experimental <NAT>

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILK 16
|||
Db 6 ILK 8

RESULT 54

S28396
T-complex protein 1 - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 04-Sep-1998
C:Accession: S28396
R:Frydman, J.; Nimmesgern, E.; Erdjument-Bromage, H.; Wall, J.S.; Tempst, P.; Hartl, R.

EMBO J. 11, 4767-4778, 1992

A>Title: Function in protein folding of TRiC, a cytosolic ring complex containing TCP

A:Reference number: S28395; MUID:93099850; PMID:1361170

A:Accession: S28396

A:Molecule type: protein

A:Residues: 1-19 <FRY>

C:Superfamily: molecular chaperone t-complex-type

Query Match 16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QDD 9
|||
Db 2 QDD 4

RESULT 55

C40634
orf21 5' of eryK - Saccharopolyspora erythraea (fragment)
C:Species: Saccharopolyspora erythraea
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 22-Oct-1999
C:Accession: C40634
R:Stassi, D.; Donadio, S.; Staver, M.J.; Katz, L.

J. Bacteriol. 175, 182-189, 1993

A>Title: Identification of a Saccharopolyspora erythraea gene required for the final

A:Reference number: A40634; MUID:93106953; PMID:8416893

A:Accession: C40634

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-19 <STA>

A:Cross-references: GB:U82823; GB:L05776; NID:G2327012; PIDN:AA45585.1; PID:G2327021

A>Note: sequence extracted from NCBI backbone (NCBIN:121243, NCBIPI:121246)

Query Match 16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEE 13
|||
Db 11 GEE 13

RESULT 56

S43624
cytochrome-c oxidase (EC 1.9.3.1) chain IV, cardiac - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 16-Jul-1999
C:Accession: S43624
R:Freund, R.; Kadenbach, B.

Eur. J. Biochem. 221, 1111-1116, 1994

A>Title: Identification of tissue-specific isoforms for subunits Vb and V1fa of cyto

A:Reference number: S43624; MUID:94237150; PMID:8181469

A:Accession: S43624
 A:Molecule type: protein
 A:Residues: 1-19 <PRE>
 A>Note: the source is designated as Salmo gairdneri
 C:Genetics:
 A:Genome: nuclear
 C:Keywords: cardiac muscle; heart; membrane-associated complex; mitochondrion; oxidoredu

Query Match 16.7%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGE 12
 ||||
 Db 3 HGE 5

RESULT 57
 A49192
 transthyretin - bullfrog (fragment)
 N:Alternate names: 3,5,3'-L-triiodothyronine-specific binding protein
 C:Species: Rana catesbeiana (bullfrog)
 C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995
 C:Accession: A49192
 R:Yamauchi, K.; Kasahara, T.; Hayashi, H.; Horiuchi, R.
 Endocrinology 132, 2254-2261, 1993
 A:Title: Purification and characterization of a 3,5,3'-L-triiodothyronine-specific binding protein
 A:Reference number: A49192; MUID:93238653; PMID:8477670
 A:Accession: A49192
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-19 <YAM>
 A:Experimental source: tadpole plasma
 A>Note: sequence extracted from NCBI backbone (NCBIP:130235)

Query Match 16.7%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGE 12
 ||||
 Db 2 HGE 4

RESULT 58
 I52721
 gene hMLH1 protein - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
 C:Accession: I52721
 R:Charbonnier, F.; Martin, C.; Scotte, M.; Sibert, L.; Moreau, V.; Frebourg, T.
 Cancer Res. 55, 1839-1841, 1995
 A:Title: Alternative splicing of MLH1 messenger RNA in human normal cells.
 A:Reference number: I52721; MUID:95246019; PMID:7728749
 A:Accession: I52721
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-19 <RES>
 A:Cross-references: GB:S77856; NID:g998493; PIDN:AAB34135.1; PID:g998494
 C:Genetics:
 A:Gene: hMLH1

Query Match 16.7%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YQD 8
 ||||
 Db 3 YQD 5

RESULT 59
 S68394

H+-transporting two-sector ATPase (EC 3.6.3.14) chain G - Chlamydomonas reinhardtii
 N:Alternate names: ATP synthase chain G
 C:Species: Chlamydomonas reinhardtii
 C>Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 03-Jun-2002
 C:Accession: S68394
 R:Fiedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.
 FEBS Lett. 377, 163-166, 1995
 A:Title: Isolation of CF(0)CF(1) from Chlamydomonas reinhardtii cw15 and the N-termi
 A:Reference number: S68388; MUID:96128220; PMID:8543042
 A:Accession: S68394
 A:Molecule type: protein
 A:Residues: 1-19 <FIE>
 A:Experimental source: strain CW15
 C:Genetics:
 A:Genome: nuclear
 C:Keywords: chloroplast; hydrolase

Query Match 16.7%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GEE 13
 ||||
 Db 16 GEE 18

RESULT 60
 B60894
 crystallin - Pacific cuttlefish (fragment)
 C:Species: Sepia esculenta (Pacific cuttlefish)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jun-1994
 C:Accession: B60894
 R:Chiou, S.H.
 J. Protein Chem. 7, 527-534, 1988
 A:Title: The protein sequence homology of gamma-crystallins among major vertebrate c
 A:Reference number: A60894; MUID:89351593; PMID:3255376
 A:Accession: B60894
 A:Molecule type: protein
 A:Residues: 1-20 <CHI>
 C:Superfamily: glutathione transferase
 C:Keywords: eye lens

Query Match 16.7%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EIL 15
 ||||
 Db 15 EIL 17

RESULT 61
 A33160
 H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 03-Jun-2002
 C:Accession: A33160
 R:Godinot, C.
 submitted to the Protein Sequence Database, February 1991
 A:Reference number: A33160
 A:Accession: A33160
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <GOD>
 C:Superfamily: H+-transporting ATP synthase gamma chain
 C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;

Query Match 16.7%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKS 17
 ||||

Db 10 LKS 12

RESULT 62

D49164

chromogranin-B - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-May-1997

C:Accession: D49164

R;Nielsen, E.; Welinder, B.S.; Madsen, O.D.

Endocrinology 129, 3147-3156, 1991

A:Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides th

A:Reference number: A49164; MUID:92063871; PMID:1954895

A:Accession: D49164

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <NIE>

A>Note: sequence extracted from NCBI backbone (NCBIP:66368)

C:Superfamily: chromogranin B precursor

Query Match 16.7%; Score 3; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEE 13

Db 17 GEE 19

RESULT 63

S00492

hemocyanin chain Ia - Japanese spiny lobster (fragment)

C:Species: Panulirus japonicus (Japanese spiny lobster)

C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 01-Aug-1997

C:Accession: S00492

R;Makino, N.; Kimura, S.

Eur. J. Biochem. 173, 423-430, 1988

A:Title: Subunits of Panulirus japonicus hemocyanin. 1. Isolation and properties.

A:Reference number: S00492; MUID:88196131; PMID:3360019

A:Accession: S00492

A:Molecule type: protein

A:Residues: 1-20 <MAK>

C:Superfamily: hemocyanin

C:Keywords: copper; hemolymph; hexamer; oxygen carrier

Query Match 16.7%; Score 3; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QDD 9

Db 17 QDD 19

RESULT 64

PN0154

groEL-like protein - Thermus aquaticus (fragment)

C:Species: Thermus aquaticus

C>Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 17-Mar-1999

C:Accession: PN0154

R;Mikulik, K.; Benada, O.

Biochem. Biophys. Res. Commun. 197, 716-721, 1993

A:Title: GroEL-like protein complex of thermophilic bacterium Thermus aquaticus.

A:Reference number: PN0154; MUID:94092153; PMID:7903530

A:Accession: PN0154

A:Molecule type: protein

A:Residues: 1-20 <MTK>

C:Comment: GroEL-like particles are homo-oligomeric complexes of two stacked seven membe

TPase activity in the presence of Mg2+ and K+.

C:Superfamily: chaperonin groEL

C:Keywords: molecular chaperone

Query Match 16.7%; Score 3; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILK 16

Db 3 ILK 5

RESULT 65

I65242

homeotic protein Hox-1 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 15-Oct-1999

C:Accession: I65242

R;Sakoyama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.

Biochem. Genet. 32, 351-360, 1994

A:Title: Cloning of rat homeobox genes.

A:Reference number: I52340; MUID:95217128; PMID:7702549

A:Accession: I65242

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-20 <RES>

A:Cross-references: GB:S76293; NID:g913078

C:Genetics:

A:Gene: Hox-A, Hox-1

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 16.7%; Score 3; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RYQ 7

Db 10 RYQ 12

RESULT 66

PL0039

outer membrane protein C class 5 - Neisseria meningitidis (fragment)

C:Species: Neisseria meningitidis

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1993

C:Accession: PL0039

R;Achman, M.; Neibert, M.; Crowe, B.A.; Strittmatter, W.; Kusecek, B.; Weyse, E.; Wa

J. Exp. Med. 168, 507-525, 1988

A:Title: Purification and characterization of eight class 5 outer membrane protein va

A:Reference number: PL0038; MUID:88316168; PMID:2457646

A:Accession: PL0039

A:Molecule type: protein

A:Residues: 1-20 <ACH>

A>Note: residues 17-18 are probably Lys-Ser

C:Comment: The Neisseria meningitidis class 5 proteins are proposed to correspond to

C:Keywords: membrane protein

Query Match 16.7%; Score 3; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKS 17

Db 16 LKS 18

RESULT 67

S65746

hypothetical protein 2 - Yersinia pseudotuberculosis (fragment)

C:Species: Yersinia pseudotuberculosis

C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 31-Mar-1997

C:Accession: S65746

R;Hobbs, M.; Reeves, P.R.

Biochim. Biophys. Acta 1245, 273-277, 1995

A:Title: Genetic organisation and evolution of Yersinia pseudotuberculosis 3,6-dideox

A:Reference number: S65746; MUID:96125720; PMID:8541300

A;Accession: S65746
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-20 <HOB>

Query Match 16.7%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKS 17
 ||||
 Db 11 LKS 13

RESULT 68

S71017
 hypothetical protein - Streptococcus pneumoniae (fragment)
 C;Species: Streptococcus pneumoniae
 C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
 C;Accession: S71017
 R;Martin, B.; Sharples, G.J.; Humbert, O.; Lloyd, R.G.; Claverys, J.P.
 Mol. Microbiol. 19, 1035-1045, 1996
 A;Title: The mmsA locus of Streptococcus pneumoniae encodes a RecG-like protein involved
 A;Reference number: S71015; MUID:96249697; PMID:8830261
 A;Accession: S71017
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-20 <MAR>
 A;Cross-references: EMBL:Z49988
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995

Query Match 16.7%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 BEI 14
 ||||
 Db 8 BEI 10

RESULT 69

PS0188
 superoxide dismutase (EC 1.15.1.1) (Cu-Zn), chloroplast - rice (fragment)
 C;Species: Oryza sativa (rice)
 C;Date: 05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change 05-Mar-1999
 C;Accession: PS0188
 R;Kawakami, T.; Tsugita, A.
 submitted to JIPID, June 1991
 A;Reference number: PS0187
 A;Accession: PS0188
 A;Molecule type: protein
 A;Residues: 1-20 <KAW>
 A;Experimental source: leaf
 C;Function:
 A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 C;Keywords: chloroplast; copper; metalloprotein; oxidoreductase; zinc

Query Match 16.7%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ILK 16
 ||||
 Db 8 ILK 10

RESULT 70

B30208
 hypothetical protein 1 (cpc-1 5' region) - Neurospora crassa
 C;Species: Neurospora crassa
 C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
 C;Accession: B30208
 R;Paluh, J.L.; Orbach, M.J.; Legerton, T.L.; Yanofsky, C.

Proc. Natl. Acad. Sci. U.S.A. 85, 3728-3732, 1988

A;Title: The cross-pathway control gene of Neurospora crassa, cpc-1, encodes a protease

A;Reference number: A30208; MUID:88234499; PMID:2967496

A;Accession: B30208

A;Molecule type: DNA

A;Residues: 1-20 <PAL>

A;Cross-references: GB:J03262

Query Match 16.7%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18
 ||||
 Db 3 KSL 5

RESULT 71

S38763
 S-adenosyl-L-methionine decarboxylase alpha chain - Acanthamoeba castellanii
 C;Species: Acanthamoeba castellanii
 C;Date: 08-Jun-1994 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
 C;Accession: S38763
 R;Hugo, E.R.; Byers, T.J.
 Biochem. J. 295, 203-209, 1993
 A;Title: S-Adenosyl-L-methionine decarboxylase of Acanthamoeba castellanii (Neff): protein
 A;Reference number: S38763; MUID:94029912; PMID:8216217
 A;Accession: S38763
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <HUG>

Query Match 16.7%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ILK 16
 ||||
 Db 12 ILK 14

RESULT 72

PC1151
 equinotoxin 1C - sea anemone (Actinia equina) (fragment)
 C;Species: Actinia equina
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: PC1151
 R;Komatsu, S.; Furukawa, K.; Abe, K.; Hirano, H.; Ueda, M.
 Chem. Pharm. Bull. 40, 2873-2875, 1992
 A;Title: Isolation and characterization of equinotoxins from the sea anemone Actinia
 A;Reference number: PC1149; MUID:93099631; PMID:1361161
 A;Accession: PC1151
 A;Molecule type: protein
 A;Residues: 1-20 <KOW>
 C;Keywords: toxin

Query Match 16.7%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TFN 4
 ||||
 Db 15 TFN 17

RESULT 73

B34016
 tenebrosin B - sea anemone (Actinia tenebrosa) (fragment)
 C;Species: Actinia tenebrosa
 C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 30-Sep-1993
 C;Accession: B34016
 R;Norton, R.S.; Bobek, G.; Ivanov, J.O.; Thomson, M.; Fiala-Beer, E.; Moritz, R.L.;
 Toxicon 28, 29-41, 1990

A:Title: Purification and characterisation of proteins with cardiac stimulatory and haem
A:Reference number: A34016; MUID:90232538; PMID:1970442
A:Accession: B34016
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <NOR>

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFN 4
|||
Db 15 TFN 17

RESULT 74

S78760
ribosomal protein MRP-L4, mitochondrial - bovine (fragments)
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: S78760
R:Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A:Reference number: S78760
A:Accession: S78760
A:Molecule type: protein
A:Residues: 1-11;12-20 <GRA>
C:Keywords: mitochondrion

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATF 3
|||
Db 6 ATF 8

RESULT 75

S56005
lysosomal protein 22K - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C:Accession: S56005
R:Kuwana, T.; Mullock, B.M.; Luzio, J.P.
Biochem. J. 308, 937-946, 1995
A:Title: Identification of a lysosomal protein causing lipid transfer, using a fluoresce
A:Reference number: S56005; MUID:97104296; PMID:8948454
A:Accession: S56005
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <KUW>

Query Match 16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
|||
Db 16 KSL 18

Search completed: November 25, 2003, 19:36:13
Job time : 13.3488 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model
Run on: November 25, 2003, 18:17:40 ; Search time 6.38372 Seconds
(without alignments)
132.600 Million cell updates/sec

Title: US-09-641-801-30
Perfect score: 18
Sequence: 1 ATFNRYQDDHGEEILKSL 18

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	22.2	10	1	TEMK_RANTE
2	3	16.7	9	1	SAMP_MUSCA
3	3	16.7	10	1	GLEM_HUMAN
4	3	16.7	10	1	SPI_HALRO
5	3	16.7	10	1	SYK_CAMUP
6	3	16.7	10	1	URAT_HUMAN
7	3	16.7	13	1	ODPA_CANFA
8	3	16.7	13	1	RS19_ASHYP
9	3	16.7	14	1	LPW_CITFR
10	3	16.7	14	1	LPW_SALTY
11	3	16.7	14	1	MAST_VRSBA
12	3	16.7	15	1	AFPS_MALPA
13	3	16.7	15	1	CKX_WHEAT
14	3	16.7	15	1	ITRB_ALBUJU
15	3	16.7	15	1	METK_MAIZE
16	3	16.7	15	1	MM01_RAT
17	3	16.7	15	1	PSAO_CUUSA
18	3	16.7	15	1	TRPA_LSUMA
19	3	16.7	16	1	ALLI_CALVO
20	3	16.7	16	1	UVSX_BPT6
21	3	16.7	17	1	GSHX_PINPS
22	3	16.7	19	1	ADC_GLOPA
23	3	16.7	19	1	COXI_ONCMY
24	3	16.7	19	1	DCAM_AACA
25	3	16.7	19	1	TRPB_KLEAE
26	3	16.7	20	1	AF2L_MALPA
27	3	16.7	20	1	FIBB_FELCA
28	3	16.7	20	1	HCVI_PANJA
29	3	16.7	20	1	M117_BOVIN
30	3	16.7	20	1	SODM_HORVU
31	3	16.7	20	1	TENB_ACTTE
32	2	11.1	5	1	BIOA_CITFR
33	2	11.1	5	1	PARP_ARTTR

34	2	11.1	5	1	PRCT_PERAM
35	2	11.1	5	1	TRM3_SCOLI
36	2	11.1	6	1	UN06_CLOPA
37	2	11.1	7	1	CIA_ENTFA
38	2	11.1	7	1	E105_LITRU
39	2	11.1	7	1	FAR1_PROCL
40	2	11.1	7	1	FAR3_HABCO
41	2	11.1	7	1	FAR3_PANRE
42	2	11.1	7	1	LANC_CARUI
43	2	11.1	7	1	UC24_MAIZE
44	2	11.1	7	1	UF03_MOUSE
45	2	11.1	8	1	AKH_TABAT
46	2	11.1	8	1	B44K_PORGI
47	2	11.1	8	1	CAD1_ENTFA
48	2	11.1	8	1	FAR4_HOMAM
49	2	11.1	8	1	HTF2_PERAM
50	2	11.1	8	1	LCK1_LEUMA
51	2	11.1	8	1	LCK3_LEUMA
52	2	11.1	8	1	LPMS_STAEP
53	2	11.1	8	1	RS1_EWCH
54	2	11.1	8	1	RT34_BOVIN
55	2	11.1	8	1	UPAA_HUMAN
56	2	11.1	9	1	AL11_CARMA
57	2	11.1	9	1	ALC_CHLRE
58	2	11.1	9	1	BS43_SERPL
59	2	11.1	9	1	D1_NEPNO
60	2	11.1	9	1	DSIP_RABIT
61	2	11.1	9	1	FAR1_CALVO
62	2	11.1	9	1	FAR2_CALVO
63	2	11.1	9	1	FAR3_CALVO
64	2	11.1	9	1	FAR4_CALVO
65	2	11.1	9	1	FAR5_ASCSU
66	2	11.1	9	1	FAR5_CALVO
67	2	11.1	9	1	FAR5_PENMO
68	2	11.1	9	1	FAR6_CALVO
69	2	11.1	9	1	FAR7_CALVO
70	2	11.1	9	1	FARA_CALVO
71	2	11.1	9	1	FARD_CALVO
72	2	11.1	9	1	FARP_CALSI
73	2	11.1	9	1	FIBB_ERYPA
74	2	11.1	9	1	FIBB_MACFU
75	2	11.1	9	1	FIBB_PAPHA
76	2	11.1	9	1	FRF1_SARBU
77	2	11.1	9	1	LITR_PHYRO
78	2	11.1	9	1	LMIP_LOEMI
79	2	11.1	9	1	LPCA_STAAU
80	2	11.1	9	1	MGMT_BOVIN
81	2	11.1	9	1	NEF_HVIZ8
82	2	11.1	9	1	NSKI_SARBU
83	2	11.1	9	1	OXYF_SCYCA
84	2	11.1	9	1	PTSP_BOMMO
85	2	11.1	9	1	RE42_LITRU
86	2	11.1	9	1	TALI_PICVA
87	2	11.1	9	1	THYF_PIG
88	2	11.1	9	1	UF02_MOUSE
89	2	11.1	9	1	UHA2_HUMAN
90	2	11.1	9	1	ULAH_HUMAN
91	2	11.1	9	1	UPA7_HUMAN
92	2	11.1	9	1	XYLA_STRSQ
93	2	11.1	10	1	AH3_PRUSE
94	2	11.1	10	1	AKHX_LOEMI
95	2	11.1	10	1	ANGT_CHICK
96	2	11.1	10	1	CAL2_LITCI
97	2	11.1	10	1	CAER_LITXA
98	2	11.1	10	1	COXA_ONCMY
99	2	11.1	10	1	COXM_RAT
100	2	11.1	10	1	COXO_RAT

ALIGNMENTS

RESULT 1

```

TEMK_RANTE
ID TEMK_RANTE STANDARD; PRT; 10 AA.
AC P56923;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tempurin K.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97179050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
temporaria."
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;

Query Match 22.2%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
DB 6 LKSL 9

RESULT 2
ID SAMP_MUSCA STANDARD; PRT; 9 AA.
AC P19095;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum amyloid P-component (SAP) (Fragment).
OS Mustelus canis (Smooth dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes; Triakidae;
OC Mustelus.
OX NCBI_TaxID=7812;
RN [1]
RP SEQUENCE.
RX MEDLINE=83160932; PubMed=6403520;
RA Robey F.A., Tanaka T., Liu T.-Y.;
RT "Isolation and characterization of two major serum proteins from the
dogfish, Mustelus canis, C-reactive protein and amyloid P
component."
RL J. Biol. Chem. 258:3889-3894(1983).
CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
DR PIR; B20569; B20569.
DR InterPro; IPR001759; Pentaxin.
DR PROSITE; PS00289; PENTAXIN; PARTIAL.
KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
FT DOMAIN 1 >9 PENTAXIN.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

```

```

Query Match 16.7%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
DB 5 KSL 7

RESULT 3
ID GLEM_HUMAN STANDARD; PRT; 10 AA.
AC P02728;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythrocyte membrane glycopeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72034940; PubMed=5286858;
RA Weiss J.B., Lote C.J., Bobinski H.;
RT "New low molecular weight glycopeptide containing triglucoylcysteine
in human erythrocyte membrane."
RL Nature New Biol. 234:25-26(1971).
CC -!- PTM: S-LINKED GLYCAN CONSISTS OF GLC-GLC-GLC TRISACCHARIDE.
CC -!- MISCELLANEOUS: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS
PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
ATTRIBUTED.
DR PIR; A03187; XGHUE.
KW Glycoprotein; Erythrocyte.
FT CARBOHYD 1 1 S-LINKED (GLC...).
SQ SEQUENCE 10 AA; 1049 MW; 239BFEEA1F5B1E8 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DHG 11
DB 7 DHG 9

RESULT 4
ID SPI_HALRO STANDARD; PRT; 10 AA.
AC Q10997;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Serine proteinase inhibitor (Fragment).
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyruidae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE.
RX TISSUE=Hemolymph; PubMed=8759295;
RA Shishikura F., Abe T., Ohtake S.-I., Tanaka K.;
RT "Purification and characterization of a 58,000-Da proteinase
inhibitor from the hemolymph of a solitary ascidian, Halocynthia
roretzi."
RL Comp. Biochem. Physiol. 114B:1-9(1996).
CC -!- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma.

```

```

FT  NON TER      10      10
SQ  SEQUENCE 10 AA; 1104 MW; 4225C73B1B187AA3 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  11 GEE 13
    |||
Db  5 GEE 7

RESULT 5
SYK_CAMUP
ID  SYK_CAMUP      STANDARD;      PRT;      10 AA.
AC  Q46464;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine-tRNA ligase) (LysRS)
DE  (Fragment).
GN  LYSS
OS  Campylobacter upsaliensis.
OC  Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC  Campylobacteraceae; Campylobacter.
OX  NCBI_TaxID=28080;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 43954;
RX  MEDLINE=97149302; PubMed=8996110;
RA  Bourke B., Rashid S.T., Bingham H.L., Chan V.L.;
RT  "Characterization of Campylobacter upsaliensis fur and its
RT  localization in a highly conserved region of the Campylobacter
RT  genome".
RL  Gene 183:219-224(1996).
CC  -!- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate
CC  + L-lysyl-tRNA(Lys).
CC  -!- COFACTOR: Binds 3 magnesium ions per subunit (By similarity).
CC  -!- SUBUNIT: Homodimer (By similarity).
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
-----
DR  EMBL; L77076; AAB41342.1; -
DR  HAMAP; MF_00252; -; 1.
DR  InterPro; IPR006195; tRNA ligase II.
DR  PROSITE; PS50862; AA_TRNA_LIGASE_II; PARTIAL.
KW  Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW  Metal-binding; Magnesium.
FT  NON TER      1
SQ  SEQUENCE 10 AA; 1218 MW; 9CEA46AB13372B05 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  15 LXS 17
    |||
Db  1 LXS 3

RESULT 6
URA7_HUMAN
ID  URA7_HUMAN      STANDARD;      PRT;      10 AA.
AC  P34990;
DT  01-FEB-1994 (Rel. 28, Created)

```

```

DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Unknown protein from 2D-page of red blood cells (Spot 2D-006HO)
DE  (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Erythrocyte;
RA  Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,
RA  Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,
RA  Balant L., Hochstrasser D.F.;
RL  Submitted (FEB-1994) to the SWISS-PROT data bank.
CC  -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC  PROTEIN IS: 4.77, ITS MW IS: 26 kDa.
DR  SWISS-2DPAGE; P34990; HUMAN.
FT  NON TER      10
SQ  SEQUENCE 10 AA; 1161 MW; F72D82E9C44B1871 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  10 HGE 12
    |||
Db  3 HGE 5

RESULT 7
ODPA_CANFA
ID  ODPA_CANFA      STANDARD;      PRT;      13 AA.
AC  P49823;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Pyruvate dehydrogenase E1 component alpha subunit, somatic form
DE  (EC 1.2.4.1) (PDHE1-A type I) (Fragment).
GN  PDHA1.
OS  Canis familiaris (Dog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX  NCBI_TaxID=9615;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Heart;
RX  MEDLINE=98163340; PubMed=9504812;
RA  Dunn M.J., Corbett J.M., Wheeler C.H.;
RT  "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT  dog heart proteins".
RL  Electrophoresis 18:2795-2802(1997).
CC  -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC  conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC  multiple copies of three enzymatic components: pyruvate
CC  dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC  lipoamide dehydrogenase (E3).
CC  -!- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-
CC  acetyldihydrolipoamide + CO(2).
CC  -!- COFACTOR: THIAMINE PYROPHOSPHATE.
CC  -!- ENZYME REGULATION: E1 ACTIVITY IS REGULATED BY PHOSPHORYLATION
CC  (INACTIVATION) AND DEPHOSPHORYLATION (ACTIVATION) OF THE ALPHA
CC  SUBUNIT (BY SIMILARITY).
CC  -!- SUBUNIT: Tetramer of two alpha and two beta subunits.
CC  -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
DR  HSC-2DPAGE; P49823; DOG
KW  Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
KW  Mitochondrion; Phosphorylation.
FT  NON TER      13
SQ  SEQUENCE 13 AA; 1510 MW; C97EEBF844085B19 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;

```



```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATF 3
Db 4 ATF 6

RESULT 8
ID RS19 ASHYP STANDARD; PRT; 13 AA.
AC Q44592;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS8 OR RPS19.
OS Ash yellows phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Achleoplasmatales;
OC Achleoplasmataceae; Phytoplasma.
OX NCBI_TaxID=35780;
RN SEQUENCE FROM N.A.
RP MEDLINE=94350802; PubMed=80711198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
their classification."
RL J. Bacteriol. 176:5244-5254(1994).
CC -!- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; L26599; AAA83936.1; -.
DR HAMAP; MF 00531; -.
DR InterPro; IPR002222; Ribosomal_S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON TRP 1
SQ SEQUENCE 13 AA; 1433 MW; CECA010B84E6305D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 ILK 16
Db 3 ILK 5

RESULT 9
LPW CITPR
ID LPW CITPR STANDARD; PRT; 14 AA.
AC P03056;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Trp operon leader peptide.
GN TRPL.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN SEQUENCE FROM N.A.
RP MEDLINE=83007061; PubMed=6749821;
RA Blumenberg M., Yanofsky C.;

"Evolutionary divergence of the Citrobacter freundii tryptophan
operon regulatory region: comparison with other enteric bacteria.";
J. Bacteriol. 152:57-62(1982).
-!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
OF TRYPTOPHAN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; J01557; -; NOT_ANNOTATED_CDS.
DR PIR; A03592; LFEBWC.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 14 AA; 1720 MW; 5B792A473E8048E7 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATF 3
Db 3 ATF 5

RESULT 10
LPW SALTY
ID LPW SALTY STANDARD; PRT; 14 AA.
AC P03054;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trp operon leader peptide.
GN TRPL OR TRPEE OR STM1722.
OC Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=78196931; PubMed=3511195;
RA Lee F., Bertrand K., Bennett G.N., Yanofsky C.;
RT "Comparison of the nucleotide sequences of the initial transcribed
regions of the tryptophan operons of Escherichia coli and Salmonella
typhimurium."
RL J. Mol. Biol. 121:193-217(1978).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2."
RL Nature 413:852-856(2001).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
OF TRYPTOPHAN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; M24960; -; NOT_ANNOTATED_CDS.
DR

```

```

DR EMBL; AE008776; AAL20640.1; -.
DR PIR; A03590; LFRBWT.
DR StvGene; SG10400; trpL.
KW Tryptophan biosynthesis, Leader peptide; Complete proteome.
SQ SEQUENCE 14 AA; 1635 MW; 49F2A47362248E7 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATP 3
Db 3 ATF 5

RESULT 11
MAST_VESBA
ID MAST_VESBA STANDARD; PRT; 14 AA.
AC P21654;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mastoparan B.
OS Vespa basalis (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7444;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=91174755; PubMed=2006909;
RA Lo C.-L., Hwang L.-L.;
RT "Structure and biological activities of a new mastoparan isolated
RL from the venom of the hornet Vespa basalis.";
RL Biochem. J. 274:453-456(1991).
CC -1- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
CC PIR; S14336; S14336.
KW Mast cell degranulation; Amidation.
FT MOD_RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA; 1613 MW; D35944CA193A19A2 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LXS 17
Db 3 LXS 5

RESULT 12
APP3_MALPA
ID APP3_MALPA STANDARD; PRT; 15 AA.
AC P83137;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antifungal protein 3 (CW-3) (Fragment).
OS Malva parviflora (little mallow) (Cheeseweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosidia I; Malvales; Malvaceae; Malvoideae; Malva.
OX NCBI_TaxID=145753;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Seed;
RX MEDLINE=21199399; PubMed=11302747;
RA Wang X., Bunkers G.J., Walters M.R., Thoma R.S.;
RT "Purification and characterization of three antifungal proteins from
RL Cheeseweed (Malva parviflora).";
RL Biochem. Biophys. Res. Commun. 282:1224-1228(2001).

-1- FUNCTION: Possesses antifungal activity against P.infestans but
not F.graminearum.
-1- MISCELLANEOUS: Antimicrobial activity is not affected by salt
concentration.
DR GO; GO:0003799; F:antifungal peptide activity; IDA.
DR GO; GO:0007275; P:development; NAS.
KW Fungicide; Antibiotic.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 2016 MW; 01D9CA069F1A52DB CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RYQ 7
Db 7 RYQ 9

RESULT 13
CKX_WHEAT
ID CKX_WHEAT STANDARD; PRT; 15 AA.
AC P58763;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2003 (Rel. 42, Last annotation update)
DE Cytokinin oxidase (EC 1.4.3.-) (CKO) (CKX) (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=cv. Samanthal;
RX MEDLINE=21099312; PubMed=11168382;
RA Galuszka P., Frebort I., Sebel M., Sauer P., Jacobsen S., Pec P.;
RT "Cytokinin oxidase or dehydrogenase? Mechanism of cytokinin
degradation in cereals.";
RL Eur. J. Biochem. 268:450-461(2001).
CC -1- FUNCTION: Catalyzes the oxidation of cytokinins, a family of N(6)-
substituted adenine derivatives that are plant hormones, where the
substituent is an isopentenyl group. Substrate preference is 2-(2-
Hydroxyethylamino)-9-methyl-N(6)-isopentenyladenine >>
isopentenyladenine > cis-zeatin = isopentenyladenosine = zeatin >>
zeatin riboside.
CC -1- CATALYTIC ACTIVITY: N(6)-(3-methylbut-2-enyl)adenine + H(2)O +
O(2) = adenine + 3-methylbut-2-enal + H(2)O(2).
CC -1- COFACTOR: FAD.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Extracellular (By similarity).
CC -1- MISCELLANEOUS: Optimal pH is 6.5.
CC -1- SIMILARITY: Belongs to the oxygen-dependent FAD-linked
oxidoreductase family.
KW Oxidoreductase; Flavoprotein; FAD.
FT UNSURE 1 1
FT UNSURE 13 15
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1709 MW; 85B589BD53FCEDEF CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
Db 4 KSL 6

RESULT 14
ITRB_ALBU
ID ITRB_ALBU STANDARD; PRT; 15 AA.
AC P24927;

```

DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trypsin inhibitor B chain (fragment).
 OS Albizzia julibrissin (Silk tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Mimosoideae; Ingeae; Albizzia.
 OX NCBI_TaxID=3813;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=80115605; PubMed=528539;
 RA Odani S., Ono T., Ikenaka T.;
 RT "Proteinase inhibitors from a mimosoideae legume, Albizzia
 RT julibrissin. Homologues of soybean trypsin inhibitor (Kunitz).";
 RL J. Biochem. 86:1795-1805(1979).
 CC -!- FUNCTION: INHIBITS TRYPSIN AND ALPHA-CHYMOTRYPSIN.
 CC -!- SUBUNIT: HETEROIDIMER OF AN "A" AND A "B" CHAIN LINKED BY A
 CC DISULFIDE BOND.
 CC -!- SIMILARITY: BELONGS TO THE LEGUMINOUS KUNITZ-TYPE INHIBITOR
 CC FAMILY.
 KW Serine protease inhibitor.
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1705 MW; 53165F7B9C45B4D0 CRC64;

 Query Match 16.7%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 8 DDH 10
 Db ||||
 2 DDH 4

 RESULT 15
 ID METK MAIZE STANDARD; PRT; 15 AA.
 AC P80616;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
 DE adenosyltransferase) (AdoMet synthetase) (Spot 178) (fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
 CC METHIONINE AND ATP.
 CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
 CC diphosphate + S-adenosyl-L-methionine.
 CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
 CC 1 potassium ion per subunit (potential).
 CC -!- PATHWAY: Activated methyl cycle.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.9, ITS MW IS: 43.3 kDa.
 CC -!- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
 DR Maize2DPAGE; P80616; COLEOPTILE.
 DR MaizeDB; 123938; -;
 DR InterPro; IPR002133; S-AdoMet synt.
 DR Pfam; PF02772; S-AdoMet syntd2; 1.
 DR PROSITE; PS00376; ADOMET SYNTHETASE 1; PARTIAL.
 DR PROSITE; PS00377; ADOMET SYNTHETASE 2; PARTIAL.

KW Transferase; One-carbon metabolism; Multigene family; ATP-binding;
 KW Magnesium; Potassium; Metal-binding.
 FT NON TER 1 1
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1601 MW; 232B07E9AC328D32 CRC64;

 Query Match 16.7%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 12 BEI 14
 Db ||||
 3 BEI 5

 RESULT 16
 ID MM01 RAT STANDARD; PRT; 15 AA.
 AC P81563;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interstitial collagenase (EC 3.4.24.7) (Matrix metalloproteinase-1)
 DE (MMP-1) (Fibroblast collagenase) (Myocardial collagenase) (fragment).
 GN MMP1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=96201136; PubMed=8605638;
 RA Tyagi S.C., Cleutjens J.P.M.;
 RT "Myocardial collagenase: purification and structural
 RT characterization.";
 RL Can. J. Cardiol. 12:165-171(1996).
 CC -!- FUNCTION: CLEAVES COLLAGENS OF TYPES I, II, AND III AT ONE SITE IN
 CC THE HELICAL DOMAIN. ALSO CLEAVES COLLAGENS OF TYPES VII AND X MAY
 CC PLAY A ROLE IN THE DETERIORATION OF THE HEART WALL EXTRACELLULAR
 CC MATRIX PROTEINS DURING THE ONSET OF DILATED CARDIOMYOPATHY.
 CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
 CC collagen. Cleavage of the triple helix of collagen at about three-
 CC quarters of the length of the molecule from the N-terminus, at
 CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
 CC substrates and alpha-macroglobulins at bonds where P1' is a
 CC hydrophobic residue.
 CC -!- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
 CC -!- ENZYME REGULATION: CAN BE ACTIVATED WITHOUT REMOVAL OF THE
 CC ACTIVATION PEPTIDE.
 CC -!- PTM: THE N-TERMINAL IS BLOCKED.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
 KW Hydrolase; Metalloprotease; Zinc; Calcium; Collagen degradation;
 KW Extracellular matrix.
 FT NON TER 1 1
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1787 MW; 15A57D24C0F6FD80 CRC64;

 Query Match 16.7%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 15 LKS 17
 Db ||||
 3 LKS 5

 RESULT 17
 ID PS00 CUCSA STANDARD; PRT; 15 AA.
 AC P42052;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Photosystem 1 reaction centre subunit 8 (Photosystem I 17.5 kDa
DE protein) (Fragment).
DE PSAM.
GN Cucumis sativus (Cucumber).
OS Cucurbitales; Cucurbitaceae; Cucumis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3659;
RN [1]
RP SEQUENCE.
RC TISSUE=Cotyledon; PubMed=1883835;
RX MEDLINE=91355209; Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;
RA "Characterization of genes that encode subunits of cucumber PS I
RT complex by N-terminal sequencing.";
RL Biochim. Biophys. Acta 1059:141-148 (1991).
CC -!- FUNCTION: ESSENTIAL FOR THE ACTIVITY OF NADP PHOTOREDUCTION.
DR PIR; E56819; E56819.
KW Photosystem I; Photosynthesis; Chloroplast; Thylakoid; Membrane.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1714 MW; CA0BF5DAD403D9F4 CRC64;
Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 QDD 9
Db 12 QDD 14

RESULT 18
TRPA_LEUMA
ID TRPA_LEUMA STANDARD; PRT; 15 AA.
AC P81753;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tachykinin-related peptide 10 (leuTRP 10).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Brain;
RX MEDLINE=97269266; PubMed=9114447;
RA Muren J.E., Naessel D.R.;
RT "Seven tachykinin-related peptides isolated from the brain of the
RT Madeira cockroach; evidence for tissue-specific expression of
RT isoforms.";
RL Peptides 18:7-15 (1997).
CC -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: BRAIN.
CC -!- MASS SPECTROMETRY: MW=1436.0; METHOD=WALDI.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide.
SQ SEQUENCE 15 AA; 1438 MW; 298572F373FA7007 CRC64;
Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATF 3
Db 9 ATF 11

RESULT 19

ALLI CALVO
ID ALLI_CALVO STANDARD; PRT; 16 AA.
AC P41839;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Callatostatin 1 (Leu-callatostatin 1) [Contains: Callatostatin 2 (Leu-callatostatin 2); Callatostatin 3 (Leu-callatostatin 3)].
DE Callatostatin 2; Callatostatin 3 (Leu-callatostatin 3)].
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain, Head, and Thoracic ganglion;
RX MEDLINE=93211980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Callatostatins: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460 (1993).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=94291167; PubMed=8020069;
RA Duve H., Thorpe A.;
RT "Distribution and functional significance of Leu-callatostatins in
RT the blowfly Calliphora vomitoria.";
RL Cell Tissue Res. 276:367-379 (1994).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC -!- TISSUE SPECIFICITY: BRAIN, SUBESOPHAGEAL GANGLION, RETROCEREBRAL
CC COMPLEX, THORACICO-ABDOMINAL GANGLION, PERIPHERAL NEUROSECRETORY
CC SYSTEM AND INTESTINE.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR PIR; A47393; A47393.
KW Neuropeptide; Amidation.
FT PEPTIDE 1 16 CALLATOSTATIN 1.
FT PEPTIDE 3 16 CALLATOSTATIN 2.
FT PEPTIDE 9 16 CALLATOSTATIN 3.
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1907 MW; A435B68C26EC3D09 CRC64;
Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 NRY 6
Db 10 NRY 12

RESULT 20
UVSX_BPT6
ID UVSX_BPT6 STANDARD; PRT; 16 AA.
AC Q06728;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Recombination and repair protein (Fragment).
DE UVSX.
GN Bacteriophage T6.
OS Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=10666;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93219141; PubMed=8464751;
RA Winkler M., Rueger W.;
RT "Cloning and sequencing of the genes of

RT beta-glucosyl-HMC-alpha-glucosyl-transferases of bacteriophages T2
RL Nucleic Acids Res. 21:1500-1500(1993).
CC -!- FUNCTION: IMPORTANT IN GENETIC RECOMBINATION, DNA REPAIR, AND
CC REPLICATION. POSSESSES PAIRING AND STRAND-TRANSFER ACTIVITY.
CC INTERACTS WITH DDA AND GENE 32 PROTEINS.
CC -!- SIMILARITY: Belongs to the recA family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X68725; CAA48668.1; -.
KW PIR; S35627; S35627.
DR DNA damage; DNA replication; DNA recombination; DNA repair;
KW ATP-binding. 16 16
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1721 MW; 48164C95D76F3CB4 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKS 17
DB 6 LKS 8

RESULT 21
GSHX_PINPS STANDARD; PRT; 17 AA.
ID GSHX_PINPS
AC P81087;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Glutathione peroxidase homolog (EC 1.1.1.9) (Water stress responsive
DE proteins 8 and 9) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]_TaxID=71647;
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=98418576; PubMed=9747804;
RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water-deficit-responsive proteins in maritime pine.";
RL Plant Mol. Biol. 38:587-596(1998).
RN [2]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=9274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
CC glutathione + 2 H(2)O.
CC -!- INDUCTION: By water stress.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 5.6 TO 6.7, ITS MW IS: 20 TO 23 kDa.
CC -!- SIMILARITY: Belongs to the glutathione peroxidase family.
DR Pfam: PF00255; GSHPX.1.
DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; PARTIAL.
DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
KW Peroxidase; Oxidoreductase.
FT NON TER 1 1

FT NON TER 17 17
SQ SEQUENCE 17 AA; 1943 MW; 4D245E9B657868C1 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EIL 15
DB 7 EIL 9

RESULT 22
ADC_CLOPA STANDARD; PRT; 19 AA.
ID ADC_CLOPA
AC P81336;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetoacetate decarboxylase (EC 4.1.1.4) (ADC) (AAD) (CP 28/CP 29)
DE (Fragment).
GN ADC.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: Catalyzes the conversion of acetoacetate to acetone and
CC carbon dioxide.
CC -!- CATALYTIC ACTIVITY: Acetoacetate + H(+) = acetone + CO(2).
CC -!- SIMILARITY: Belongs to the ADC family.
DR HAMAP; MF_00597; -; 1.
KW Lyase; Decarboxylase.
FT NON TER 19 19
SQ SEQUENCE 19 AA; 2078 MW; 6ACDAA91103AEC31 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKS 17
DB 2 LKS 4

RESULT 23
COX4_ONCMY STANDARD; PRT; 19 AA.
ID COX4_ONCMY
AC P80327;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide IV (EC 1.9.3.1) (Fragments).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and Vila
RT of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).

CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE IV FAMILY.
 CC PIR: S43624; S43624.
 CC Oxidoreductase; Inner membrane; Mitochondrion.
 KW
 DR
 FT NON_CONS 9 10
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 1963 MW; 9280E1D8EC77987E CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 HGE 12
 DB 3 HGE 5
 RESULT 24
 DCAM ACACA STANDARD; PRT; 19 AA.
 ID DCAM ACACA
 AC P34039;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE S-adenosylmethionine decarboxylase alpha subunit (EC 4.1.1.50)
 DE (AdoMetDC) (SamDC) (Fragment).
 OS Acanthamoeba castellanii (Amoeba).
 OC Eukaryota; Acanthamoebidae; Acanthamoeba.
 OX NCBI_TaxID=5755;
 [1]
 SEQUENCE, AND CHARACTERIZATION.
 RX MEDLINE=94029912; PubMed=8216217;
 RA Hugo E.R., Byers T.J.;
 RT "S-adenosyl-L-methionine decarboxylase of Acanthamoeba castellanii
 RT (Neff): purification and properties.";
 RL Biochem. J. 295:203-209(1993).
 CC -!- FUNCTION: S-ADENOSYLMETHIONINE DECARBOXYLASE IS ESSENTIAL FOR THE
 CC BIOSYNTHESIS OF SPERMINE AND SPERMIDINE. THE ALPHA SUBUNIT
 CC CONTAINS THE ACTIVE SITE.
 CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-
 CC adenosyl) (3-aminopropyl) methylsulfonium salt + CO(2).
 CC -!- COFACTOR: Pyruvoyl group.
 CC -!- PATHWAY: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES THE
 CC AMINOPOPYL MOIETY REQUIRED FOR SPERMIDINE AND SPERMINE
 CC BIOSYNTHESIS FROM PUTRESCINE.
 CC -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED ONLY DURING EXPONENTIAL GROWTH.
 CC -!- INDUCTION: STIMULATED BY PUTRESCINE. INHIBITED BY AROMATIC
 CC DIAMIDINES BERENIL, PENTAMIDINE, PROPAMIDINE, HYDROXYSTILBAMIDINE,
 CC BY ETHIDIUM BROMIDE AND METHYLGLYOXAL.
 CC -!- SIMILARITY: BELONGS TO THE EUKARYOTIC ADOMETDC FAMILY.
 CC PIR: S38763; S38763.
 CC InterPro; IPR001985; SAM decarbox.
 CC Pfam; PF01536; SAM decarbox; 1.
 CC PROSITE; PS01336; ADOMETDC; PARTIAL.
 KW Spermidine biosynthesis; Lyase; Decarboxylase; Pyruvate.
 FT MOD_RES 1 1 CONVERTED TO A PYRUVOYL GROUP.
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2153 MW; 88B18AD9B6142AEF CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 ILK 16
 DB 11 ILK 13

RESULT 25
 TRPB_KLEAE STANDARD; PRT; 19 AA.
 ID TRPB_KLEAE
 AC P14552;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tryptophan synthase beta chain (EC 4.2.1.20) (Fragment).
 GN TRPB.
 OS Klebsiella aerogenes.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=28451;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81199002; PubMed=6262736;
 RA Nichols B.P., Blumenberg M., Yanofsky C.;
 RT "Comparison of the nucleoside sequence of trpA and sequences
 RT immediately beyond the trp operon of Klebsiella aerogenes. Salmonella
 RT typhimurium and Escherichia coli.";
 RL Nucleic Acids Res. 9:1743-1755(1981).
 CC -!- FUNCTION: The beta subunit is responsible for the synthesis of L-
 CC tryptophan from indole and L-serine.
 CC -!- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate
 CC = L-tryptophan + glyceraldehyde 3-phosphate.
 CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -!- PATHWAY: Tryptophan biosynthesis; fifth (last) step.
 CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (By
 CC similarity).
 CC -!- SIMILARITY: BELONGS TO THE TRPB FAMILY.
 CC
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; V00630; CAA23901.1; -
 CC EMBL; J01738; AAA25144.1; -
 CC HSSP; P00933; 2TYS.
 CC HAMAP; MF_00133; -; 1.
 CC InterPro; IPR006653; Trp synth b_rel.
 CC PROSITE; PS00168; TRP SYNTHASE BETA; PARTIAL.
 KW Tryptophan biosynthesis; Pyridoxal phosphate; Lyase.
 FT NON_TER 1 1
 SQ SEQUENCE 19 AA; 2183 MW; 82864627BF574E2C CRC64;
 Query Match 16.7%; Score 3; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 ILK 16
 DB 12 ILK 14
 RESULT 26
 AP2L_MALPA STANDARD; PRT; 20 AA.
 ID AP2L_MALPA
 AC P83143;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Antifungal protein 2 large subunit (CW-2) (Fragment).
 OS Malva parviflora (Little mallow) (Cheeseweed).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.
 OX NCBI_TaxID=145753;
 RN [1]

```

RP SEQUENCE, AND FUNCTION.
RC TISSUE=Seed;
RX MEDLINE=20568734; PubMed=11118343;
RA Wang X., Bunkers G.J.;
RT "Potent heterologous antifungal proteins from cheeseweed (Malva
RL Biochem. Biophys. Res. Commun. 279:669-673(2000)).
CC -!- FUNCTION: Possesses antifungal activity against P.infestans but
CC not P.graminearum.
CC -!- SUBUNIT: Heterodimer of a large and a small subunit.
CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC concentration.
KW GO:0003799; F:antifungal peptide activity; IDA.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2303 MW; 6E766A5E342036DA CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RYQ 7
DB 7 RYQ 9

RESULT 27
FIBB_FELCA STANDARD; PRT; 20 AA.
AC P14469;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals. ";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW Blood coagulation; Plasmas.
FT PEPTIDE 1 20
FT NON_TER 20 FIBRINOPEPTIDE B.
SQ SEQUENCE 20 AA; 2328 MW; A829E393B8F627D0 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEE 13
DB 8 GEE 10

RESULT 28
HCYA_PANJA STANDARD; PRT; 20 AA.
ID HCYA_PANJA
AC P82310;

```

```

DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hemocyanin subunit Ia (Fragment).
OS Panulirus japonicus (Japanese spiny lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;
OC Palinuroidea; Palinuridae; Panulirus.
OX NCBI_TaxID=6736;
RN [1]
RP SEQUENCE.
RC TISSUE=Serum;
RX MEDLINE=88196131; PubMed=3360019;
RA Makino N., Kimura S.;
RT "Subunits of Panulirus japonicus hemocyanin. 1. Isolation and
RT properties. ";
RL Eur. J. Biochem. 173:423-430(1988).
CC -!- FUNCTION: Hemocyanins are copper-containing oxygen carriers
CC occurring freely dissolved in the hemolymph of many mollusks and
CC arthropods.
CC -!- SUBUNIT: Composed of 3 major subunits (IB, II and III) and 1 minor
CC subunit (IA) which form homohexamers and heterohexamers. May also
CC form larger structures.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Hemolymph.
CC -!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
CC SUBFAMILY.
DR PIR; S00492; S00492.
DR InterPro; IPR000896; Hemocyanin.
DR InterPro; IPR002227; Tyrosinase.
DR PROSITE; PS00209; HEMOCYANIN_1; PARTIAL.
DR PROSITE; PS00210; HEMOCYANIN_2; PARTIAL.
DR PROSITE; PS00497; TYROSINASE_1; PARTIAL.
DR PROSITE; PS00498; TYROSINASE_2; PARTIAL.
KW Transport; Oxygen transport; Copper; Hemolymph.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2154 MW; 313BE8E456DDDE09 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QDD 9
DB 17 QDD 19

RESULT 29
M117_BOVIN STANDARD; PRT; 20 AA.
ID M117_BOVIN
AC P35451;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 17 kDa milk glycoprotein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Milk;
RX MEDLINE=93308294; PubMed=8320368;
RA Soerensen E.S., Petersen T.E.;
RT "Purification and characterization of three proteins isolated from
RT the protease peptone fraction of bovine milk. ";
RL J. Dairy Res. 60:189-197(1993).
CC -!- PTM: N-GLYCOSYLATED.
CC -!- SIMILARITY: TO CAMEL WHEY PROTEIN.
KW Glycoprotein; Milk.
FT NON_TER 1 1
FT NON_TER 20 20

```

```

SQ SEQUENCE 20 AA; 2233 MW; 4CCA589404C62C27 CRC64;
Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILK 16
    |||
Db 16 ILK 18

RESULT 30
SODM_HORVU STANDARD; PRT; 20 AA.
AC P28524;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1) (Fragment).
GN SODA.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. CM 72; TISSUE=Root;
RA Harkman W.J., Tao H.P., Tanaka C.K.;
RT "germin-like polypeptides increase in barley roots during salt
RT stress.";
RL Plant Physiol. 97:366-374 (1991).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Manganese (By similarity).
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Manganese; Mitochondrion.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2152 MW; 7F7CAE8DF1C9657 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATF 3
    |||
Db 2 ATF 4

RESULT 31
TENB_ACTTE STANDARD; PRT; 20 AA.
AC P30834;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tenebrosin B (Fragment).
OS Actinia tenebrosa (Australian red waratah sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Actinia.
OX NCBI_TaxID=6105;
RN [1]
RP SEQUENCE.
RX MEDLINE=90232538; PubMed=1970442;
RA Norton R.S., Bobek G., Ivanov J.O., Thomson M., Fiala-Beer E.,
RA Moritz R.L., Simpson R.J.;

```

```

RT "Purification and characterisation of proteins with cardiac
RT stimulatory and haemolytic activity from the anemone Actinia
RT tenebrosa.";
RL Toxicon 28:29-41 (1990).
CC -!- FUNCTION: This cardiac stimulatory and hemolytic protein is a
CC channel-forming and/or membrane-penetrating protein.
CC -!- SUBCELLULAR LOCATION: Secreted; Cnidocyst.
CC -!- SIMILARITY: BELONGS TO THE TENEBROSIN FAMILY.
DR PIR; B34016; B34016.
KW Cytolysis; Hemolysis; Toxin; Cnidocyst; Transmembrane.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 1960 MW; FA32B426009FF5FA CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFN 4
    |||
Db 15 TFN 17

RESULT 32
BIOA_CITFR STANDARD; PRT; 5 AA.
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
DE aminotransferase) (Fragment).
GN BIOA.
OC Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89006280; PubMed=2971595;
RA Shiuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211 (1988).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC diaminononanoate.
CC -!- COFACTOR: Pyridoxal phosphate.
CC -!- PATHWAY: Biotin biosynthesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
CC aminotransferases.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; M21922; -; NOT_ANNOTATED_CDS.
DR PIR; I40697; I40697.
DR InterPro; IPR005814; Aminotrans_3.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KW Biotin biosynthesis; Transferase; Aminotransferase;
KW Pyridoxal phosphate.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



```

QY      8 DD 9
      ||
Db      4 DD 5

RESULT 33
FARP ARTTR
ID_FARP ARTTR STANDARD; PRT; 5 AA.
AC P41853;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE FMRFamide-like neuropeptide RYRF-amide.
OS Artiopesthia triangulata (New Zealand flatworm).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Terricola; Geoplanidae; Arthurdendyus.
OX NCBI_TaxID=132421;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=94211927; PubMed=7909164;
RA Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
RT "RYRFamide: a turbellarian FMRFamide-related peptide (FARP).";
RL Regul. Pept. 50:37-43(1994)
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA; 754 MW; 69D4004B44600000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 RY 6
      ||
Db      1 RY 2

RESULT 34
PRCT PERAM
ID_PRCT PERAM STANDARD; PRT; 5 AA.
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES=P.americana;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569(1981).
RN [3]
RP SEQUENCE.
RC SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;

```

```

RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
horsehoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).
RN [4]
RP SEQUENCE.
RC SPECIES=C.maenas; PubMed=2872661;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangier J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72(1986).
CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
THE CRAB PERICARDIAL ORGANS.
CC PIR; A01644; HOROHA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 RY 6
      ||
Db      1 RY 2

RESULT 35
TRM3 ECOLI
ID_TRM3 ECOLI STANDARD; PRT; 5 AA.
AC P13973;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trm protein (Fragment).
OS Escherichia coli.
OG Plasmid IncFII R100.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88227859; PubMed=2836369;
RA Inamoto S., Yoshioka Y., Ohtsubo E.;
RT "Identification and characterization of the products from the traj
and tray genes of plasmid R100.";
RL J. Bacteriol. 170:2749-2757(1988).
CC -!- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE TRAM FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M20941; -; NOT ANNOTATED_CDS.
DR PIR; A32014; A32014.
KW Conjugation; Plasmid; DNA-binding.
FT NON_TER 1
RN [1]
RP SEQUENCE 5 AA; 634 MW; 6B1B1AA443500000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;

```

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EI 13
Db 4 EI 5

RESULT 36
UN06_CLOPA STANDARD; PRT; 6 AA.
ID UN06_CLOPA
AC P81351;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 6 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=WS;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum WS.";
RL Electrophoresis 19:802-806(1998).
CC -/- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.
FT NON TER 6
FT MOD RES 6
SQ SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EI 14
Db 5 EI 6

RESULT 37
CIA_ENTFA STANDARD; PRT; 7 AA.
ID CIA_ENTFA
AC P11932;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone cAM373 (Clumping-inducing agent) (CIA).
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=87005252; PubMed=3093276;
RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
RA White B.A., An F.Y., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the Streptococcus faecalis sex pheromone,
RT cAM373.";
RL FEBS Lett. 206:69-72(1986).
CC -/- FUNCTION: cAM373 INDUCES MATING RESPONSE OF DONOR CELLS
CC HARBORING pAM373.
CC -/- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR
CC SPECIFICITY OF PHEROMONES TO PLASMIDS.
CC -/- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
DR PIR; A25269; A25269.
KW Pheromone.
SQ SEQUENCE 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 IL 15
Db 4 IL 5

RESULT 38
EI05_LITRU STANDARD; PRT; 7 AA.
ID EI05_LITRU
AC P82101;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 5
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -/- SUBCELLULAR LOCATION: Secreted.
CC -/- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 7
FT MOD RES 7
SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EI 14
Db 5 EI 6

RESULT 39
FARI_PROCL STANDARD; PRT; 7 AA.
ID FARI_PROCL
AC P38499;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Cardioexcitatory FMRamide homolog NFL.
OS Procamburus clarkii (Red swamp crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidea; Cambaridae; Procamburus.
OX NCBI_TaxID=6728;
RN [1]
RP SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=93248032; PubMed=8387183;
RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;
RT "Isolation of two FMRamide-related peptides from crayfish
RT pericardial organs.";
RL Peptides 14:137-143(1993).
CC -/- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
CC -/- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 7
FT MOD RES 7
SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540420 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.3e+05; Mismatches 0; Indels 0; Gaps 0;

QY 4 NR 5
||
1 NR 2

RESULT 40

ID FAR3_HAECO STANDARD; PRT; 7 AA.
 AC P81298;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRFamide-like neuropeptide PF3 (KSAYMRF-amide).
 OS Haemochus contortus (Barber pole worm).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
 OC Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
 OX NCBI_TaxID=6289;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Neuron;
 RX MEDLINE=99318264; PubMed=10391380;
 RA Marks N.J., Sangster N.C., Maule A.G., Halton D.W., Thompson D.P.,
 RA Geary T.G., Shaw C.;
 RT "Structural characterisation and pharmacology of KHEYLRamide (AF2)
 and KSAYMRFamide (PF3/AF8) from Haemonchus contortus.";
 RL Mol. Biochem. Parasitol. 100:185-194(1999).
 CC -!- FUNCTION: ACTIVE ON NEUROMUSCULATURE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 FAMILY.
 CC Neuropeptide; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 902 MW; 69D4068B5DC5B350 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KS 17
||
1 KS 2

RESULT 41

ID FAR3_PANRE STANDARD; PRT; 7 AA.
 AC P41874;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE FMRFamide-like neuropeptide PF3 (KSAYMRF-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=94235053; PubMed=8179635;
 RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,
 RA Geary T.G., Thim L.;
 RT "KSAYMRFamide: a novel FMRFamide-related heptapeptide from the free-
 living nematode, Panagrellus redivivus, which is myoactive in the
 parasitic nematode, Ascaris suum.";
 RL Biochem. Biophys. Res. Commun. 200:973-980(1994).
 CC -!- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT
 MUSCLE TENSION INCREASE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 FAMILY.
 CC PIR; PC2132; PC2132.
 DR Neuropeptide; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 902 MW; 69D4068B5DC5B350 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ SEQUENCE 7 AA; 902 MW; 69D4068B5DC5B350 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KS 17
||
1 KS 2

RESULT 42

ID LANC_CARUI STANDARD; PRT; 7 AA.
 AC P36960;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lantibiotic carnocin UI49 (Fragment).
 OS Carnobacterium sp. (strain UI49).
 OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
 OC Carnobacterium.
 OX NCBI_TaxID=35782;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92321768; PubMed=1622206;
 RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
 RA Nes I.F.;
 RT "Purification and characterization of a new bacteriocin isolated from
 a Carnobacterium sp.";
 RL Appl. Environ. Microbiol. 58:1417-1422(1992).
 CC -!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
 CC ACTIVE ON GRAM-POSITIVE BACTERIA.
 KW Antibiotic; Bacteriocin; Lantibiotic.
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EI 14
||
3 EI 4

RESULT 43

ID UC24_MAIZE STANDARD; PRT; 7 AA.
 AC P80630;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 447)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 genome analysis program";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 6.0, ITS MW IS: 30.0 kDa.
 DR Maize-2DPAGE; P80630; COLEOPTILE.
 DR MaizeDB; 123956; --
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

FT  NON TER      7      7
SQ  SEQUENCE      7 AA;  665 MW;  6DC1B5B33DC1B5D0 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  16 KS 17
    |||
Db  4 KS 5

RESULT 44
UF03 MOUSE      STANDARD;      PRT;      7 AA.
ID  UF03 MOUSE
AC  P38641;
DT  01-OCT-1994 (Rel. 30, Created)
DT  01-OCT-1994 (Rel. 30, Last sequence update)
DT  01-FEB-1995 (Rel. 31, Last annotation update)
DE  Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Fibroblast; PubMed=7523108;
RA  Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT  "Separation and sequencing of familial and novel murine proteins
RT  using preparative two-dimensional gel electrophoresis.";
RL  Electrophoresis 15:735-745(1994).
CC  -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC  PROTEIN IS: 5.1, ITS MW IS: 36 kDa.
FT  NON TER      7
SQ  SEQUENCE      7 AA;  842 MW;  6AA72B1DDB1B1180 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  12 EE 13
    |||
Db  2 EE 3

RESULT 45
AKH TABAT      STANDARD;      PRT;      8 AA.
ID  AKH TABAT
AC  P14595;
DT  01-JAN-1990 (Rel. 13, Created)
DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
DE  (DCC I).
OC  Tabanus atratus (Horse fly).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC  Tabanus.
OX  NCBI_TaxID=7207;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Corpora cardiaca;
RA  Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA  Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT  "Primary structure of two neuropeptide hormones with adipokinetic and
RT  hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT  flies (Diptera).";
RL  Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC  -I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC  CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC  DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT

```

```

CC  MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC  -I- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR  PIR; A33995; A33995.
DR  InterPro; IPR002047; AKH.
DR  PROSITE; PS00256; AKH; 1.
KW  Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT  MOD_RES      1 1  PYRROLIDONE CARBOXYLIC ACID.
FT  MOD_RES      8 8  AMIDATION.
SQ  SEQUENCE      8 AA;  949 MW;  86786771A9D1A736 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 TF 3
    |||
Db  3 TF 4

RESULT 46
B44K PORGI      STANDARD;      PRT;      8 AA.
ID  B44K PORGI
AC  P81886;
DT  30-MAY-2000 (Rel. 39, Created)
DT  30-MAY-2000 (Rel. 39, Last sequence update)
DT  30-MAY-2000 (Rel. 39, Last annotation update)
DE  44 kDa immunogenic protein (Fragment).
OS  Porphyromonas gingivalis (Bacteroides gingivalis).
OC  Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales;
OC  Porphyromonadaceae; Porphyromonas.
OX  NCBI_TaxID=837;
RN  [1]
RP  SEQUENCE.
RC  STRAIN=VPB 3492;
RX  MEDLINE=20198497; PubMed=10731616;
RA  Norris J.M., Love D.N.;
RT  "Serum antibody responses of cats to soluble whole cell antigens of
RT  feline Porphyromonas gingivalis.";
RL  Vet. Microbiol. 73:37-49(2000).
CC  -I- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
KW  Antigen.
FT  NON TER      8
SQ  SEQUENCE      8 AA;  989 MW;  9554540326CB476D CRC64;

Query Match      11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 YQ 7
    |||
Db  3 YQ 4

RESULT 47
CAD1_ENTFA      STANDARD;      PRT;      8 AA.
ID  CAD1_ENTFA
AC  P13268;
DT  01-JAN-1990 (Rel. 13, Created)
DT  01-JAN-1990 (Rel. 13, Last sequence update)
DT  01-FEB-1991 (Rel. 17, Last annotation update)
DE  Sex pheromone CAD1.
OC  Enterococcus faecalis (Streptococcus faecalis).
OC  Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX  NCBI_TaxID=1351;
RN  [1]
RP  SEQUENCE.
RA  Mori M., Sakagami Y., Narita M., Isogai A., Fujino M., Kitada C.,
RA  Craig R.A., Clewell D.B., Suzuki A.;
RT  "Isolation and structure of the bacterial sex pheromone, cAD1, that
RT  induces plasmid transfer in Streptococcus faecalis.";
RL  FEBS Lett. 178:97-100(1984).
CC  -I- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE

```

```

CC      HEMOLYSIN PLASMID PAD1.
KW      Pheromone. 8 AA; 819 MW; 047DD732C735B9C7 CRC64;
SQ      SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      17 SL 18
Db      3 SL 4

RESULT 48
FAR4_HOMAM
ID      FAR4_HOMAM      STANDARD;      PRT;      8 AA.
AC      P41487;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DE      01-NOV-1995 (Rel. 32, Last annotation update)
DE      FMRFamide-like neuropeptide 4 (FLI 4) (FLI).
OS      Homarus americanus (American lobster).
OC      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC      Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC      Nephropoidea; Nephropidae; Homarus.
OX      NCBI_TaxID=6706;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Pericardial organs;
RX      MEDLINE=89116164; PubMed=34297114;
RA      Trimmer B.A., Kobierski L.A., Kravitz E.A.;
RT      "Purification and characterization of FMRFamide-like immunoreactive
RT      substances from the lobster nervous system: isolation and sequence
RT      analysis of two closely related peptides.";
RL      J. Comp. Neurol. 266:16-26(1987).
CC      -!- FUNCTION: CAN ACT AS A MODULATOR OF EXOSKELETAL AND CARDIAC
CC      NEUROMUSCULAR JUNCTIONS.
CC      -!- SIMILARITY: BELONGS TO THE FAP (FMRFAMIDE RELATED PEPTIDE)
CC      FAMILY.
KW      Neuropeptide; Amidation.
FT      MOD RES      8
SQ      SEQUENCE 8 AA; 1067 MW; DDD40729C4540451 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 NR 5
Db      2 NR 3

RESULT 49
HTF2_PERAM
ID      HTF2_PERAM      STANDARD;      PRT;      8 AA.
AC      P04549;
DT      13-AUG-1987 (Rel. 05, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Hypertrehalosaemic factor II (Neuropeptide M-II) (Pexiplanetin CC-2)
DE      (PeA-CAH-II) (Leb-CC-II) (Hypertrehalosaemic neuropeptide II).
OS      Pexiplaneta americana (American cockroach).
OS      Lepidoptera decemlineata (Colorado potato beetle), and
OS      Blatta orientalis (Oriental cockroach).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC      Blattidae; Pexiplaneta.
OX      NCBI_TaxID=6978, 7539, 6976;
RN      [1]
RP      SEQUENCE.
RC      SPECIES=P.americana;
RX      MEDLINE=85046530; PubMed=6548628;
RA      Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,

Rinehart K.L. Jr.;
"Structures of two cockroach neuropeptides assigned by fast atom
bombardment mass spectrometry.";
RL      Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN      [2]
RP      SEQUENCE.
RC      SPECIES=P.americana;
RX      MEDLINE=84298179; PubMed=6591205;
RA      Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA      Miller C.A., Schooley D.A.;
RT      "Isolation and primary structure of two peptides with
RT      cardioacceleratory and hyperglycemic activity from the corpora
RT      cardiaca of Periplaneta americana.";
RL      Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN      [3]
RP      SEQUENCE.
RC      SPECIES=L.declineata; TISSUE=Corpora cardiaca;
RX      MEDLINE=90160053; PubMed=2576128;
RA      Gaede G., Kellner R.;
RT      "The metabolic neuropeptides of the corpus cardiaca from the potato
RT      beetle and the American cockroach are identical.";
RL      Peptides 10:1287-1289(1989).
RN      [4]
RP      SEQUENCE.
RC      SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX      MEDLINE=90253659; PubMed=2340112;
RA      Gaede G., Rinehart K.L. Jr.;
RT      "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT      the corpora cardiaca of the cockroaches Leucophaea maderae
RT      Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT      and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT      atom bombardment mass spectrometry.";
RL      Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC      -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC      ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYPH (TREHALOSE IS
CC      THE MAJOR CARBOHYDRATE IN THE HEMOLYPH OF INSECTS).
CC      -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR      PIR; B44960; B49620.
DR      PIR; B49823; B49823.
DR      PIR; S08996; S08996.
DR      InterPro; IPR002047; AKH.
DR      PROSITE; PS00256; AKH; 1.
KW      Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT      MOD RES      1 1
FT      MOD RES      8 8
SQ      SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TF 3
Db      3 TF 4

RESULT 50
LCK1_LEUMA
ID      LCK1_LEUMA      STANDARD;      PRT;      8 AA.
AC      P21140;
DT      01-MAY-1991 (Rel. 18, Created)
DT      01-MAY-1991 (Rel. 18, Last sequence update)
DT      01-MAY-1991 (Rel. 18, Last annotation update)
DE      Leucokinin I (L-I).
OS      Leucophaea maderae (Madeira cockroach).
OS      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC      Blaberidae; Leucophaea.
OX      NCBI_TaxID=6988;
RN      [1]
RP      SEQUENCE, AND SYNTHESIS.
RC      TISSUE=Head;
RA      Holman G.W., Cook B.J., Nachman R.J.;

```

RT "Isolation, primary structure and synthesis of two neuropeptides
 RT from Leucophaea maderae: members of a new family of
 RL Cephalomyotropins.";
 RL Comp. Biochem. Physiol. 84C:205-211 (1986).
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
 CC Neuropeptide; Amidation.
 KW MOD_RES 8 AMIDATION.
 FT SEQUENCE 8 AA; 993 MW; DC6365B449C676A CRC64;
 SQ

Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FN 4
 ||
 Db 4 FN 5

RESULT 51
 LCK3_LEUMA STANDARD; PRT; 8 AA.
 ID LCK3_LEUMA
 AC P21142;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE Leucokinin III (L-III).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Primary structure and synthesis of two additional neuropeptides
 RT from Leucophaea maderae: members of a new family of
 RL Cephalomyotropins.";
 RL Comp. Biochem. Physiol. 84C:271-276 (1986).
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 910 MW; DC6365B449C66DA CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FN 4
 ||
 Db 4 FN 5

RESULT 52
 LPMS_STAEP STANDARD; PRT; 8 AA.
 ID LPMS_STAEP
 AC P23211;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-MAR-1992 (Rel. 21, Last annotation update)
 DE Probable msrA leader peptide.
 OS Staphylococcus epidermidis.
 OQ Plasmid pUL5050.
 OC Bacteri; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=968;
 RX MEDLINE=91041730; PubMed=2233255;

RA Ross J.I., Eady E.A., Cove J.H., Cunliffe W.J., Baumberg S.,
 RA Wootton J.C.;
 RT "Inducible erythromycin resistance in staphylococci is encoded by a
 RT member of the ATP-binding transport super-gene family.";
 RL Mol. Microbiol. 4:1207-1214 (1990).
 CC -!- FUNCTION: MAY REGULATE EXPRESSION OF THE ERYTHROMYCIN RESISTANCE
 CC PROTEIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).

CC EMBL; X52085; CAA36303.1; -.
 DR PIR; S11157; LFSAME.
 KW Leader peptide; Plasmid.
 SQ SEQUENCE 8 AA; 937 MW; FA37340685BDC1A6 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LK 16
 ||
 Db 7 LK 8

RESULT 53
 RSL_ERWCH STANDARD; PRT; 8 AA.
 ID RSL_ERWCH
 AC P37985;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE 30S ribosomal protein S1 (Fragment).
 GN RPSA.
 OS Brwinia chrysanthemi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Pectobacterium.
 OX NCBI_TaxID=556;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3937;
 RA Douillie A., Toussaint A., Faelen M.;
 RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: BINDS MRNA; THUS FACILITATING RECOGNITION OF THE
 CC INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT
 CC SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).

CC EMBL; X74750; CAA52769.1; -.
 DR PIR; S37141; S37141.
 KW Ribosomal protein; Repeat; RNA-binding.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 837 MW; 9E18733DCSB339CD CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GE 12
 ||

```

Db          7 GE 8

RESULT 54
RT34_BOVIN
ID UPAA_HUMAN STANDARD; PRT; 8 AA.
AC P82929;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S34 (S34mt) (MRP-S34) (Fragment).
GN MRPS34.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
RN NCBI_TaxID=9913;
RP SEQUENCE.
RC TISSUE=Liver;
RA MEDLINE=21276436; PubMed=11279123;
RA Koc E.C.; Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrion.
KW Ribosomal protein; Mitochondrial.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          2 TF 3
Db          6 TF 7

RESULT 55
UPAA_HUMAN
ID UPAA_HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN NCBI_TaxID=9606;
RP SEQUENCE.
RC TISSUE=Plasma;
RA MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7, ITS MW IS: 12 kDa.
DR SWISS-2DPAGE; P30096; HUMAN.
FT NON TER 1 1
FT VARIANT 5 5 F -> P.
FT VARIANT 8 8 /FTID=VAR_000004.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;

```

```

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          2 TF 3
Db          4 TF 5

RESULT 56
AL11_CARMA
ID AL11_CARMA STANDARD; PRT; 9 AA.
AC P81814;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 11.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
[1]
RN NCBI_TaxID=6759;
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RA MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestros J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 927 MW; 832D79CDB46D861 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 AT 2
Db          1 AT 2

RESULT 57
ALC_CHLRE
ID ALC_CHLRE STANDARD; PRT; 9 AA.
AC P82678;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Allantoicase (EC 3.5.3.4) (Allantoate amidinohydrolase) (Fragment).
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
[1]
RN NCBI_TaxID=3055;
RP SEQUENCE.
RC STRAIN=6145C;
RA MEDLINE=20318328; PubMed=10860551;
RA Piedras P., Munoz A., Aguilar M., Pineda M.;
RT "Allantoate amidinohydrolase (Allantoicase) from Chlamydomonas
RT reinhardtii: its purification and catalytic and molecular
RT characterization.";
RL Arch. Biochem. Biophys. 378:340-348(2000).
CC -!- FUNCTION: Catalyzes the degradation of allantoate to (-)-
CC ureidoglycolate and (+)-ureidoglycolate to glyoxylate.
CC -!- CATALYTIC ACTIVITY: Allantoate + H(2)O = (-)-ureidoglycolate +
CC urea.
CC -!- PATHWAY: Degradation of allantoin (purine catabolism); second
CC step.
CC -!- SUBUNIT: Homohexamer.

```

CC -!- MISCELLANEOUS: Optimum pH is 6.5 and 8 for the reactions with
 CC allantoinase and uridyloglycolate, respectively.
 CC -!- SIMILARITY: BELONGS TO THE ALLANTOICASE FAMILY.
 KW Hydrolase; Purine metabolism. OR Y.
 FT UNSURE 5 5
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 943 MW; D934ADD9D6D871F2 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AT 2
 ||
 7 AT 8

Db

RESULT 58

BS43_SERPL STANDARD; PRT; 9 AA.
 AC P83375;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bacteriocin serracin P 43 kDa subunit (Fragment).
 OS Serratia plymuthica.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Serratia.
 OC NCBI_TaxID=82996;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC STRAIN=J7;
 RX MEDLINE=22293561; PubMed=12406768;
 RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenberghe I.,
 RA Van Beemuen J., Thonart P.;
 RT "Characterization of serracin P, a phage-tail-like bacteriocin, and
 RT its activity against *Erwinia amylovora*, the fire blight pathogen.";
 RL Appl. Environ. Microbiol. 68:5704-5710(2002).
 CC -!- FUNCTION: Major component of a prophage tail sheath (Probable).
 CC -!- FUNCTION: Antibacterial activity against Gram-negative bacterium
 CC *E. amylovora*.
 DR InterPro; IPR006498; Tail tube.
 DR Pfam; PF04985; Phage_tube; 1.
 KW Antibiotic; Bacteriocin.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1095 MW; 1E66D412C871E1FB CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HG 11
 ||
 4 HG 5

Db

RESULT 59

DI_NEPNO STANDARD; PRT; 9 AA.
 AC P24816;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-MAR-1992 (Rel. 21, Last annotation update)
 DE Gastrin/cholecystokinin-like peptide DI.
 OS Nephrops norvegicus (Norway lobster).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Plecocyemata; Astacidea;
 OC Nephropoidea; Nephropidae; Nephrops.
 OC NCBI_TaxID=6829;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=92082847; PubMed=1747388;

RA Favrel P., Kegel G., Sedlmeier D., Keller R., van Wormhoudt A.;
 RT "Structure and biological activity of crustacean gastrointestinal
 RT peptides identified with antibodies to gastrin/cholecystokinin.";
 RL Biochimie 73:1233-1239(1991).
 CC -!- FUNCTION: MAY CONTROL DIGESTION PROCESSES IN CRUSTACEANS.
 CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR PIR; S47432; S47432.
 KW Hormone.
 SQ SEQUENCE 9 AA; 1038 MW; 60EC79CAB6D8787B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QD 8
 ||
 5 QD 6

Db

RESULT 60

DSIP_RABIT STANDARD; PRT; 9 AA.
 AC P01156;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Delta sleep-inducing peptide (DSIP).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77185324; PubMed=862769;
 RA Monnier M., Dudler L., Gachter R., Maier P.F., Tobler H.J.,
 RA Schoenberger G.A.;
 RT "The delta sleep inducing peptide (DSIP). Comparative properties of
 RT the original and synthetic nonapeptide.";
 RL Experientia 33:548-552(1977).
 RN [2]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=79054421; PubMed=568769;
 RA Schoenberger G.A., Maier P.F., Tobler H.J., Wilson K., Monnier M.;
 RT "The delta EEG (sleep)-inducing peptide (DSIP). XI. Amino-acid
 RT analysis, sequence, synthesis and activity of the nonapeptide.";
 RL Pflugers Arch. 376:119-129(1978).
 RN [3]
 RP REVIEW.
 RX MEDLINE=87175129; PubMed=3550726;
 RA Graf M.V., Kastin A.J.;
 RT "Delta-sleep-inducing peptide (DSIP): an update.";
 RL Peptides 7:1165-1187(1986).
 CC -!- FUNCTION: WHEN INFUSED INTO THE MESODIENCEPHALIC VENTRICLE OF
 CC RECIPIENT RABBITS INDUCES SPINDLE AND DELTA EEG ACTIVITY AND
 CC REDUCED MOTOR ACTIVITIES.
 CC -!- MISCELLANEOUS: THIS PEPTIDE WAS OBTAINED FROM DIALYSATES OF
 CC OCCIPITAL VENOUS SINUS BLOOD FROM RABBITS KEPT ASLEEP BY ELECTRIC
 CC STIMULATION OF THE THALAMUS.
 CC -!- DATABASE: NAME=Protein Spotlight;
 CC NOTE=Issue 8 of March 2001;
 CC WWW="http://www.expasy.org/spotlight/articles/sptlt008.html".
 DR PIR; A01422; QDRB.
 SQ SEQUENCE 9 AA; 849 MW; DDD365BDDAA8787D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GE 12
 ||
 8 GE 9

Db


```
RESULT 61
FAR3 CALVO
ID FAR3 CALVO STANDARD; PRT; 9 AA.
AC P41856;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC -!- SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A41978; A41978.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QD 8
DB 4 QD 5

RESULT 62
FAR2 CALVO
ID FAR2 CALVO STANDARD; PRT; 9 AA.
AC P41857;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 2.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC -!- SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; B41978; B41978.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1128 MW; 29D00699CAB6C5A7 CRC64;
```

```
Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QD 8
DB 4 QD 5

RESULT 63
FAR3 CALVO
ID FAR3 CALVO STANDARD; PRT; 9 AA.
AC P41858;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 3.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC -!- SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; C41978; C41978.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1114 MW; 2F0B0699CAB6C5A7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QD 8
DB 4 QD 5

RESULT 64
FAR4 CALVO
ID FAR4 CALVO STANDARD; PRT; 9 AA.
AC P41859;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 4.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
```

CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR PIR; D41978; D41978.
 KW Neuropeptide; Amidation.
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 1182 MW; 31730699CAB6D457 CRC64;
 Amidation.

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QD 8
 ||
 Db 4 QD 5

RESULT 65
 FARS_ASCSU
 ID_FARS_ASCSU STANDARD; PRT; 9 AA.
 AC P43170;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRFamide-like neuropeptide AF5.
 DE FMRFamide-like neuropeptide AF5.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoidea).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OC NCBI_TaxID=6253;
 RN [1]
 RN SEQUENCE.
 RP MEDLINE=95380362; PubMed=7651904;
 RX Cowden C., Strutton A.O.W.;
 RA "Right novel FMRFamide-like neuropeptides isolated from the nematode
 RT Ascaris suum.";
 RL Peptides 16:491-500(1995).
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 1052 MW; 34080059D1B76338 CRC64;
 Amidation.

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TF 3
 ||
 Db 5 TF 6

RESULT 66
 FARS_CALVO
 ID_FARS_CALVO STANDARD; PRT; 9 AA.
 AC P41860;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CallifMRamide 5.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OC NCBI_TaxID=27454;
 RN [1]
 RN SEQUENCE.
 RP TISSUE=Thoracic ganglion;
 RC MEDLINE=92196111; PubMed=1549595;
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated callifMRamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).

CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR PIR; E41978; E41978.
 KW Neuropeptide; Amidation.
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 1068 MW; 39D10699CAB6D867 CRC64;
 Amidation.

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QD 8
 ||
 Db 4 QD 5

RESULT 67
 FARS_PENMO
 ID_FARS_PENMO STANDARD; PRT; 9 AA.
 AC P83320;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRFamide-like neuropeptide FLPS (SMPSLRLEF-amide).
 DE FMRFamide-like neuropeptide FLPS (SMPSLRLEF-amide).
 OS Penaeus monodon (Penaeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OC NCBI_TaxID=6687;
 RN [1]
 RN SEQUENCE, AND MASS SPECTROMETRY.
 RP TISSUE=Eyestalk;
 RC MEDLINE=21956277; PubMed=11959015;
 RX Sithigorngul P., Pupuem J., Krungkarn C., Longyant S.,
 RA Chaivitsuthangkura P., Sithigorngul W., Petsom A.;
 RA "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
 RT of the giant tiger prawn Penaeus monodon.";
 RT Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;
 Amidation.

Query Match 11.1%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 SL 18
 ||
 Db 4 SL 5

RESULT 68
 FARS_CALVO
 ID_FARS_CALVO STANDARD; PRT; 9 AA.
 AC P41861;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CallifMRamide 6.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OC NCBI_TaxID=27454;
 RN [1]
 RN SEQUENCE.
 RP TISSUE=Thoracic ganglion;
 RC MEDLINE=92196111; PubMed=1549595;
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,

```
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated callifWRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY
DR PIR; F41978; F41978.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1058 MW; 96D10699CAB6D865 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QD 8
DB 4 QD 5

RESULT 69
FARP CALVO
ID FARP CALVO STANDARD; PRT; 9 AA.
AC P41862;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 7.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; G41978; G41978.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1081 MW; E1D10699CAB6D86A CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QD 8
DB 4 QD 5

RESULT 70
FARP CALVO
ID FARP CALVO STANDARD; PRT; 9 AA.
AC P41865;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 10.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
```

```
RN SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A44787; A44787.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
FT UNSURE 1 1
SQ SEQUENCE 9 AA; 1183 MW; 29D00699CAB40457 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NR 5
DB 3 NR 4

RESULT 71
FARP CALVO
ID FARP CALVO STANDARD; PRT; 9 AA.
AC P41858;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 13.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; D44787; D44787.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1028 MW; 22D10699C87AB6D8 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QD 8
DB 3 QD 4

RESULT 72
FARP CALSI
ID FARP CALSI STANDARD; PRT; 9 AA.
AC P38495;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
```

DE FMRamide-like neuropeptide.
OS Callinectes sapidus (Blue crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Callinectes.
RN NCBI_TaxID=6763;
RN [1]
RP SEQUENCE.
RX MEDLINE=92270479; PubMed=1815216;
RA Krajniak K.G.;
RT "The identification and structure-activity relations of a
RT cardioactive FMRamide-related peptide from the blue crab Callinectes
RT sapidus".
RL Peptides 12:1295-1302(1991).
CC -!- FUNCTION: CARDIOACTIVE PEPTIDE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION
SQ SEQUENCE 9 AA; 1159 MW; 134F0729D5A4045B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NR 5
DB 3 NR 4

RESULT 73
FIBB_ERYPA
ID FIBB_ERYPA STANDARD; PRT; 9 AA.
AC P19346;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocybus.
OX NCBI_TaxID=9538;
OX [1]
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocybus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons".
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D24180; D24180.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1020 MW; 69FF7879C732CB1B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NR 5
DB 3 NR 4

RESULT 74
FIBB_MACFU
ID FIBB_MACFU STANDARD; PRT; 9 AA.
AC P19345;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9543;
OX [1]
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocybus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons".
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; C24180; C24180.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1038 MW; 69FE65B9C735BB1B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EE 13
DB 2 EE 3

RESULT 75
FIBB_PAPHA
ID FIBB_PAPHA STANDARD; PRT; 9 AA.
AC P19343;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9557;
OX [1]
RN RN
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;

QY 12 EE 13
DB 2 EE 3

RESULT 74
FIBB_MACFU
ID FIBB_MACFU STANDARD; PRT; 9 AA.
AC P19345;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9543;
OX [1]
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocybus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons".
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; C24180; C24180.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1038 MW; 69FE65B9C735BB1B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EE 13
DB 2 EE 3

RESULT 75
FIBB_PAPHA
ID FIBB_PAPHA STANDARD; PRT; 9 AA.
AC P19343;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9557;
OX [1]
RN RN
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;

"Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, RT and Theropithecus gelada): their amino acid sequences and RT evolutionary rates and a molecular phylogeny for the baboons."; RL J. Biochem. 94:1973-1978(1983).

CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET CC AGGREGATION.

CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

DR PIR: E28854; E28854. Fibrinogen C. DR InterPro; IPR002181; Fibrinogen C. DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL. KW Blood coagulation; Plasma. FT PEPTIDE 1 9 FIBRINOPEPTIDE B. FT NON_TER 9 9 SQ SEQUENCE 9 AA; 1057 MW; DDFE71E9C7287B06 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HG 11
||
Db 7 HG 8

Search completed: November 25, 2003, 19:28:26
Job time : 7.45515 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 33.8023 Seconds
(without alignments)
137.415 Million cell updates/sec

Title: US-09-641-801-30

Perfect score: 18

Sequence: 1 ATFNRYQDDHGERILKSL 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	22.2	18	2	Q9R4V9
2	4	22.2	20	2	Q9R417
3	4	22.2	20	6	Q9TR34
4	4	22.2	20	6	Q9TR33
5	4	22.2	20	10	Q9S8X5
6	4	22.2	20	13	Q9RPN6
7	4	22.2	20	15	Q993P2
8	4	22.2	20	15	Q993Q0
9	4	22.2	20	15	Q993Q4
10	4	22.2	20	15	Q993P4
11	4	22.2	20	15	Q993N6
12	4	22.2	20	15	Q993P8
13	4	22.2	20	15	Q993N8
14	4	22.2	20	15	Q993Q6
15	3	16.7	7	4	Q15897
16	3	16.7	8	2	Q51594

17 3 16.7 8 2 Q8GL21
18 3 16.7 8 4 Q15895
19 3 16.7 8 8 P93963
20 3 16.7 8 8 P92384
21 3 16.7 8 8 P93973
22 3 16.7 8 8 P92215
23 3 16.7 8 8 P93957
24 3 16.7 8 8 P92222
25 3 16.7 8 8 P92388
26 3 16.7 8 8 P92441
27 3 16.7 8 8 P92404
28 3 16.7 8 8 P93961
29 3 16.7 8 8 P93970
30 3 16.7 8 8 P93955
31 3 16.7 8 8 P93965
32 3 16.7 8 8 P92394
33 3 16.7 8 8 P92382
34 3 16.7 8 8 P93966
35 3 16.7 8 8 P92227
36 3 16.7 8 8 P92373
37 3 16.7 8 8 P92211
38 3 16.7 8 8 P92428
39 3 16.7 8 8 P92386
40 3 16.7 8 8 P93959
41 3 16.7 8 8 P93965
42 3 16.7 8 8 P92443
43 3 16.7 8 8 P92391
44 3 16.7 8 8 P93981
45 3 16.7 8 8 P93992
46 3 16.7 8 8 P92426
47 3 16.7 8 8 P92431
48 3 16.7 8 8 P92422
49 3 16.7 8 10 Q40530
50 3 16.7 8 11 Q9ERD2
51 3 16.7 8 13 Q90ZV5
52 3 16.7 9 2 Q8GL31
53 3 16.7 9 12 Q9IBY9
54 3 16.7 10 8 Q8W704
55 3 16.7 10 11 Q63056
56 3 16.7 10 11 Q8VIL8
57 3 16.7 10 11 Q9JLI5
58 3 16.7 11 2 Q9L4F7
59 3 16.7 11 2 Q9S618
60 3 16.7 11 2 Q8GL19
61 3 16.7 11 4 Q16234
62 3 16.7 11 10 Q8RV30
63 3 16.7 11 12 Q8JS92
64 3 16.7 12 2 Q93A08
65 3 16.7 12 2 Q93U04
66 3 16.7 12 2 Q9L4M9
67 3 16.7 12 2 Q47251
68 3 16.7 12 6 Q9TRU1
69 3 16.7 12 8 P82164
70 3 16.7 12 11 Q62966
71 3 16.7 12 12 Q84268
72 3 16.7 13 2 Q9R3R6
73 3 16.7 13 4 Q9UDE0
74 3 16.7 13 5 Q8I2E2
75 3 16.7 13 10 Q945C1
76 3 16.7 13 12 Q86129
77 3 16.7 14 2 Q9R517
78 3 16.7 14 2 Q9LCS1
79 3 16.7 14 2 Q44847
80 3 16.7 14 10 P82341
81 3 16.7 15 2 Q9R5H5
82 3 16.7 15 2 Q9R543
83 3 16.7 15 4 Q16297
84 3 16.7 15 4 Q9UR90
85 3 16.7 15 5 Q9UCC2
86 3 16.7 15 5 Q9TWF3
87 3 16.7 15 5 Q9TWF3
88 3 16.7 15 6 Q9RTR6
89 3 16.7 15 6 Q9N0G0

Q8GL21 borrelia bu
Q15895 homo sapien
P93963 peathyrosta
P92384 hordeum mur
P93973 eremopyrum
P92215 amblyopyrum
P93957 festucopsis
P92222 bromus iner
P92388 henrardia p
P92441 thincopyrum
P92404 lophopyrum
P93961 peathyrosta
P93970 eremopyrum
P93955 festucopsis
P93965 secale stri
P92394 hordeum vul
P92382 hordeum bra
P93966 aegilops sp
P92227 crithopsis
P92373 haynaldia v
P92211 agropyron c
P92428 peridictyon
P92386 hordeum mar
P93959 hordeum ere
P93985 aegilops co
P92443 taeniatheir
P92391 heteranthe
P93981 crithodium
P93992 australopyr
P92426 pseudoeegn
P92431 aegilops ta
P92422 peathyrosta
Q40530 nicotiana t
Q9ERD2 mus musculu
Q90ZV5 fulica leuc
Q8GL31 borrelia bu
Q9IBY9 kaposi's sa
Q8W704 anolis nite
Q63056 rattus norv
Q8VIL8 mus musculu
Q9JLI5 mus musculu
Q9L4F7 bacillus ce
Q9S618 prochloroco
Q8GL19 borrelia bu
Q16234 homo sapien
Q8RV30 zea mays (m
Q8JS92 hepatitis b
Q93A08 thibacilla
Q93U04 escherichia
Q9L4M9 streptococc
Q47251 escherichia
Q9TRU1 bos taurus
P82164 spinacia ol
Q62966 rattus norv
Q84268 human papil
Q9R3R6 prochloroco
Q9UDE0 homo sapien
Q8I2E2 plasmodium
Q945C1 cryptescodi
Q86129 vesicular s
Q9R517 escherichia
Q9LCS1 bacillus bu
Q44847 borrelia bu
P82341 pisum sativ
Q9R5H5 rhodospiril
Q9R543 mycobacteri
Q9UR90 saccharomyc
Q16297 homo sapien
Q9UCC2 homo sapien
Q9TWF3 dictyosteli
P82207 bombyx mori
Q9RTR6 sus scrofa
Q9N0G0 canis fami

90 Q9tr54 ovis aries
 91 P82665 bos taurus
 92 Q8hz79 bos taurus
 93 Q8wk21 bolidomonas
 94 Q8cj29 mus musculus
 95 Q88954 vaccinia vi
 96 Q9prz9 micropogoni
 97 Q9k4j0 arthrobacte
 98 Q54357 bacillus am
 99 Q937k1 escherichia
 100 Q8v1x6 thermus the

ALIGNMENTS

RESULT 1
 Q9R4V9 ID Q9R4V9 PRELIMINARY; PRT; 18 AA.
 AC Q9R4V9;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
 DE 10 kDa heat shock- and alkaline PH-induced protein (Fragment).
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=197;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95012609; PubMed=7927682;
 RA Wu Y.L.; Lee L.H.; Rollins D.M.; Ching W.M.;
 RT "Heat shock- and alkaline PH-induced proteins of Campylobacter jejuni:
 RT characterization and immunological properties."
 RL Infect. Immun. 62:4256-4260(1994).
 SQ SEQUENCE 18 AA; 2056 MW; 9E4FED7B4DA76C4 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13
 Db 14 HGEE 17

RESULT 2
 Q9R4L7 ID Q9R4L7 PRELIMINARY; PRT; 20 AA.
 AC Q9R4L7;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Dextranucrase (EC 2.4.1.5) (Fragment).
 OS Leuconostoc mesenteroides.
 OC Bacteria; Firmicutes; Lactobacillales; Leuconostoc.
 OX NCBI_TaxID=1245;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95306915; PubMed=7540436;
 RA Funane K.; Yamada M.; Shiraiwa M.; Takahara H.; Yamamoto N.;
 RA Ichishima E.; Kobayashi M.;
 RT "Aggregated form of dextranucrases from Leuconostoc mesenteroides
 RT NRRL B-512F and its constitutive mutant."
 RL Biosci. Biotechnol. Biochem. 59:776-780(1995).
 DR InterPro; IPR003318; Glyco_hydro_70.
 DR Pfam; PF02324; Glyco_hydro_70; 1.
 SQ SEQUENCE 20 AA; 2356 MW; 701179A7AC89957F CRC64;

Query Match 22.2%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YQDD 9
 Db 12 YQDD 15

RESULT 3
 Q9TR34 ID Q9TR34 PRELIMINARY; PRT; 20 AA.
 AC Q9TR34;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
 DE Cytochrome c oxidase subunit VIA-L (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96092035; PubMed=8529022;
 RA Linder D.; Freund R.; Kadenbach B.;
 RT "Species-specific expression of cytochrome c oxidase isozymes."
 RL Comp. Biochem. Physiol. 112B:461-469(1995).
 FT NON TER 1
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2079 MW; 97E5DDCAB5076C26 CRC64;

Query Match 22.2%; Score 4; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13
 Db 5 HGEE 8

RESULT 4
 Q9TR33 ID Q9TR33 PRELIMINARY; PRT; 20 AA.
 AC Q9TR33;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
 DE Cytochrome c oxidase subunit VIA-L (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96092035; PubMed=8529022;
 RA Linder D.; Freund R.; Kadenbach B.;
 RT "Species-specific expression of cytochrome c oxidase isozymes."
 RL Comp. Biochem. Physiol. 112B:461-469(1995).
 FT NON TER 1
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2109 MW; 97E5C71075076C26 CRC64;

Query Match 22.2%; Score 4; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13
 Db 5 HGEE 8

RESULT 5
 Q9S8X5 ID Q9S8X5 PRELIMINARY; PRT; 20 AA.
 AC Q9S8X5;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Vegetative storage protein 94 peptide 2, WSP94=LIPXYGENASE
 DE (fragment).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OC NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92361246; PubMed=1822994;
 RA Tranbarger T.J., Franceschi V.R., Hildebrand D.F., Grimes H.D.;
 RT "The soybean 94-kilodalton vegetative storage protein is a
 RT lipoxigenase that is localized in paraveinal mesophyll cell
 RT vacuoles."
 RL Plant Cell 3:973-987(1991).
 FT NON_TER 1 1
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2330 MW; B889AB684EA09968 CRC64;
 Query Match 22.2%; Score 4; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 LKSL 18
 DB 6 LKSL 9
 RESULT 6
 Q9PRN6 PRELIMINARY; PRT; 20 AA.
 ID Q9PRN6
 AC Q9PRN6
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Urotensin I homolog.
 OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
 OC Scyllorhinidae; Scyllorhinus.
 OC NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96051495; PubMed=8536945;
 RA Waugh D., Anderson G., Armour K.J., Baiment R.J., Hazon N.,
 RA Conlon J.M.;
 RT "A peptide from the caudal neurosecretory system of the dogfish
 RT Scyllorhinus canicula that is structurally related to urotensin I."
 RL Gen. Comp. Endocrinol. 99:333-339(1995).
 SQ SEQUENCE 20 AA; 2305 MW; 77A92D52817E97B7 CRC64;
 Query Match 22.2%; Score 4; DB 13; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TFNR 5
 DB 11 TFNR 14
 RESULT 7
 Q993P2 PRELIMINARY; PRT; 20 AA.
 ID Q993P2
 AC Q993P2
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Gag protein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PRB670;
 RX MEDLINE=21136890; PubMed=11238855;
 RA Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;
 RT "Individual Contributions of Mutant Protease and Reverse Transcriptase
 RT to Viral Infectivity, Replication, and Protein Maturation of
 RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1."
 RL J. Virol. 75:3291-3300(2001).
 DR ENBL; AF316847; AAK21098.1; --
 FT NON_TER 1 1
 SQ SEQUENCE 20 AA; 2167 MW; B9EBC80E8A2AE340 CRC64;
 Query Match 22.2%; Score 4; DB 15; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 LKSL 18
 DB 9 LKSL 12
 RESULT 8
 Q993Q0 PRELIMINARY; PRT; 20 AA.
 ID Q993Q0
 AC Q993Q0
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Gag protein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PR-RTB497;
 RX MEDLINE=21136890; PubMed=11238855;
 RA Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;
 RT "Individual Contributions of Mutant Protease and Reverse Transcriptase
 RT to Viral Infectivity, Replication, and Protein Maturation of
 RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1."
 RL J. Virol. 75:3291-3300(2001).
 DR ENBL; AF316843; AAK21090.1; --
 FT NON_TER 1 1
 SQ SEQUENCE 20 AA; 2194 MW; B9EBC80E8A3B1340 CRC64;
 Query Match 22.2%; Score 4; DB 15; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 LKSL 18
 DB 9 LKSL 12
 RESULT 9
 Q993Q4 PRELIMINARY; PRT; 20 AA.
 ID Q993Q4
 AC Q993Q4
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Gag protein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PRB497;
 RX MEDLINE=21136890; PubMed=11238855;


```
RA Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;  
RT "Individual Contributions of Mutant Protease and Reverse Transcriptase  
RT to Viral Infectivity, Replication, and Protein Maturation of  
RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1.";  
RL J. Virol. 75:3291-3300(2001).  
DR EMBL; AF316840; AAK21086.1; -.  
FT NON TER 1  
SQ SEQUENCE 20 AA; 2194 MW; B9EBC80E8A3B1340 CRC64;  
  
Query Match 22.2%; Score 4; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 15 LKSL 18  
Db 9 LKSL 12  
|||||  
RESULT 10  
Q993P4 PRELIMINARY; PRT; 20 AA.  
ID Q993P4  
AC Q993P4  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Gag protein (Fragment).  
GN GAG.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI_TaxID=11676;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PR-B670;  
RX MEDLINE=21136890; PubMed=11238855;  
RA Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;  
RT "Individual Contributions of Mutant Protease and Reverse Transcriptase  
RT to Viral Infectivity, Replication, and Protein Maturation of  
RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1.";  
RL J. Virol. 75:3291-3300(2001).  
DR EMBL; AF316846; AAK21096.1; -.  
FT NON TER 1  
SQ SEQUENCE 20 AA; 2194 MW; B9EBC80E8A3B1340 CRC64;  
  
Query Match 22.2%; Score 4; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 15 LKSL 18  
Db 9 LKSL 12  
|||||  
RESULT 11  
Q993N6 PRELIMINARY; PRT; 20 AA.  
ID Q993N6  
AC Q993N6  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Gag protein (Fragment).  
GN GAG.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI_TaxID=11676;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PR-RTB670;  
RX MEDLINE=21136890; PubMed=11238855;  
RA Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;  
RT "Individual Contributions of Mutant Protease and Reverse Transcriptase  
RT to Viral Infectivity, Replication, and Protein Maturation of  
RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1.";  
RL J. Virol. 75:3291-3300(2001).
```

```
DR EMBL; AF316851; AAK21104.1; -.  
FT NON TER 1  
SQ SEQUENCE 20 AA; 2194 MW; B9EBC80E8A3B1340 CRC64;  
  
Query Match 22.2%; Score 4; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 15 LKSL 18  
Db 9 LKSL 12  
|||||  
RESULT 12  
Q993P8 PRELIMINARY; PRT; 20 AA.  
ID Q993P8  
AC Q993P8  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Gag protein (Fragment).  
GN GAG.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI_TaxID=11676;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PR-RTB497;  
RX MEDLINE=21136890; PubMed=11238855;  
RA Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;  
RT "Individual Contributions of Mutant Protease and Reverse Transcriptase  
RT to Viral Infectivity, Replication, and Protein Maturation of  
RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1.";  
RL J. Virol. 75:3291-3300(2001).  
DR EMBL; AF316844; AAK21092.1; -.  
FT NON TER 1  
SQ SEQUENCE 20 AA; 2194 MW; B9EBC80E8A3B1340 CRC64;  
  
Query Match 22.2%; Score 4; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 15 LKSL 18  
Db 9 LKSL 12  
|||||  
RESULT 13  
Q993N8 PRELIMINARY; PRT; 20 AA.  
ID Q993N8  
AC Q993N8  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Gag protein (Fragment).  
GN GAG.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI_TaxID=11676;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PR-RTB670;  
RX MEDLINE=21136890; PubMed=11238855;  
RA Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;  
RT "Individual Contributions of Mutant Protease and Reverse Transcriptase  
RT to Viral Infectivity, Replication, and Protein Maturation of  
RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1.";  
RL J. Virol. 75:3291-3300(2001).  
DR EMBL; AF316850; AAK21102.1; -.  
FT NON TER 1  
SQ SEQUENCE 20 AA; 2194 MW; B9EBC80E8A3B1340 CRC64;  
  
Query Match 22.2%; Score 4; DB 15; Length 20;
```

```
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
Db 9 LKSL 12

RESULT 14
Q99306 PRELIMINARY; PRT; 20 AA.
AC Q99306;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag protein (Fragment).
GN GAG
OS Human immunodeficiency virus 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRB497;
RX MEDLINE=21136890; PubMed=11238855;
RA Bleiber G.; Munoz M.; Cluffi A.; Meylan P.; Telenti A.;
RT "Individual Contributions of Mutant Protease and Reverse Transcriptase
to Viral Infectivity, Replication, and Protein Maturation of
RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1.";
RL J. Virol. 75:3291-3300(2001).
DR EMBL; AF316839; AAK21084.1; -.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2194 MW; B9EBC80E8A3B1340 CRC64;

Query Match 22.2%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
Db 9 LKSL 12

RESULT 15
Q15897 PRELIMINARY; PRT; 7 AA.
AC Q15897;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP6A11A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C.; Yazdani A.; Wehnert M.; Bailey J.; Couch L.; Xiong M.;
RA Coolbaugh M.I.; Chinault C.A.; Baldini A.; Lindeay E.A.; Zhao Z.-Y.;
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32077; AAA73887.1; -.
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 814 MW; 672B1DD337204650 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILK 16
```

```
Db 2 ILK 4

RESULT 16
Q51594 PRELIMINARY; PRT; 8 AA.
AC Q51594;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CopB protein (Fragment).
OS Escherichia coli.
OG Plasmid ColV2-K94.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86223772; PubMed=2423502;
RA Weber P.C.; Palchaudhuri S.;
RT "Incompatibility repressor in a repA-like replicon of the IncFI
RT plasmid ColV2-K94.";
RL J. Bacteriol. 166:1106-1112(1986).
DR EMBL; M13472; AAR23194.1; -.
KW Plasmid.
FT NON_TER 1
SQ SEQUENCE 8 AA; 998 MW; 0F37205AA73416D7 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILK 16
Db 6 ILK 8

RESULT 17
Q8GL21 PRELIMINARY; PRT; 8 AA.
AC Q8GL21;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-8.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sh-2-82;
RA Stevenson B.; Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
RT prophages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV142094; AAN17903.1; -.
KW Plasmid.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1042 MW; 1437244337204373 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILK 16
Db 3 ILK 5

RESULT 18
```

```

Q15895
ID Q15895 PRELIMINARY; PRT; 8 AA.
AC Q15895;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP6A10A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32075; AAA73885.1; -.
FT NON TER 1
FT NON TER 8
FT NON TER 8
SQ SEQUENCE 8 AA; 921 MW; C6C735B33686C1AA CRC64;

Query Match 16.7%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18
Db 5 KSL 7

RESULT 19
P93963
ID P93963 PRELIMINARY; PRT; 8 AA.
AC P93963;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PeD protein (Fragment).
GN PETD.
OS Psathyrostachys stoloniformis.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Psathyrostachys.
OX NCBI_TaxID=58873;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H9182; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77754; CAB01341.1; -.
FT NON TER 1
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18
Db 1 KSL 3

RESULT 20
P92384
ID P92384 PRELIMINARY; PRT; 8 AA.
AC P92384;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PeD protein (Fragment).
GN PETD.
OS Hordeum murinum subsp. glaucum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=98113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H801; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77762; CAB01365.1; -.
FT NON TER 1
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18
Db 1 KSL 3

RESULT 22
P93973
ID P93973 PRELIMINARY; PRT; 8 AA.
AC P93973;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PeD protein (Fragment).
GN PETD.
OS Eremopyrum distans.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Eremopyrum.
OX NCBI_TaxID=58936;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5552; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77745; CAB01314.1; -.
FT NON TER 1
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18
Db 1 KSL 3

RESULT 20
P92384

```

```

P92215          PRELIMINARY;          PRT;          8 AA.
ID P92215;
AC P92215;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Amblyopyrum muticum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Amblyopyrum.
OX NCBI_TaxID=4595;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5572; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77756; CAB01347.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match          16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
DB 1 KSL 3

RESULT 23
P93957          PRELIMINARY;          PRT;          8 AA.
ID P93957;
AC P93957;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Pestucopsis serpentina.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Pestucopsis.
OX NCBI_TaxID=72456;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6511; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z79501; CAB01777.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match          16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
DB 1 KSL 3

P92215          PRELIMINARY;          PRT;          8 AA.
ID P92215;
AC P92215;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Amblyopyrum muticum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Amblyopyrum.
OX NCBI_TaxID=4595;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5572; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77756; CAB01347.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match          16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
DB 1 KSL 3

P92222          PRELIMINARY;          PRT;          8 AA.
ID P92222;
AC P92222;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Bromus inermis (Smooth brome grass).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Bromus.
OX NCBI_TaxID=15371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OSA414; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77759; CAB01356.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match          16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
DB 1 KSL 3

RESULT 25
P92388          PRELIMINARY;          PRT;          8 AA.
ID P92388;
AC P92388;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Henrardia persica.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Henrardia.
OX NCBI_TaxID=37678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5556; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77748; CAB01323.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match          16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
DB 1 KSL 3
```

RESULT 26

P92441 PRELIMINARY; PRT; 8 AA.
 AC P92441
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PetD protein (Fragment).
 GN PETD.
 OS Thinopyrum bessarabicum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Thinopyrum.
 OC NCBI_TaxID=4601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H6725; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; 277769; CAB01386.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
 |||
 Db 1 KSL 3

RESULT 27

P92404 PRELIMINARY; PRT; 8 AA.
 ID P92404
 AC P92404
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PetD protein (fragment).
 GN PETD.
 OS Lophopyrum elongatum (Tall wheatgrass) (Argopyrum elongatum).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Lophopyrum.
 OC NCBI_TaxID=4588;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H6692; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; 277743; CAB01308.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
 |||
 Db 1 KSL 3

RESULT 28

P93961 PRELIMINARY; PRT; 8 AA.
 ID P93961
 AC P93961
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PetD protein (Fragment).
 GN PETD.
 OS Psathyrostachys rupestris.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Psathyrostachys.
 OC NCBI_TaxID=58938;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H6703; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; 277755; CAB01344.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
 |||
 Db 1 KSL 3

RESULT 29

P93970 PRELIMINARY; PRT; 8 AA.
 ID P93970
 AC P93970
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PetD protein (Fragment).
 GN PETD.
 OS Eremopyrum triticeum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Eremopyrum.
 OC NCBI_TaxID=58937;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H5553; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; 277746; CAB01315.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
 |||

Db 1 KSL 3

RESULT 30

P93955 PRELIMINARY; PRT; 8 AA.

AC P93955; (TREMBlrel. 03, Created)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE PetD protein (Fragment).

GN PETD.

OS Festucopsis festucoeides.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Triticeae; Festucopsis.

OX NCBI_TaxID=72455;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H6731; TISSUE=Leaf;

RX MEDLINE=97271648; PubMed=9126564;

RA Petersen G., Seberg O.;

RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA

RT sequence data.";

RL Mol. Phylogenet. Evol. 7:217-230(1997).

DR EMBL; Z77770; CAB01389.1; -.

KW Chloroplast.

FT NON TER

SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18

Db 1 KSL 3

RESULT 31

P93965 PRELIMINARY; PRT; 8 AA.

AC P93965; (TREMBlrel. 03, Created)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE PetD protein (Fragment).

GN PETD.

OS Secale strictum.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Triticeae; Secale.

OX NCBI_TaxID=58866;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H4342; TISSUE=Leaf;

RX MEDLINE=97271648; PubMed=9126564;

RA Petersen G., Seberg O.;

RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA

RT sequence data.";

RL Mol. Phylogenet. Evol. 7:217-230(1997).

DR EMBL; Z77765; CAB01373.1; -.

KW Chloroplast.

FT NON TER

SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18

Db 1 KSL 3

RESULT 32

P92394 PRELIMINARY; PRT; 8 AA.

AC P92394; (TREMBlrel. 03, Created)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE PetD protein (Fragment).

GN PETD.

OS Hordeum vulgare (Barley).

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Triticeae; Hordeum.

OX NCBI_TaxID=4513;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H3139; TISSUE=Leaf;

RX MEDLINE=97271648; PubMed=9126564;

RA Petersen G., Seberg O.;

RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA

RT sequence data.";

RL Mol. Phylogenet. Evol. 7:217-230(1997).

DR EMBL; Z77764; CAB01371.1; -.

KW Chloroplast.

FT NON TER

SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18

Db 1 KSL 3

RESULT 33

P92382 PRELIMINARY; PRT; 8 AA.

AC P92382; (TREMBlrel. 03, Created)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE PetD protein (Fragment).

GN PETD.

OS Hordeum brachyantherum.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Triticeae; Hordeum.

OX NCBI_TaxID=52712;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H3139; TISSUE=Leaf;

RX MEDLINE=97271648; PubMed=9126564;

RA Petersen G., Seberg O.;

RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA

RT sequence data.";

RL Mol. Phylogenet. Evol. 7:217-230(1997).

DR EMBL; Z77761; CAB01362.1; -.

KW Chloroplast.

FT NON TER

SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18
Db 1 KSL 3

RESULT 34

P93966 PRELIMINARY; PRT; 8 AA.
AC P93966;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PeD protein (Fragment).
GN PEID.
OS Agilops speltoides (Goat grass).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Agilops.
OX NCBI_TaxID=4573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4523; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77766; CAB01377.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18
Db 1 KSL 3

RESULT 35

P92227 PRELIMINARY; PRT; 8 AA.
AC P92227;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PeD protein (Fragment).
GN PEID.
OS Crithopsis delileana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Crithopsis.
OX NCBI_TaxID=37674;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5558; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77751; CAB01332.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18
Db 1 KSL 3

RESULT 36

P92373 PRELIMINARY; PRT; 8 AA.
AC P92373;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PeD protein (Fragment).
GN PEID.
OS Haynaldia villosa.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Haynaldia.
OX NCBI_TaxID=40247;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5561; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77741; CAB01302.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18
Db 1 KSL 3

RESULT 37

P92211 PRELIMINARY; PRT; 8 AA.
AC P92211;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PeD protein (Fragment).
GN PEID.
OS Agropyron cristatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Agropyron.
OX NCBI_TaxID=4593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4349; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77771; CAB01392.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
|||
Db 1 KSL 3

RESULT 38

P92428 P92428 PRELIMINARY; PRT; 8 AA.
AC P92428;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Peridictyon sanctum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Peridictyon.
OX NCBI_TaxID=37683;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5575; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77749; CAB01326.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
|||
Db 1 KSL 3

RESULT 39

P92386 P92386 PRELIMINARY; PRT; 8 AA.
AC P92386;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Hordeum marinum subsp. gussoneanum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=98114;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H299; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77763; CAB01368.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 884 MW; 1EDAB8773AE735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
|||
Db 1 KSL 3

RESULT 40

P93959 P93959 PRELIMINARY; PRT; 8 AA.
AC P93959;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Hordeum erectifolium.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=58926;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H1150; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z79500; CAB01776.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
|||
Db 1 KSL 3

RESULT 41

P93985 P93985 PRELIMINARY; PRT; 8 AA.
AC P93985;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Aegilops comosa.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=4485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6673; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77742; CAB01305.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18
 Db 1 KSL 3

RESULT 42

P92443 ID P92443 PRELIMINARY; PRT; 8 AA.
 AC P92443;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE PeD protein (Fragment).
 GN PEID.
 OS Taeniatherum caput-medusae (Medusaehead).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Taeniatherum.
 OC NCBI_TaxID=37687;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H10254; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; Z77760; CAB01359.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18
 Db 1 KSL 3

RESULT 43

P92391 ID P92391 PRELIMINARY; PRT; 8 AA.
 AC P92391;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE PeD protein (Fragment).
 GN PEID.
 OS Heteranthelium piliferum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Heteranthelium.
 OC NCBI_TaxID=37679;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H5557; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; Z77750; CAB01329.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18
 Db 1 KSL 3

RESULT 44

P93981 ID P93981 PRELIMINARY; PRT; 8 AA.
 AC P93981;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE PeD protein (Fragment).
 GN PETD.
 OS Crithodium monococcum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Crithodium.
 OC NCBI_TaxID=72428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H4547; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; Z77757; CAB01350.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18
 Db 1 KSL 3

RESULT 45

P93992 ID P93992 PRELIMINARY; PRT; 8 AA.
 AC P93992;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE PeD protein (Fragment).
 GN PETD.
 OS Australopyrum velutinum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Australopyrum.
 OC NCBI_TaxID=58935;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H6724; TISSUE=Leaf;
 RX MEDLINE=97271648; PubMed=9126564;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
 DR EMBL; Z77768; CAB01383.1; -.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 1 1

```

SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;
Query Match 16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
DB 1 KSL 3

RESULT 46
P92426 ID P92426 PRELIMINARY; PRT; 8 AA.
AC P92426;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Psudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Psudoroegneria.
OX NCBI_TaxID=4604;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H9082; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230 (1997).
DR EMBL; Z77744; CAB01311.1; -.
KW Chloroplast.
FT NON TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
DB 1 KSL 3

RESULT 47
P92431 ID P92431 PRELIMINARY; PRT; 8 AA.
AC P92431;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Aegilops tauschii (Aegilops squarrosa).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=37682;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6668; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230 (1997).
DR EMBL; Z77758; CAB01353.1; -.
KW Chloroplast.

SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;
Query Match 16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
DB 1 KSL 3

RESULT 48
P92422 ID P92422 PRELIMINARY; PRT; 8 AA.
AC P92422; P92420;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
DE Chloroplast rpoA gene (Fragment).
GN PETD.
OS Psathyrostachys fragilis.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Psathyrostachys.
OX NCBI_TaxID=37729;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4372; and H917; TISSUE=Leaf;
RA Petersen G., Seberg O.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z77753; CAB01338.1; -.
DR EMBL; Z77752; CAB01335.1; -.
KW Chloroplast.
FT NON TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
DB 1 KSL 3

RESULT 49
Q40530 ID Q40530 PRELIMINARY; PRT; 8 AA.
AC Q40530;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE P20 n with a leader peptide.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87089808; PubMed=3540612;
RA Herman L.M.F., Montagu M.C.V., Depicker A.G.;
RT "Isolation of tobacco DNA segments with plant promoter activity.";
RL Mol. Cell. Biol. 6:4486-4492 (1986).
DR EMBL; M14685; AAA34090.1; -.
SQ SEQUENCE 8 AA; 1109 MW; E257205B19C9C9C6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 13 EIL 15
|||
Db 5 EIL 7

RESULT 50

Q9ERD2 PRELIMINARY; PRT; 8 AA.
AC Q9ERD2; (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Galactose-1-phosphate uridylyl transferase (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/D3;
RA Leslie N.D., Bai S.;
RT "Functional analysis of the mouse galactose-1-phosphate uridylyl transferase (GALT) promoter."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF314226; AAG31161.1; -.
KW Transferase.
FT NON_TER
SQ SEQUENCE 8 AA; 854 MW; EC8DC409DIADDD6 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATF 3
|||
Db 3 ATF 5

RESULT 51

Q90ZV5 PRELIMINARY; PRT; 8 AA.
AC Q90ZV5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE Adenylate kinase (Fragment).
OS Fulica leucopetra.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Gruiformes; Rallidae; Fulica.
OX NCBI_TaxID=156758;
RN [1]
RP SEQUENCE FROM N.A.
RA Shapiro L.H., Dumbacher J.P.;
RT "Adenylate kinase intron 5: a new nuclear locus for avian systematics."
RL Auk 118:248-255 (2001).
RW EMBL; AF307898; AAK43537.1; -.
KW Kinase.
FT NON_TER
SQ SEQUENCE 8 AA; 994 MW; 96333B19CB1B1866 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEE 13
|||
Db 2 GEE 4

RESULT 52

Q8GLJ31

ID Q8GLJ31 PRELIMINARY; PRT; 9 AA.
AC Q8GLJ31;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-1.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sh-2-82;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32 prophages: conservation amidst diversity."
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142089; AAN17869.1; -.
KW Plasmid.
FT NON_TER
SQ SEQUENCE 9 AA; 1206 MW; 5A4A244337204373 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILK 16
|||
Db 4 ILK 6

RESULT 53

Q9IBY9 PRELIMINARY; PRT; 9 AA.
AC Q9IBY9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ORF 10-like protein (Fragment).
OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KS187;
RX MEDLINE=20240083; PubMed=10775636;
RA Schultz E.N., Rankin G.W. Jr., Blanc M.P., Raden B.W., Tsai C.C., Rose T.M.;
RT "Characterization of two divergent lineages of macaque rhadinoviruses related to Kaposi's sarcoma-associated herpesvirus."
RL J. Virol. 74:4919-4928 (2000).
RW EMBL; AF005477; AAF78823.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 1053 MW; CD1959D1ADDB01B6 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATF 3
|||
Db 5 ATF 7

RESULT 54

Q8W7U4 PRELIMINARY; PRT; 10 AA.
AC Q8W7U4;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

```

DE Cytochrome oxidase subunit 1 (Fragment).
GN COL.
OS Anolis nitens.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_taxID=174262;
RN [1]
RP SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337800; AAL72083.1; -.
DR EMBL; AF337801; AAL72085.1; -.
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1349 MW; C9348E29D3640449 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FNR 5
Db |||
3 FNR 5

RESULT 55
Q63056 PRELIMINARY; PRT; 10 AA.
ID Q63056;
AC Q63056;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rat asialoglycoprotein receptor (ASGP) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Liver;
RX MEDLINE=87026895; PubMed=2945599;
RA Watts C.;
RT "Isolation and expression of cDNA clones for a rat liver
RT asialoglycoprotein receptor."
RL Biosci. Rep. 6:527-534(1986).
DR EMBL; M21739; AAA40763.1; -.
KW Receptor.
FT NON TER 10
SQ SEQUENCE 10 AA; 1312 MW; 56ADE0CAB6CB5AA3 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YQD 8
Db |||
5 YQD 7

RESULT 56
Q8VIL8 PRELIMINARY; PRT; 10 AA.
ID Q8VIL8;
AC Q8VIL8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Immediate early gene protein Homer1A (Fragment).
GN HOMER1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxID=10090;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RA Bottai D., Guzowski J.F., Schwarz M.K., Kang S.H., Xiao B.,
RA Lanahan A., Worley P.F., Seeburg P.H.;
RT "Synaptic Activity-Induced Conversion of Intronic to Exonic Sequence
RT in Homer1 Immediate Early Gene Expression.";
RL J. Neurosci. 0:0-0(2002).
DR EMBL; AF425674; AAL34511.1; -.
DR MGD; MGI:1347345; Homer1.
FT NON TER 1
SQ SEQUENCE 10 AA; 1187 MW; CD7A2B905DC5B449 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TFN 4
Db |||
2 TFN 4

RESULT 57
Q9JLI5 PRELIMINARY; PRT; 10 AA.
ID Q9JLI5;
AC Q9JLI5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Melanocortin type 1 receptor MC1R (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STEAIN=C57BL/6;
RX MEDLINE=20090876; PubMed=10623832;
RA Adachi S., Morii E., Kim D.-K., Ogihara H., Jippo T., Ito A., Lee Y.M.,
RA Kitamura Y.;
RT "Involvement of mi-transcription factor in expression of alpha-
RT melanocyte-stimulating hormone receptor in cultured mast cells of
RT mice.";
RL J. Immunol. 164:855-860(2000).
DR EMBL; AF176016; AAF37323.1; -.
KW Receptor.
FT NON TER 10
SQ SEQUENCE 10 AA; 1148 MW; 95B58A26C76B06C1 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18
Db |||
8 KSL 10

RESULT 58
Q9L4F7 PRELIMINARY; PRT; 11 AA.
ID Q9L4F7;
AC Q9L4F7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 15, Last annotation update)
DE Phosphatidylinositol-specific phospholipase C (PI-PLC)
DE (Fragment).
GN PLCA.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_taxID=1396;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN-ATCC 14579 type strain;
RX MEDLINE=20055637; PubMed=10589720;
RA Oktad O., Gominet M., Purnelle B., Rose M., Lereclus D., Koisto A.B.;
RT "sequence analysis of three Bacillus cereus loci under PICR-regulated
RL genes encoding degradative enzymes and enterotoxin.";
RL Microbiology 145:3129-3138(1999).
DR EMBL; AC243711; CAB69804.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1335 MW; 4277A30E20572333 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 2; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILK 16
Db 7 ILK 9

RESULT 59
Q9S618
ID Q9S618 PRELIMINARY; PRT; 11 AA.
AC Q9S618;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Cytochrome b6/f complex subunit IV (Fragment).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanog. 43:1615-1630(1998).
DR EMBL; AF070132; AAD20740.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1297 MW; 5CC38013B7633337 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 2; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILK 16
Db 3 ILK 5

RESULT 60
Q8GL19
ID Q8GL19 PRELIMINARY; PRT; 11 AA.
AC Q8GL19;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Bacterium group cp32-11.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sh-2-82.
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
RT prophages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142096; AAN17880.1; -.
KW Plasmid.

```

```

FT NON_TER 1
SQ SEQUENCE 11 AA; 1366 MW; 4E441D5337204373 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 2; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILK 16
Db 6 ILK 8

RESULT 61
Q16234
ID Q16234 PRELIMINARY; PRT; 11 AA.
AC Q16234;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE HuD protein (Fragment).
GN HUD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94349312; PubMed=8069866;
RA Sekido Y., Bader S.A., Carbone D.P., Johnson B.E., Minna J.D.;
RT "Molecular analysis of the HuD gene encoding a paraneoplastic
RT encephalomyelitis antigen in human lung cancer cell lines.";
RL Cancer Res. 54:4988-4992(1994).
DR EMBL; S73887; AAD14142.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1289 MW; 2EDCF20E204415A7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 4; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILK 16
Db 7 ILK 9

RESULT 62
Q8RV30
ID Q8RV30 PRELIMINARY; PRT; 11 AA.
AC Q8RV30;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Methionine adenosyltransferase 1-like protein (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Various strains;
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
RA Morgante M., Rafalski J.A.;
RT "SNP frequency, haplotype structure and linkage disequilibrium in
RT elite maize inbred lines.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF486085; AAL85893.1; -.
DR EMBL; AF486086; AAL85894.1; -.
DR EMBL; AF486087; AAL85895.1; -.
DR EMBL; AF486088; AAL85896.1; -.
DR EMBL; AF486089; AAL85897.1; -.
DR EMBL; AF486090; AAL85898.1; -.
DR EMBL; AF486091; AAL85899.1; -.

```

DR	EMBL; AF486092; AAL85900.1; -
DR	EMBL; AF486093; AAL85901.1; -
DR	EMBL; AF486094; AAL85902.1; -
DR	EMBL; AF486095; AAL85903.1; -
DR	EMBL; AF486096; AAL85904.1; -
DR	EMBL; AF486097; AAL85905.1; -
DR	EMBL; AF486098; AAL85906.1; -
DR	EMBL; AF486099; AAL85907.1; -
DR	EMBL; AF486100; AAL85908.1; -
DR	EMBL; AF486101; AAL85909.1; -
DR	EMBL; AF486102; AAL85910.1; -
DR	EMBL; AF486104; AAL85911.1; -
DR	EMBL; AF486105; AAL85912.1; -
DR	EMBL; AF486106; AAL85913.1; -
DR	EMBL; AF486107; AAL85914.1; -
DR	EMBL; AF486108; AAL85915.1; -
DR	EMBL; AF486109; AAL85916.1; -
DR	EMBL; AF486110; AAL85917.1; -
DR	EMBL; AF486111; AAL85918.1; -
DR	EMBL; AF486112; AAL85919.1; -
DR	EMBL; AF486113; AAL85920.1; -
DR	EMBL; AF486114; AAL85921.1; -
DR	EMBL; AF486115; AAL85922.1; -
DR	EMBL; AF486116; AAL85923.1; -
DR	EMBL; AF486117; AAL85924.1; -
DR	EMBL; AF486118; AAL85925.1; -
FT	NON_TPR
SQ	SEQUENCE 11 AA; 1183 MW; 448D42ED3B05B337 CRC64;
Query Match	
Best Local Similarity 16.7%; Score 3; DB 10; Length 11;	
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	15 LKS 17
Db	4 LKS 6
RESULT 63	
Q8JS92	PRELIMINARY; PRT; 11 AA.
ID	Q8JS92
AC	Q8JS92;
DT	01-OCT-2002 (TrEMBLrel. 22, Created)
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE	X protein (fragment).
OS	Hepatitis B virus.
OC	Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=34;
RC	PubMed=15185284;
RX	Hou J., Luo Y., Waters J., Wang Z., Min J., Liao H., Jiang J., Chen J., Lin K., Karayianis P.;
RA	"Detection and significance of a G1862T variant of hepatitis B virus
RT	in Chinese patients with fulminant hepatitis.";
RL	J. Gen. Virol. 83:2291-2298(2002).
RJ	EMBL; AF495895; AAM34089.1; -
FT	NON_TPR
SQ	SEQUENCE 11 AA; 1315 MW; DC70528AB5B73412 CRC64;
Query Match	
Best Local Similarity 16.7%; Score 3; DB 12; Length 11;	
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	11 GEE 13
Db	1 GEE 3
RESULT 64	

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OX Streptococcus.

NCBI_TaxID=119602;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=H46A;

RX MEDLINE=20123454; PubMed=10660058;

RA Ceyer A., Schmidt K.H.;

RT "Genetic organisation of the M protein region in human isolates of

group C and G streptococci: two types of multigene regulator-Like

(mgrC) regions.";

RL Mol. Gen. Genet. 262:965-974(2000).

DR EMBL; AJ133440; CAB70616.1; -

FT NON_TER 12 12

SQ SEQUENCE 12 AA; 1334 MW; 0A82EC4258A72440 CRC64;

Query Match

Best Local Similarity 16.7%; Score 3; DB 2; Length 12;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEE 13

Db 9 GEE 11

RESULT 67

Q47251

ID Q47251 PRELIMINARY; PRT; 12 AA.

AC Q47251;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE HEMC protein (Fragment).

GN HEMC.

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RX MEDLINE=88096587; PubMed=3320969;

RA Jordan P.M., Mgebeje B.I.A., Alwan A.F., Thomas S.D.;

RT "Nucleotide sequence of hemD, the second gene in the hem operon of

Escherichia coli K-12.";

RL Nucleic Acids Res. 15:10583-10583(1987).

DR EMBL; Y00883; CAA68775.1; -

FT NON_TER 1 1

FT NON_TER 12 12

SQ SEQUENCE 12 AA; 1375 MW; 5D2DEB339BA045B3 CRC64;

Query Match

Best Local Similarity 16.7%; Score 3; DB 2; Length 12;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LXS 17

Db 4 LXS 6

RESULT 68

Q9TRU1

ID Q9TRU1 PRELIMINARY; PRT; 12 AA.

AC Q9TRU1;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE 43 kDa CYANOGEN bromide fragment PEAK 7 (Fragment).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Ruminantia; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE.

RX MEDLINE=92132498; PubMed=1734497;

RA Veiby O.P., Sletten K., Husby G., Nordstoga K.;

RT "Amino acid sequence analyses of non-AA proteins from amyloid fibrils

of bovine kidney.";

RL Scand. J. Immunol. 35:63-69(1992).

FT NON_TER 1 1

FT NON_TER 12 12

SQ SEQUENCE 12 AA; 1257 MW; 0D5C94FDE9B76AAA CRC64;

Query Match

Best Local Similarity 16.7%; Score 3; DB 6; Length 12;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFN 4

Db 3 TFN 5

RESULT 69

P82164

ID P82164 PRELIMINARY; PRT; 12 AA.

AC P82164;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE Chloroplast 30S ribosomal protein S14 beta (Fragment).

OS Spinacia oleracea (Spinach).

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.

OX NCBI_TaxID=3562;

RN [1]

RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.

RC STRAIN=cv. ALVARO; TISSUE=Leaf;

RX MEDLINE=20435797; PubMed=10874039;

RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;

RT "The plastid ribosomal proteins. Identification of all the proteins in

the small subunit of an organelle ribosome (chloroplast).";

RL J. Biol. Chem. 37:28455-28465(2000).

CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.

CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.

CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.

CC -!- MISCELLANEOUS: S14 ALPHA AND BETA FORMS DIFFER IN P.I. S14 ALPHA

FORM IS THE LEAST BASIC FORM.

CC -!- MASS SPECTROMETRY: MW=11745.9; METHOD=ELECTROSPRAY.

CC -!- MASS SPECTROMETRY: MW=11947; METHOD=MALDI.

CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 14 KDA.

CC -!- SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOMAL PROTEINS.

DR InterPro; IPR001209; Ribosomal_S14.

DR Pfam; PF00253; Ribosomal_S14; PARTIAL.

DR PROSITE; PS00057; RIBOSOMAL_S18; PARTIAL.

KW Ribosomal protein; Chloroplast; rRNA-binding.

FT NON_TER 12 12

SQ SEQUENCE 12 AA; 1513 MW; 5E84D3F10116D057 CRC64;

Query Match

Best Local Similarity 16.7%; Score 3; DB 8; Length 12;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18

Db 3 KSL 5

RESULT 70

Q62966

ID Q62966 PRELIMINARY; PRT; 12 AA.

AC Q62966;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT	01-NOV-1996	(TrEMBLrel. 01, last sequence update)
DT	01-DEC-2001	(TrEMBLrel. 19, last annotation update)
DE	Interstitial collagenase [Fragment].	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OX	NCBI_TaxID=10116;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Sprague-Dawley;	
RX	MEDLINE=96408720; PubMed=8813727;	
RA	Rajakumar R.A., Quinn C.O.;	
RT	"Parathyroid hormone induction of rat interstitial collagenase mRNA in	
RL	osteosarcoma cells is mediated through an AP-1-binding site.";	
RL	Mol. Endocrinol. 10:867-878(1996).	
DR	EMBL; U53605; AAB47407.1; -.	
KW	Collagen.	
FT	NON TER	
SQ	SEQUENCE	
	12 AA; 1432 MW; 148A4DFEE8ADD720 CRC64;	
	Query Match	16.7%; Score 3; DB 11; Length 12;
	Best Local Similarity	100.0%; Pred.No. 1.le+04;
	Matches	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATF 3	
DB	7 ATF 9	
RESULT 71		
ID	Q84268	PRELIMINARY; PRT; 12 AA.
AC	Q84268;	
DT	01-NOV-1996	(TrEMBLrel. 01, Created)
DT	01-NOV-1996	(TrEMBLrel. 01, last sequence update)
DT	01-DEC-2001	(TrEMBLrel. 19, last annotation update)
DE	E1 ORF (fragment).	
OS	Human papillomavirus.	
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;	
OC	Papillomavirus.	
OX	NCBI_TaxID=10566;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=89095007; PubMed=2536104;	
RA	Choo K.-B., Cheung W.-F., Liew L.-N., Lee H.-H., Han S.-H.;	
RT	"Presence of Caenated Human Papillomavirus Type 16 Episomes in a	
RL	Cervical Carcinoma Cell Line.";	
RL	J. Virol. 63:782-789(1989).	
DR	EMBL; M24215; AAA46945.1; -.	
FT	NON TER	
SQ	SEQUENCE	
	12 AA; 1178 MW; 993F1F424D5D1A861 CRC64;	
	Query Match	16.7%; Score 3; DB 12; Length 12;
	Best Local Similarity	100.0%; Pred.No. 1.le+04;
	Matches	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	11 GEE 13	
DB	9 GEE 11	
RESULT 72		
ID	Q9R3R6	PRELIMINARY; PRT; 13 AA.
AC	Q9R3R6;	
DT	01-MAY-2000	(TrEMBLrel. 13, Created)
DT	01-MAY-2000	(TrEMBLrel. 13, last sequence update)
DT	01-MAY-2000	(TrEMBLrel. 13, Last annotation update)
DE	Cytochrome B6/F complex subunit IV (Fragment).	
GN	PETD	
OS	Prochlorococcus sp.	
OC	Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;	
OC	Prochlorococcus.	


```

RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrell B.G;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531(2002).
DR EMBL; AL031744; CAD48947.1; -.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 13 AA; 1619 MW; 50E352E2F7FED1A7 CRC64;

Query Match 16.7%; Score 3; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EIL 15
Db |||
4 EIL 6

RESULT 75
Q945CI PRELIMINARY; PRT; 13 AA.
AC Q945C1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Dip5 protein (Fragment).
OS Cryptocodium cohni (Dinoflagellate).
OC Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Cryptocodiniaceae;
OC Cryptocodium.
CX NCBI_TaxID=2866;
RN [1]_-
RP SEQUENCE FROM N.A.
RX MEDLINE=21428164; PubMed=11545436;
RA Guillebaud D., Derelle E., Bhaud Y., Moreau H.;
RT "Role of nuclear WW domains and proline-rich proteins in
RT dinoflagellate transcription.";
RL Protist 152:127-138(2001).
DR EMBL; AF417570; AAL15908.1; -.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1225 MW; 322FA05EE70CB327 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
Db |||
7 KSL 9

Search completed: November 25, 2003, 19:34:12
Job time : 35.8023 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 45.9419 Seconds
(without alignments)
62.189 Million cell updates/sec

Title: US-09-641-801-30

Perfect score: 18

Sequence: 1 ATFNRYQDDHGHEILKSL 18

Scoring table:

OLIGO Gapop 60.0 , Capext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A Geneseq 19Jun03.*
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	22	Colostrinin derive
2	18	100.0	18	22	Colostrinin peptid
3	18	100.0	18	22	Colostrinin peptid
4	18	100.0	18	22	Colostrinin peptid
5	18	100.0	18	22	Ewe colostrinin pe
6	18	100.0	18	23	Colostrinin consti
7	18	100.0	18	23	Colostrinin consti
8	18	100.0	18	23	Neural cell regula
9	6	33.3	11	22	Ewe colostrinin pe
					Rat SNS1 ion chann

10	6	33.3	18	23	ABJ04200	Kinase-associated
11	6	33.3	18	24	ABU54247	Jak2 protein kinase
12	5	27.8	17	24	ABP59049	Chlamydia trachoma
13	4	22.2	4	21	AAV43756	Amino acid sequenc
14	4	22.2	5	21	AAW90997	N. denitrificans a
15	4	22.2	5	21	AAV92081	C-terminal peptide
16	4	22.2	5	21	AAV92083	C-terminal peptide
17	4	22.2	5	21	AAV92085	C-terminal peptide
18	4	22.2	5	22	AAV55641	Monocyte surface r
19	4	22.2	5	22	AAV57488	CD61 C-terminal co
20	4	22.2	5	22	AAV57898	CD61 C-terminal co
21	4	22.2	5	23	ABJ05120	T-cell surface rec
22	4	22.2	5	23	ABP63413	Monocyte surface r
23	4	22.2	6	20	AAV21763	Conserved peptide
24	4	22.2	6	20	AAV21768	Conserved peptide
25	4	22.2	6	20	AAV21752	Conserved peptide
26	4	22.2	6	22	AAE08967	Mammalian ced-3 ho
27	4	22.2	6	22	AAE08978	CPP32 peptide frag
28	4	22.2	6	22	AAE08983	CEB-3 peptide frag
29	4	22.2	6	22	AAV55642	Monocyte surface r
30	4	22.2	6	22	AAV57489	CD61 C-terminal co
31	4	22.2	6	22	AAV57899	CD61 C-terminal co
32	4	22.2	6	23	ABJ05121	T-cell surface rec
33	4	22.2	6	23	ABP63414	Monocyte surface r
34	4	22.2	6	23	ABJ01256	Human caspase cons
35	4	22.2	6	23	ABJ01267	Human caspase cons
36	4	22.2	6	23	ABJ01272	Human caspase cons
37	4	22.2	6	23	AAO17301	A thaliana recepto
38	4	22.2	7	22	AAU28695	DPI tryptic digest
39	4	22.2	7	22	AAU25065	Schizophrenia-Asso
40	4	22.2	7	22	AAU26343	Depression-Asso
41	4	22.2	7	22	AAW44583	H11 binding site c
42	4	22.2	7	22	AAW44588	H11 binding site c
43	4	22.2	7	22	AAU15409	Schizophrenia-asso
44	4	22.2	7	22	AAV55643	Monocyte surface r
45	4	22.2	7	22	AAV57490	CD61 C-terminal co
46	4	22.2	7	22	AAV57900	CD61 C-terminal co
47	4	22.2	7	23	ABJ05122	T-cell surface rec
48	4	22.2	7	23	ABP63415	Monocyte surface r
49	4	22.2	8	22	ABP11644	HIV A01 super moti
50	4	22.2	8	22	ABP12644	HIV A02 super moti
51	4	22.2	8	22	ABP12645	HIV A02 super moti
52	4	22.2	8	22	ABP15564	HIV A04 super moti
53	4	22.2	8	22	ABP15565	HIV A04 super moti
54	4	22.2	8	22	ABP15567	HIV A04 super moti
55	4	22.2	8	22	ABP17830	HIV B58 super moti
56	4	22.2	8	22	ABP17849	HIV B58 super moti
57	4	22.2	8	22	ABP17869	HIV B58 super moti
58	4	22.2	8	22	ABP20480	HIV A03 motif gag
59	4	22.2	8	22	ABP20520	HIV A03 motif gag
60	4	22.2	8	22	ABP23517	HIV A11 motif pol
61	4	22.2	8	22	AAV55644	Monocyte surface r
62	4	22.2	8	22	AAV57491	CD61 C-terminal co
63	4	22.2	8	22	AAV57901	CD61 C-terminal co
64	4	22.2	8	23	ABJ05123	T-cell surface rec
65	4	22.2	8	23	ABU06021	Hepatitis B virus
66	4	22.2	8	23	ABJ06547	Hepatitis B virus
67	4	22.2	8	23	ABJ07394	Hepatitis B virus
68	4	22.2	8	23	ABP63416	Monocyte surface r
69	4	22.2	9	15	AAV66006	Peptide which bind
70	4	22.2	9	15	AAV65863	Antidioxynucle
71	4	22.2	9	16	AAV70537	HIV peptide fragme
72	4	22.2	9	16	AAV70544	HIV peptide fragme
73	4	22.2	9	16	AAV77554	HIV(B35)GAG-29, hu
74	4	22.2	9	17	AAW49244	Human leucocyte an
75	4	22.2	9	21	AAV96353	HIV A3 binding pep
76	4	22.2	9	21	AAV96358	HIV A11 binding pe
77	4	22.2	9	21	AAV86698	Telomerase peptide
78	4	22.2	9	21	AAV86757	Telomerase peptide
79	4	22.2	9	21	AAV86794	Telomerase peptide
80	4	22.2	9	21	AAV86795	Telomerase peptide
81	4	22.2	9	21	AAV86838	Telomerase peptide
82	4	22.2	9	22	ABP11665	HIV A01 super moti

83 4 22.2 9 22 ABP11666 HIV A01 super moti
 84 4 22.2 9 22 ABP14749 HIV A03 super moti
 85 4 22.2 9 22 ABP15634 HIV A24 super moti
 86 4 22.2 9 22 ABP15635 HIV A24 super moti
 87 4 22.2 9 22 ABP16714 HIV B07 super moti
 88 4 22.2 9 22 ABP16716 HIV B07 super moti
 89 4 22.2 9 22 ABP16718 HIV B07 super moti
 90 4 22.2 9 22 ABP16719 HIV B07 super moti
 91 4 22.2 9 22 ABP18759 HIV B62 super moti
 92 4 22.2 9 22 ABP18782 HIV B62 super moti
 93 4 22.2 9 22 ABP20454 HIV A03 motif gag
 94 4 22.2 9 22 ABP20529 HIV A03 motif gag
 95 4 22.2 9 22 ABP21628 HIV A03 motif pol
 96 4 22.2 9 22 ABP21734 HIV A03 motif pol
 97 4 22.2 9 22 ABP23604 HIV A11 motif pol
 98 4 22.2 9 22 AAU24975 Schizophrenia-Asso
 99 4 22.2 9 22 AAU15319 Schizophrenia-Asso
 100 4 22.2 9 22 AAB05198 Human HLA-A1 bindi

ALIGNMENTS

RESULT_1
 AAB72275
 ID AAB72275 standard; peptide; 18 AA.
 XX AC
 XX AAB72275;
 DT 14-MAY-2001 (first entry)
 XX DE
 DE Colostrinin derived cytokine inducing peptide SEQ ID 30.
 KW Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.
 XX OS
 OS Synthetic.
 XX WO200111937-A2.
 XX 22-FEB-2001.
 XX PF
 PF 17-AUG-2000; 2000WO-US22818.
 XX PR
 PR 17-AUG-1999; 99US-0149311.
 XX PA
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX PA (REGG-) REGEN THERAPEUTICS PLC.
 XX PI
 PI Stanton GU, Hughes TK, Boldogh I, Georgiades J;
 XX WPI; 2001-202804/20.
 XX PT
 PT Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator -
 XX PS
 PS Claim 1; Page 34; 50pp; English.
 XX CC
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrinin and its derived peptides are useful for
 CC inducing cytokine production, for modulating an immunological response
 CC and for inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies.

XX SQ Sequence 18 AA;
 Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.7e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATFNRYQDDHGEILKSL 18
 DB 1 ATFNRYQDDHGEILKSL 18
 RESULT 2
 AAB72528
 ID AAB72528 standard; Peptide; 18 AA.
 XX AC
 AC AAB72528;
 XX DT
 DT 09-MAY-2001 (first entry)
 XX DE
 DE Colostrinin peptide #29.
 XX KW
 KW Dermatological; oxidative stress regulator; colostrinin.
 XX OS
 OS Unidentified.
 XX XX
 XX WO200112650-A2.
 XX PD
 PD 22-FEB-2001.
 XX PP
 PP 17-AUG-2000; 2000WO-US22665.
 XX PR
 PR 17-AUG-1999; 99US-0149310.
 XX PA
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX WPI; 2001-218342/22.
 XX PT
 PT Modulating oxidative stress level in a cell, involves contacting the
 PT cell with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations -
 XX PS
 PS Claim 6; Page 26; 48pp; English.
 XX CC
 CC The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidizing species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient.
 XX SQ Sequence 18 AA;
 Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.7e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATFNRYQDDHGEILKSL 18
 DB 1 ATFNRYQDDHGEILKSL 18
 RESULT 3
 AAB72560
 ID AAB72560 standard; Peptide; 18 AA.
 XX AC
 AC AAB72560;
 XX DT
 DT 09-MAY-2001 (first entry)
 XX

DE Colostrinin peptide #29.
XX
KW Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX
OS Unidentified.
XX
PN WO200112651-A2.
XX
PD 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22774.
PF
XX 17-AUG-1999; 99US-0149633.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
PA
XX Boldogh I;
PI
XX
XX WPI; 2001-226545/23.
DR
XX
XX Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating
PT damaged neural cells in a patient -
XX
XX
PS Claim 6; Page 22; 35pp; English.
XX
XX The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATFNRYQDDHGHEILKSL 18
DB |||||
1 ATFNRYQDDHGHEILKSL 18
RESULT 4
AAB59340
ID AAB59340 standard; Peptide; 18 AA.
XX
XX AAB59340;
AC
DT 21-MAR-2001 (first entry)
XX
XX Ewe colostrinin peptide fragment D-1.
DE
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
KW
XX Ovis sp.
OS
XX WO200075173-A2.
PN
XX 14-DEC-2000.
PD
XX 02-JUN-2000; 2000WO-GB02128.
PF
XX 02-JUN-1999; 99GB-0012852.
PR
XX (REGE-) REGEN THERAPEUTICS PLC.
PA
XX Georgiades JA;
PI
XX WPI; 2001-071059/08.
DR
XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
XX characterized by amyloid plaques -
XX
PS Claim 7; Page 27; 63pp; English.
XX
XX The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
XX promote the dissolution of beta-amyloid plaques.
XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATFNRYQDDHGHEILKSL 18
DB |||||
1 ATFNRYQDDHGHEILKSL 18
RESULT 5
AAE20257
ID AAE20257 standard; peptide; 18 AA.
XX
XX AAE20257;
AC
XX 18-JUN-2002 (first entry)
DT
XX Colostrinin constituent peptide #29.
DE
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulneryary.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 18
FT /note= "Optionally C-terminal amide"
FT
XX WO200213850-A1.
PN
XX 21-FEB-2002.
PD
XX 17-AUG-2000; 2000WO-US22776.
PF
XX 17-AUG-2000; 2000WO-US22776.
PR
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Stanton GJ, Hughes TK, Boldogh I;
PI
XX WPI; 2002-269151/31.
DR
XX Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog -
XX
XX Claim 6; Page 26; 51pp; English.
PS
XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present
CC sequence is a colostrinin constituent peptide.

SQ Sequence 18 AA;
Query Match 100.0%; Score 18; DB 23; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATFNRYYQDDHGEEILKSL 18
|||||
Db 1 ATFNRYYQDDHGEEILKSL 18
|||||

RESULT 6
AAW51064
ID AAW51064 standard; Peptide; 18 AA.

AC AAW51064;

DT 30-MAY-2002 (first entry)

DE Colostrinin constituent peptide (annexin amino acids 203-220).

KW Colostrinin; colostrum; immunomodulator; cardiovascular;

KW blood cell regulator; cytokine inducer; annexin; human.

OS Homo sapiens.

Key Location/Qualifiers

FT Modified-site 18 /note= "optional C-terminal amidation"

FN WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

PA (TEXA) UNIV TEXAS SYSTEM.

PI (REG-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

DR WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of

PT blood cell regulator selected from colostrinin, its constituent peptide

PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
CC that is used as an immunological regulator and as a blood cell
CC regulator in claimed methods of the invention. It is classified
CC as having an annexin precursor, and corresponds to annexin amino
CC acids 203-220. Methods are claimed for: inducing a cytokine in a
CC cell by contact with an immunological regulator, where the cell is
CC present in a cell culture, a tissue, an organ or an organism, and
CC the cell is mammalian, including human; modulating an immune
CC response in a cell by contact with the immunological regulator

CC under conditions effective to induce a cytokine; modulating an
CC immune response in a patient by administering an immunological
CC regulator under conditions effective to induce a cytokine, where
CC the immunological regulator is administered topically or as part
CC of a dietary supplement, and where the immune response is specific
CC or non specific, an interferon response or an antibody response;
CC modulating blood cell proliferation by contacting blood cells with
CC a blood cell regulator, where the blood cells are present in a cell
CC culture or an organism, are mammalian or human, and where the blood
CC cells are increased in number or differentiated; and a method for
CC modulating blood cell proliferation in a patent. A claimed
CC cytokine-inducing composition comprises a pharmaceutical carrier
CC and an active agent such as the present peptide.

SQ Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.7e-12;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATFNRYYQDDHGEEILKSL 18

|||||

Db 1 ATFNRYYQDDHGEEILKSL 18

|||||

RESULT 7

AAO14606

ID AAO14606 standard; peptide; 18 AA.

XX AAO14606;

XX 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 29.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;

XX neural cell formation; proline-rich polypeptide aggregate; colostrum;

XX Unidentified.

Key Location/Qualifiers

FT Modified-site 18 /note= "Optional C-terminal amide"

FT WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell

PT regulator selected from colostrinin, its constituent peptide and/or

PT analog -

XX Claim 7; Page 22; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention.

XX Sequence 18 AA;

SQ Query Match 100.0%; Score 18; DB 23; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.7e-12; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATFNRYQDDHGEILKSL 18

|||||

Db 1 ATFNRYQDDHGEILKSL 18

RESULT 8

AAB59357

ID AAB59357 standard; Peptide; 19 AA.

XX AC AAB59357;

XX DT 21-MAR-2001 (first entry)

XX DE Ewe colostrinin peptide fragment derived sequence #17.

XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;

XX KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS Ovis sp.

XX WO200075173-A2.

XX PN 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-GB02128.

XX PR 02-JUN-1999; 99GB-0012852.

XX PA (REG-) REGEN THERAPEUTICS PLC.

XX PI Georgiades JA;

XX WPI; 2001-071058/08.

XX PT Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system

PT and immune system, viral and bacterial infections, and diseases

PT characterized by amyloid plaques -

XX Claim 8; Page 27; 63pp; English.

XX CC The present invention provides the sequences of a number of peptides

CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide

CC fragment of colostrum. These peptides can be used in the treatment of

CC central nervous system disorders such as senile dementia, Parkinson's

CC disease, Alzheimer's disease, psychosis and neurosis, immune system

CC disorders such as bacterial and viral infections, to improve the

CC development of a child's immune system, as a dietary supplement, and to

CC promote the dissolution of beta-amyloid plaques.

XX Sequence 19 AA;

Query Match 100.0%; Score 18; DB 22; Length 19;

Best Local Similarity 100.0%; Pred. No. 3.8e-12;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATFNRYQDDHGEILKSL 18

|||||

Db 2 ATFNRYQDDHGEILKSL 19

RESULT 9

AAG5972

ID AAG5972 standard; peptide; 11 AA.

XX

AC AAG5972;

XX DT 11-FEB-2002 (first entry)

XX DE Rat SNS1 ion channel protein mutant 2 (A1560E).

XX KW Ion channel protein; gating; sensory neurone specific protein; SNS;

XX analgesic; antiinflammatory; immunosuppressive; rat; mutant.

XX OS Rattus sp.

XX WO200168681-A2.

XX PD 20-SEP-2001.

XX PF 14-MAR-2001; 2001WO-GB01108.

XX PR 14-MAR-2000; 2000GB-0006024.

XX PA (GLAX) GLAXO GROUP LTD.

XX PI Aitken AJ, Chen MX, Gladwell ZM, Powell AJ, Tate SN;

XX WPI; 2001-590038/66.

XX DR N-PSDB; AA167050.

XX PT Altered ion channel protein useful for screening modulators that are

PT useful in the manufacture of a medicament for the treatment of pain,

PT inflammation and hypersensitivity, has acquired sensitivity to gating

PT agent -

XX Disclosure; Fig 3; 64pp; English.

XX CC The invention provides an altered ion channel protein having acquired

CC sensitivity to a gating agent. The altered ion channel protein can be

CC expressed by standard recombinant methodology. The altered ion channel

CC protein can be derived from a rat, mouse or human unaltered, gating agent

CC insensitive ion channel proteins. The altered protein is useful in

CC screening assay for the identification of modulators capable of

CC modulating an unaltered gating agent insensitive ion channel protein. The

CC modulator identified by the assay is preferably an antagonist of the

CC altered protein, which is useful in the manufacture of a medicament for

CC the treatment of pain, inflammation or hypersensitivity, and for treating

CC a mammalian patient, particularly human. The present sequence represents

CC a mutant fragment of the rat sensory neurone specific (SNS) 1 protein.

XX Sequence 11 AA;

Query Match 33.3%; Score 6; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILKSL 18

|||||

Db 6 EILKSL 11

RESULT 10

ABJ04200

ID ABJ04200 standard; Peptide; 18 AA.

XX AC ABJ04200;

XX DT 24-OCT-2002 (first entry)

XX DE Kinase-associated signal transduction modulating peptide 33.

XX KW Kinase-associated signal transduction; diabetes; cancer; obesity;

XX restenosis; bone healing; alopecia; osteoporosis;

XX neurodegenerative disease; autoimmune disease; inflammation;

XX atherosclerosis; skin disorder; central nervous system disease;

XX inflammatory disorder; autoimmune disease; cardiovascular disease.

XX

OS Unidentified.
 XX WO200248336-A2.
 XX
 XX
 PD 20-JUN-2002.
 XX
 XX
 FF 11-DEC-2001; 2001WO-US47443.
 XX
 PR 11-DEC-2000; 2000US-0734520.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 XX (YISS) YISSUM RES & DEV CO.
 FI Ben-sasson S;
 XX
 XX WPI; 2002-583508/62.
 XX
 XX Identifying compounds for modulating kinase-associated signal
 PT transduction and treating cancer, by synthesizing compounds having
 PT short sequences identical to native sequences appearing in specific
 PT region of a kinase -
 XX
 PS Claim 36; Fig 1; 143pp; English.
 XX
 CC The invention comprises a method for identifying compounds for the
 CC modulation of kinase-associated signal transduction. The invention also
 CC comprises a number of peptides which modulate kinase-associated signal
 CC transduction. The method of the invention is useful for identifying
 CC compounds for the modulation of kinase-associated signal transduction.
 CC The kinase-associated signal transduction modulating peptides of the
 CC invention are useful for treating: diabetes; cancer; obesity;
 CC bone healing; alopecia; osteoporosis; neurodegenerative disease;
 CC autoimmune disease; inflammation; restenosis; atherosclerosis; skin
 CC disorders; central nervous system disease; inflammatory disorders;
 CC autoimmune diseases; and cardiovascular diseases. The peptides ABJ04168 -
 CC ABJ04300 represent the kinase-associated signal transduction modulating
 CC peptides of the invention.
 XX
 SQ Sequence 18 AA;
 XX
 Query Match 33.3%; Score 6; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 EILKSL 18
 Db 2 EILKSL 7
 |||||
 |||||
 RESULT 11
 ABUS4247
 ID ABUS4247 standard; Peptide; 18 AA.
 XX
 AC ABUS4247;
 XX
 DT 06-MAR-2003 (first entry)
 XX
 DE Jak2 protein kinase A-region peptide.
 XX
 KW Kinase; A-region; PKA; PKA-Calpha; signal transduction; inhibitor;
 KW stimulator; proliferation; differentiation; oncogenesis; cancer;
 KW arteriosclerosis; psoriasis; septic shock; therapeutic; diabetes;
 KW obesity; restenosis; tissue remodeling; bone healing; alopecia; scarring;
 KW osteoporosis; neurodegenerative disease; autoimmune disease;
 KW inflammation; atherosclerosis; skin disorder; central nervous system;
 KW cardiovascular disease; dermatological; neuroprotective;
 KW immunosuppressive.
 XX
 OS Unidentified.
 OS Synthetic.
 XX
 PN US2002137141-A1.
 XX

PD 26-SEP-2002.
 XX
 PF 11-DEC-2001; 2001US-0012034.
 XX
 XX
 PR 11-DEC-2000; 2000US-0734520.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 FI Ben-Sasson S;
 XX
 XX WPI; 2003-110601/10.
 XX
 XX Identifying candidate compounds for the modulation of kinase-associated
 PT signal transduction, useful for treating diabetes, cancer, obesity, and
 PT osteoporosis, autoimmune disorders, atherosclerosis and cardiovascular
 PT diseases -
 XX
 XX Claim 36; Fig 1; 79pp; English.
 XX
 CC The invention discloses compounds, or variants of them, and methods for
 CC identifying and synthesizing the candidate compounds which comprise a
 CC peptide region in the protein kinase A-region (PKA). This region is
 CC determined by aligning catalytic subunits of the kinase and PKA-Calpha
 CC and determining the sequence of the kinase corresponding to positions
 CC 92-109 of PKA-Calpha. The capacity of the compound to modulate the signal
 CC transduction associated with the kinase (as a kinase inhibitor or
 CC stimulator) is then determined. Protein kinases mediate signal
 CC transduction in a wide variety of cellular events, such as cell
 CC proliferation, differentiation, oncogenesis and immune/inflammatory
 CC responses. Enhanced stimulation can lead to proliferative diseases, such
 CC as cancer, arteriosclerosis, psoriasis and septic shock. The methods and
 CC compositions are useful for detecting A-region ligands and for treating a
 CC disease where a therapeutically beneficial effect may be evident by the
 CC modulation of a signal transduction associated with a kinase, where the
 CC kinase from which the A-region is determined is the kinase associated
 CC with the signal transduction, and where the disease is diabetes, cancer,
 CC obesity, restenosis, tissue remodeling including improved bone healing,
 CC prevention of alopecia, reduced scarring, osteoporosis, neurodegenerative
 CC disease, autoimmune disease, inflammation, atherosclerosis, skin
 CC disorders, diseases of the central nervous system and cardiovascular
 CC diseases. The sequences presented in ABUS4215-ABUS4336 are the A-region
 CC peptides disclosed in the invention which are N-myristylated and
 CC C-amidated.
 XX
 SQ Sequence 18 AA;
 XX
 Query Match 33.3%; Score 6; DB 24; Length 18;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 EILKSL 18
 Db 2 EILKSL 7
 |||||
 |||||
 RESULT 12
 ABP59049
 ID ABP59049 standard; Peptide; 17 AA.
 XX
 AC ABP59049;
 XX
 DT 20-FEB-2003 (first entry)
 XX
 DE Chlamydia trachomatis peptide epitope #90.
 XX
 KW Antibacterial; secreted protein; intracellular bacterium.
 XX
 OS Chlamydia trachomatis.
 XX
 XX WO200282091-A2.
 XX
 PD 17-OCT-2002.
 XX

CC production of alpha-1,6-branched alpha-1,4-glucans. It is also used to
 CC prepare transgenic plants that produce starches with modified properties.
 CC (III) are used as binders for tablets, carriers for pharmaceuticals,
 CC flavors and perfumes and powdered additives, packaging materials,
 CC ultra-violet light adsorbers in sunscreens and also for any of the usual
 CC applications of starch in foods, papermaking, as textile size, in soil
 CC stabilization, as wetting agent for agricultural chemicals, as polymer
 CC additives etc. Fragments of (I) are useful as PCR primers and antisense
 CC molecules or ribozymes for inhibiting expression of (I), and the
 CC regulatory region of (II) can be used to control expression of
 CC heterologous sequences in host cells. (I) provides an inexpensive method
 CC for producing alpha-1,6-branched alpha-1,4-glucans (III), producing
 CC products that can be tailored for particular applications, particularly
 CC by controlling the degree of branching. Starch from transgenic plants
 CC has increased gel strength; reduced phosphate content; reduced peak
 CC viscosity; lower pasting temperature and granule size and/or altered
 CC sidechain distribution. This sequence represents an alpha-1,6-branched
 CC alpha-1,4-glucan protein fragment isolated from *Neisseria dentrificans*
 CC which is described in the method of the invention.

XX Sequence 5 AA;

Query Match 22.2%; Score 4; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DDHG 11
 Db 1 DDHG 4

RESULT 15

AAAY92081
 ID AAY92081 standard; Peptide; 5 AA.

XX AC AAY92081;

XX DT 01-AUG-2000 (first entry)

XX DE C-terminal peptide of recombinant human DKR-3 expressed in *E. coli*.

XX KW DKR-3; dkk-1; dickkopf-1; antagonist; wnt-8 signaling; morphogenesis;
 XX KW growth factor; cytostatic; sonic hedgehog; tissue differentiation;
 XX KW bacterial expression.

XX OS Synthetic.

XX PN WO200018914-A2.

XX PD 06-APR-2000.

XX PF 17-SEP-1999; 99WO-US21647.

XX PR 25-SEP-1998; 98US-0161241.

XX PA (AMGE-) AMGEN INC.

XX PI Bass MB, Sullivan JK, Theill LE, Wang D;

XX DR WPI; 2000-293153/25.

XX PT New nucleic acid molecule encoding a biologically active DKR
 XX PT polypeptide, useful in treatment of cancer, e.g. mammary tumors and
 XX PT stem cell tumors

XX PS Example 9; Page 78; 143pp; English.

XX CC DKR-1 is a human ortholog of dkk-1 (dickkopf-1), a novel gene identified
 CC in *Xenopus* and mouse, purportedly an antagonist of wnt-8 signaling.
 CC DKR-2, -3 and -4 are each related to DKR-1 by their cysteine pattern.
 CC Dkk-1 is also involved in morphogenesis in the developing embryo, and
 CC therefore a growth factor, by inference DKR polypeptides are also
 CC growth-factors. The DKR polypeptides are useful for treating cancer,

CC e.g. mammary tumors, stem cell tumors, or other cancers in which the wnt
 CC and/or sonic hedgehog (shh) signal transduction pathways are activated.
 CC They can also be used to enhance tissue differentiation, such as bone
 CC formation and hematopoietic cell formation.

XX Sequence 5 AA;

Query Match 22.2%; Score 4; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GEEI 14
 Db 2 GEEI 5

RESULT 16

AAAY92083

ID AAY92083 standard; Peptide; 5 AA.

XX AC AAY92083;

XX DT 01-AUG-2000 (first entry)

XX DE C-terminal peptide of recombinant human DKR-3 expressed in *E. coli*.

XX KW DKR-3; dkk-1; dickkopf-1; antagonist; wnt-8 signaling; morphogenesis;
 XX KW growth factor; cytostatic; sonic hedgehog; tissue differentiation;
 XX KW bacterial expression.

XX OS Synthetic.

XX PN WO200018914-A2.

XX PD 06-APR-2000.

XX PF 17-SEP-1999; 99WO-US21647.

XX PR 25-SEP-1998; 98US-0161241.

XX PA (AMGE-) AMGEN INC.

XX PI Bass MB, Sullivan JK, Theill LE, Wang D;

XX DR WPI; 2000-293153/25.

XX PT New nucleic acid molecule encoding a biologically active DKR
 XX PT polypeptide, useful in treatment of cancer, e.g. mammary tumors and
 XX PT stem cell tumors

XX PS Example 9; Page 79; 143pp; English.

XX CC DKR-1 is a human ortholog of dkk-1 (dickkopf-1), a novel gene identified
 CC in *Xenopus* and mouse, purportedly an antagonist of wnt-8 signaling.
 CC DKR-2, -3 and -4 are each related to DKR-1 by their cysteine pattern.
 CC Dkk-1 is also involved in morphogenesis in the developing embryo, and
 CC therefore a growth factor, by inference DKR polypeptides are also
 CC growth factors. The DKR polypeptides are useful for treating cancer,
 CC e.g. mammary tumors, stem cell tumors, or other cancers in which the wnt
 CC and/or sonic hedgehog (shh) signal transduction pathways are activated.
 CC They can also be used to enhance tissue differentiation, such as bone
 CC formation and hematopoietic cell formation.

XX Sequence 5 AA;

Query Match 22.2%; Score 4; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GEEI 14
 Db 2 GEEI 5

RESULT 17
 AAY92085
 ID AAY92085 standard; Peptide; 5 AA.
 XX AC AAY92085;
 XX 01-AUG-2000 (first entry)
 DT DT
 XX C-terminal peptide of recombinant human DKR-3-42-350.
 DE
 XX DKR-3; dkk-1; dickkopf-1; antagonist; wnt-8 signaling; morphogenesis;
 KW growth factor; cytostatic; sonic hedgehog; tissue differentiation;
 KW bacterial expression.
 XX
 OS Synthetic.
 XX WO200018914-A2.
 PN 06-APR-2000.
 XX
 PD 17-SEP-1999; 99WO-US21647.
 PF
 XX 25-SEP-1998; 98US-0161241.
 XX (AMGE-) AMGEN INC.
 PA
 XX Bass MB, Sullivan JK, Theill LE, Wang D;
 PI WPI; 2000-293153/25.
 XX
 DR New nucleic acid molecule encoding a biologically active DKR
 PT polypeptide, useful in treatment of cancer, e.g. mammary tumors and
 PT stem cell tumors
 PS Example 9; Page 79; 143pp; English.
 XX
 CC DKR-1 is a human ortholog of dkk-1 (dickkopf-1), a novel gene identified
 CC in Xenopus and mouse, purportedly an antagonist of wnt-8 signaling.
 CC DKR-2, -3 and -4 are each related to DKR-1 by their cysteine pattern.
 CC Dkk-1 is also involved in morphogenesis in the developing embryo, and
 CC therefore a growth factor, by inference DKR polypeptides are also
 CC growth factors. The DKR polypeptides are useful for treating cancer,
 CC e.g. mammary tumors, stem cell tumors, or other cancers in which the wnt
 CC and/or sonic hedgehog (shh) signal transduction pathways are activated.
 CC They can also be used to enhance tissue differentiation, such as bone
 CC formation and hematopoietic cell formation.
 XX
 SQ Sequence 5 AA;
 Query Match 22.2%; Score 4; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GEEI 14
 Db |||||
 2 GEEI 5
 RESULT 18
 AAB55641
 ID AAB55641 standard; Peptide; 5 AA.
 XX AC AAB55641;
 XX 07-MAR-2001 (first entry)
 DT
 XX Monocyte surface receptor PDZ domain sequence #12.
 DE
 XX Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;
 KW allergy; asthma; multiple sclerosis; cancer; infection.
 XX
 OS Synthetic.

XX WO200069896-A2.
 XX 23-NOV-2000.
 PD
 XX 12-MAY-2000; 2000WO-US13161.
 PF
 XX 14-MAY-1999; 99US-0134114.
 PR 14-MAY-1999; 99US-0134117.
 PR 14-MAY-1999; 99US-0134118.
 PR 21-OCT-1999; 99US-0160860.
 PR 29-OCT-1999; 99US-0162498.
 PR 13-DEC-1999; 99US-0170453.
 PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.
 XX (ARBO-) ARBOR VITA CORP.
 PA
 XX Lu PS;
 PI
 XX WPI; 2001-080245/09.
 DR
 XX Modulating a biological function of an endothelial cell or
 PT hematopoietic cell, useful for treating autoimmune diseases and
 PT infectious diseases, by administering an antagonist that inhibits
 PT binding between a PDZ protein and a PL protein -
 XX Disclosure; Page 87-94; 141pp; English.
 PS
 XX The present invention relates to a new method for modulating a
 CC biological function of an endothelial cell or hematopoietic cell. The
 CC method involves introducing into a cell, an antagonist that inhibits
 CC binding between a PDZ protein and a PL protein. The inhibitor is used
 CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune
 CC disease. It may also be used to prevent transplantation rejection of
 CC a solid organ transplant. The method may also be used in the treatment
 CC of inflammation, allergy, inflammatory bowel diseases, ulcerative
 CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,
 CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,
 CC graft rejection, transplantation rejection), atherosclerosis, cancers,
 CC infectious diseases, ischemia, vasculitis and Crohn's disease.
 XX
 SQ Sequence 5 AA;
 Query Match 22.2%; Score 4; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 LKSL 18
 Db |||||
 1 LKSL 4
 RESULT 19
 AAB57488
 ID AAB57488 standard; Peptide; 5 AA.
 XX AC AAB57488;
 XX 12-MAR-2001 (first entry)
 DT
 XX CD61 C-terminal core sequence #2.
 DE
 XX Endothelial cell; hematopoietic cell; PDZ domain protein;
 KW PL domain protein; leukocyte activation; T cell surface receptor;
 KW synapse formation; transmembrane neurotransmitter receptor;
 KW autoimmune disease; transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
 KW ischaemia; vasculitis; Crohn's disease.

```

XX OS Homo sapiens.
XX PN WO200069897-A2.
XX PD 23-NOV-2000.
XX PF 12-MAY-2000; 2000WO-US13166.
XX PR 14-MAY-1999; 99US-0134114.
XX PR 14-MAY-1999; 99US-0134117.
XX PR 14-MAY-1999; 99US-0134118.
XX PR 21-OCT-1999; 99US-0160860.
XX PR 29-OCT-1999; 99US-0162498.
XX PR 13-DEC-1999; 99US-0170453.
XX PR 14-FEB-2000; 2000US-0176195.
XX PR 14-FEB-2000; 2000US-0182296.
XX PR 11-APR-2000; 2000US-0196460.
XX PR 11-APR-2000; 2000US-0196527.
XX PA (ARBO-) ARBOR VITA CORP.
XX PI Lu PS;
XX XX WPI; 2001-025003/03.
XX XX
XX XX New inhibitors of binding of a PDZ protein and PL protein for
XX XX inhibiting T cell-mediated response by hematopoietic cells, or for
XX XX treating diseases characterized by inflammatory and humoral immune
XX XX responses, e.g. inflammation, cancer -
XX XX
XX XX Disclosure; Page 90; 139pp; English.
XX XX
XX CC The present invention relates to a method for modulating a biological
XX CC function of an endothelial cell or hematopoietic cell, comprises
XX CC introducing into a cell an antagonist that inhibits binding between a
XX CC PDZ domain protein and a PL domain protein to result in inhibition of
XX CC leukocyte activation. The present sequence is a core sequence of a PL
XX CC domain protein (a T cell surface receptor). PDZ domains of proteins are
XX CC named after three prototypical proteins: PSD95, Drosophila large disc
XX CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved
XX CC in synapse formation by organising transmembrane neurotransmitter
XX CC receptors through intracellular interactions. The inhibitors identified
XX CC by the present invention can be used to treat a disease mediated by
XX CC hematopoietic cells, e.g. autoimmune disease, inflammation, allergy
XX CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
XX CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
XX CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
XX CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
XX CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
XX CC viral infection), ischaemia, vasculitis and Crohn's disease. The
XX CC inhibitors can also be used to prevent transplantation rejection of a
XX CC solid organ transplant.
XX XX
XX SQ Sequence 5 AA;
XX XX
XX XX Query Match 22.2%; Score 4; DB 22; Length 5;
XX XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX Qy 15 LKSL 18
XX Db 1 LKSL 4
XX XX
XX XX RESULT 20
XX XX AAB57898
XX XX ID AAB57898 standard; Peptide; 5 AA.
XX XX AC AAB57898;
XX XX XX
XX XX 12-MAR-2001 (first entry)
XX XX

```

```

DE CD61 C-terminal core sequence #2.
XX Endothelial cell; hematopoietic cell; PDZ domain protein;
XX PL domain protein; leukocyte activation; T cell surface receptor;
XX synapse formation; transmembrane neurotransmitter receptor;
XX autoimmune disease; transplantation rejection; inflammation; allergy;
XX inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
XX asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
XX ischaemia; vasculitis; Crohn's disease.
XX OS Homo sapiens.
XX XX WO200069898-A2.
XX PD 23-NOV-2000.
XX PF 12-MAY-2000; 2000WO-US13205.
XX PR 14-MAY-1999; 99US-0134114.
XX PR 14-MAY-1999; 99US-0134117.
XX PR 14-MAY-1999; 99US-0134118.
XX PR 21-OCT-1999; 99US-0160860.
XX PR 29-OCT-1999; 99US-0162498.
XX PR 13-DEC-1999; 99US-0170453.
XX PR 14-JAN-2000; 2000US-0176195.
XX PR 14-FEB-2000; 2000US-0182296.
XX PR 11-APR-2000; 2000US-0196460.
XX PR 11-APR-2000; 2000US-0196527.
XX PA (ARBO-) ARBOR VITA CORP.
XX PI Lu PS;
XX XX WPI; 2001-061214/07.
XX XX
XX XX Modulating a biological function of a hematopoietic cell for treating
XX XX an allergic response, or diseases mediated by immune system cells,
XX XX comprises introducing into the cell a PDZ-PL interaction enhancer or
XX XX inhibitor -
XX XX
XX XX Disclosure; Page 93; 143pp; English.
XX XX
XX CC The present invention relates to a method for modulating a biological
XX CC function of an endothelial cell or hematopoietic cell, comprises
XX CC introducing into a cell an antagonist that inhibits binding between a
XX CC PDZ domain protein and a PL domain protein to result in inhibition of
XX CC leukocyte activation. The present sequence is a core sequence of a PL
XX CC domain protein (a T cell surface receptor). PDZ domains of proteins are
XX CC named after three prototypical proteins: PSD95, Drosophila large disc
XX CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved
XX CC in synapse formation by organising transmembrane neurotransmitter
XX CC receptors through intracellular interactions. The inhibitors identified
XX CC by the present invention can be used to treat a disease mediated by
XX CC hematopoietic cells, e.g. autoimmune disease, inflammation, allergy
XX CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
XX CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
XX CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
XX CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
XX CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
XX CC viral infection), ischaemia, vasculitis and Crohn's disease. The
XX CC inhibitors can also be used to prevent transplantation rejection of a
XX CC solid organ transplant.
XX XX
XX SQ Sequence 5 AA;
XX XX
XX XX Query Match 22.2%; Score 4; DB 22; Length 5;
XX XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX Qy 15 LKSL 18
XX Db 1 LKSL 4
XX XX
XX XX RESULT 20
XX XX AAB57898
XX XX ID AAB57898 standard; Peptide; 5 AA.
XX XX AC AAB57898;
XX XX XX
XX XX 12-MAR-2001 (first entry)
XX XX

```

RESULT 21
 AB05120
 ID AB05120 standard; Peptide; 5 AA.
 XX AC
 XX AB05120;
 DT 07-NOV-2002 (first entry)
 XX
 DE T-cell surface receptor C-terminal core peptide SEQ ID No 115.
 XX
 XX Immunosuppressive; antiinflammatory; affinity; Kd; binding; PDZ domain;
 KW ligand; Ki; inhibitor; K-enhancer; leukocyte; autoimmune disease;
 KW inflammatory; humoral immune response; inflammation; C-terminal core;
 KW T-cell surface receptor.
 XX
 OS Unidentified.
 XX
 XX WO200231512-A2.
 PN
 XX
 PD 18-APR-2002.
 XX
 XX 11-OCT-2001; 2001WO-US32150.
 PF
 XX 13-OCT-2000; 2000US-0688017.
 PR
 XX (ARBO-) ARBOR VITA CORP.
 PA
 XX Rabinowitz JD, Lu PS, Schweizer J;
 PI WPI; 2002-416878/44.
 DR
 XX Assays for determining the affinity of binding between a PDZ domain and
 PT a ligand, and determining the Ki of an inhibitor of the binding,
 PT comprises using a polypeptide comprising a PDZ domain and a non-PDZ
 PT domain -
 XX
 PS Disclosure; Page 114; 164pp; English.
 XX
 CC The invention relates to methods and reagents for determining the
 CC apparent affinity (Kd) of binding between a PDZ domain and a ligand. The
 CC invention also relates to methods and reagents for determining the Ki of
 CC an inhibitor of binding between a PDZ domain and a ligand, identifying an
 CC agent that enhances binding of a PDZ domain and a ligand, and determining
 CC the potency (K-enhancer) of binding between a PDZ domain and a ligand, by
 CC determining the ligand bound with an immobilised polypeptide comprising a
 CC PDZ domain and a non-PDZ domain on a surface. The modulator (preferably,
 CC an inhibitor) of interaction between PDZ and PL is useful for treating a
 CC disease characterised by leukocyte activation, e.g., an autoimmune
 CC disease that is characterised by inflammatory or humoral immune response,
 CC and for reducing inflammation in a subject. This sequence represents a T-
 CC cell surface receptor C-terminal core peptide relating to the PDZ
 CC containing proteins of the invention.
 XX
 SQ Sequence 5 AA;
 Query Match 22.2%; Score 4; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 LKSL 18
 DB 1 LKSL 4
 RESULT 22
 ABP63413
 ID ABP63413 standard; Peptide; 5 AA.
 XX AC
 XX ABP63413;
 DT 28-OCT-2002 (first entry)
 XX

DE Monocyte surface receptor PDZ motif (PL) peptide SEQ ID NO:115.
 XX
 KW Molecular interaction; haematopoietic cell; immune response; T cell;
 PDZ domain; B cell; endothelial cell; PDZ protein; PSD95; PDZ ligand;
 KW Drosophila large disc protein; Zonula Occludin 1 protein; PL protein;
 KW immunosuppressive; antiinflammatory; antiallergic; antiatherosclerotic;
 KW antitumor; antipsoriatic; dermatological; antiasthmatic; cyostatic;
 KW antimicrobial; vasotropic; inflammatory immune response; inflammation;
 KW humoral immune response; autoimmune disease; allergy; ulcerative colitis;
 KW inflammatory bowel disease; ileitis; enteritis; psoriasis; scleroderma;
 KW inflammatory dermatosis; respiratory allergic disease; asthma; cancer;
 KW allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia;
 XX angiogenesis-dependent disorder; infectious disease.
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200242422-A2.
 XX
 PD 30-MAY-2002.
 XX
 XX 09-NOV-2001; 2001WO-US44138.
 PF
 XX 11-NOV-2000; 2000US-0710059.
 PR
 XX 24-NOV-2000; 2000US-0721915.
 PR
 XX 28-NOV-2000; 2000US-0722069.
 PR
 XX 28-NOV-2000; 2000US-0724553.
 PA
 XX (ARBO-) ARBOR VITA CORP.
 PI
 XX Lu P, Rabinowitz JD, Schweizer J;
 PI WPI; 2002-609221/65.
 DR
 XX Modulating the biological function of an endothelial cell or
 PT hematopoietic cell e.g., a T-cell or B-cell comprises introducing into
 PT the cell, an agent that inhibits binding of a PDZ protein and a PDZ
 PT ligand protein in the cell -
 XX
 PS Disclosure; Page 132; 207pp; English.
 XX
 CC The present invention describes a method (M1) for modulating a biological
 CC function of an endothelial cell or haematopoietic cell. M1 comprises
 CC introducing into the cell, an agent that inhibits binding of a PDZ
 CC (PSD95, Drosophila large disc protein, and Zonula Occludin 1 protein)
 CC protein and a PDZ ligand (PL) protein in the cell, and so modulates the
 CC biological function. Also described is a method (M2) for determining
 CC whether a test compound is an inhibitor of binding between a PDZ protein
 CC and a PL protein. M1 is used for modulating a biological function of an
 CC endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an
 CC inflammatory or humoral immune response, or an autoimmune disease. An
 CC inhibitor (I) is useful for treating a disease characterised by leukocyte
 CC activation, where the disease is characterised by an inflammatory or
 CC humoral immune response, e.g., an autoimmune disease. The compounds
 CC e.g., PL-PDZ interaction inhibitors are useful for treating (ameliorating
 CC symptoms of) a variety of diseases and conditions characterised by
 CC inflammatory and humoral immune responses e.g., inflammation, allergy,
 CC inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis,
 CC psoriasis and inflammatory dermatoses, scleroderma, respiratory allergic
 CC diseases such as asthma, allergic rhinitis, transplantation rejection
 CC (cardiac, kidney, lung, liver, small bowel, cornea, pancreas, cadaver,
 CC autologous, bone marrow, xenotransplantation), atherosclerosis, cancers,
 CC angiogenesis-dependent disorders, infectious diseases and ischaemia.
 CC AB096620 to AB096732 and ABP63153 to ABP63578 represent sequences used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 5 AA;
 Query Match 22.2%; Score 4; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 LKSL 18

```

Db      ||||
      1 LKSL 4

RESULT 23
AAY21763
ID  AAY21763 standard; peptide; 6 AA.
XX
AC  AAY21763;
XX
DT  10-SEP-1999 (first entry)
XX
DE  Conserved peptide sequence of CYP32 (caspase-3).
XX
KW  Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
KW  autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
KW  tumour cell; myocardial infarction; human.
XX
OS  Homo sapiens.
XX
PN  WO9935277-A2.
XX
PD  15-JUL-1999.
XX
PF  11-JAN-1999; 99WO-US00632.
XX
PR  09-JAN-1998; 98US-0070987.
XX
PA  (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI  Alnemri ES;
XX
DR  WPI; 1999-419353/35.
XX
PF  11-JAN-1999; 99WO-US00632.
XX
PR  09-JAN-1998; 98US-0070987.
XX
PA  (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI  Alnemri ES;
XX
DR  WPI; 1999-419353/35.
XX
PT  New isolated nucleic acid molecule encoding a rev-caspase - used
PT  for screening and identifying inhibitors or enhancers for treating
PT  cancer or autoimmune disease
XX
PS  Disclosure; Fig 6; 74pp; English.
XX
CC  The invention relates to nucleic acid molecules encoding rev-caspases.
CC  Rev-caspases are cysteine proteases that specifically cleave proteins
CC  after Asp residues and is expressed as a zymogen, in which the small
CC  subunit is N-terminal to a large subunit. A gene delivery vehicle
CC  comprising a rev-caspase coding sequence is useful for the treatment of
CC  cancer, where the gene delivery vehicle is internalised by tumour cells.
CC  The gene delivery vehicle can also be used to treat autoimmune diseases.
CC  Cells transfected with a rev-caspase expressing vector can be used in
CC  identification of inhibitors or enhancers of caspase-mediated apoptosis.
CC  In vitro translated rev-caspase can be used to identify an inhibitor or
CC  enhancer of caspase processing activity. Caspase inhibitors are useful
CC  for treating neurodegenerative diseases as well as for inhibiting
CC  apoptosis in the heart following myocardial infarction. Sequences
CC  AAY21734 -AAY21795 represent conserved peptide sequences in various
CC  caspases.
XX
SQ  Sequence 6 AA;
      Query Match      22.2%; Score 4; DB 20; Length 6;
      Best Local Similarity 100.0%; Pred. No. 9.3e+05;
      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  10 HGEE 13
      ||||
Db  3 HGEE 6

RESULT 24
AAY21768
ID  AAY21768 standard; peptide; 6 AA.
XX
AC  AAY21768;
XX
DT  10-SEP-1999 (first entry)
XX
DE  Conserved peptide sequence of Mch3 (caspase-7).
XX
KW  Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
KW  autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
KW  tumour cell; myocardial infarction; human.
XX
OS  Homo sapiens.
XX

```

```

DT  10-SEP-1999 (first entry)
XX
DE  Conserved peptide sequence of CED3.
XX
KW  Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
KW  autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
KW  tumour cell; myocardial infarction; human.
XX
OS  Homo sapiens.
XX
PN  WO9935277-A2.
XX
PD  15-JUL-1999.
XX
PF  11-JAN-1999; 99WO-US00632.
XX
PR  09-JAN-1998; 98US-0070987.
XX
PA  (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI  Alnemri ES;
XX
DR  WPI; 1999-419353/35.
XX
PT  New isolated nucleic acid molecule encoding a rev-caspase - used
PT  for screening and identifying inhibitors or enhancers for treating
PT  cancer or autoimmune disease
XX
PS  Disclosure; Fig 6; 74pp; English.
XX
CC  The invention relates to nucleic acid molecules encoding rev-caspases.
CC  Rev-caspases are cysteine proteases that specifically cleave proteins
CC  after Asp residues and is expressed as a zymogen, in which the small
CC  subunit is N-terminal to a large subunit. A gene delivery vehicle
CC  comprising a rev-caspase coding sequence is useful for the treatment of
CC  cancer, where the gene delivery vehicle is internalised by tumour cells.
CC  The gene delivery vehicle can also be used to treat autoimmune diseases.
CC  Cells transfected with a rev-caspase expressing vector can be used in
CC  identification of inhibitors or enhancers of caspase-mediated apoptosis.
CC  In vitro translated rev-caspase can be used to identify an inhibitor or
CC  enhancer of caspase processing activity. Caspase inhibitors are useful
CC  for treating neurodegenerative diseases as well as for inhibiting
CC  apoptosis in the heart following myocardial infarction. Sequences
CC  AAY21734 -AAY21795 represent conserved peptide sequences in various
CC  caspases.
XX
SQ  Sequence 6 AA;
      Query Match      22.2%; Score 4; DB 20; Length 6;
      Best Local Similarity 100.0%; Pred. No. 9.3e+05;
      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  10 HGEE 13
      ||||
Db  3 HGEE 6

RESULT 25
AAY21752
ID  AAY21752 standard; peptide; 6 AA.
XX
AC  AAY21752;
XX
DT  10-SEP-1999 (first entry)
XX
DE  Conserved peptide sequence of Mch3 (caspase-7).
XX
KW  Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
KW  autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
KW  tumour cell; myocardial infarction; human.
XX
OS  Homo sapiens.
XX

```

PN WO9935277-R2.
 XX 15-JUL-1999.
 XX 11-JAN-1999; 99WO-US00632.
 XX 09-JAN-1998; 98US-0070987.
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX Alnemri ES;
 XX WPI; 1999-419353/35.
 XX New isolated nucleic acid molecule encoding a rev-caspase - used
 PT for screening and identifying inhibitors or enhancers for treating
 PT cancer or autoimmune disease
 XX Disclosure; Fig 6; 74pp; English.
 XX The invention relates to nucleic acid molecules encoding rev-caspases.
 CC Rev-caspases are cysteine proteases that specifically cleave proteins
 CC after Asp residues and is expressed as a zymogen, in which the small
 CC subunit is N-terminal to a large subunit. A gene delivery vehicle
 CC comprising a rev-caspase coding sequence is useful for the treatment of
 CC cancer, where the gene delivery vehicle is internalised by tumour cells.
 CC The gene delivery vehicle can also be used to treat autoimmune diseases.
 CC Cells transfected with a rev-caspase expressing vector can be used in
 CC identification of inhibitors or enhancers of caspase-mediated apoptosis.
 CC In vitro translated rev-caspase can be used to identify an inhibitor or
 CC enhancer of caspase processing activity. Caspase inhibitors are useful
 CC for treating neurodegenerative diseases as well as for inhibiting
 CC apoptosis in the heart following myocardial infarction. Sequences
 CC AAY21734 -AAY21795 represent conserved peptide sequences in various
 CC caspases.
 XX
 SQ Sequence 6 AA;
 Query Match 22.2%; Score 4; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 HGEE 13
 DB |||||
 3 HGEE 6
 RESULT 26
 AAE08967
 ID AAE08967 standard; peptide; 6 AA.
 XX AAE08967;
 XX 15-NOV-2001 (first entry)
 DT
 DE Mammalian ced-3 homologue 3 (Mch3) peptide fragment #2.
 XX
 KW Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer;
 KW aspartate-specific cysteine protease; ASCP; apoptosis; therapy;
 KW autoimmune disease; cerebellar degeneration; Alzheimer's disease;
 KW cytostatic; Parkinson's disease; immunomodulator; antimicrobial;
 KW viral infection; cell death-mediated disease; neuroprotective.
 XX
 OS Unidentified.
 XX
 PN US6271361-B1.
 XX
 PD 07-AUG-2001.
 XX
 PF 25-FEB-1999; 99US-0257218.
 XX
 PR 29-MAY-1997; 97US-0865579.
 XX
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX Alnemri ES, Fernandes-alnemri T, Litwack G;
 XX WPI; 2001-528686/58.
 XX New apoptotic genes and their apoptotic protease products, useful for
 PT modulating apoptosis for the therapeutic treatment of human diseases,
 PT e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's
 PT disease -

PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX Alnemri ES, Fernandes-alnemri T, Litwack G;
 XX WPI; 2001-528686/58.
 XX New apoptotic genes and their apoptotic protease products, useful for
 PT modulating apoptosis for the therapeutic treatment of human diseases,
 PT e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's
 PT disease -
 XX Disclosure; Column 35; 36pp; English.
 XX The invention relates to an isolated gene encoding apoptotic protease,
 CC mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the
 CC aspartate-specific cysteine protease (ASCP) family. Mch6 DNA and
 CC protein sequences are useful for modulating apoptosis for the
 CC therapeutic treatment of human diseases. Mch6 sequences are useful
 CC for upregulating apoptosis (e.g. for treating cancers, autoimmune
 CC disease or viral infections) or downregulating apoptosis (e.g. for
 CC treating Alzheimer's disease, Parkinson's disease or cerebellar
 CC degeneration). The Mch6 sequence is useful for diagnosing, treating
 CC or reducing the severity of cell death-mediated diseases, as well as
 CC other diseases mediated by either increased or decreased programmed
 CC cell death. The present amino acid sequence is Mch3 peptide fragment.
 XX Sequence 6 AA;
 SQ
 Query Match 22.2%; Score 4; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 HGEE 13
 DB |||||
 3 HGEE 6
 RESULT 27
 AAE08978
 ID AAE08978 standard; peptide; 6 AA.
 XX AAE08978;
 XX 15-NOV-2001 (first entry)
 DT
 DE CPP32 peptide fragment #2.
 XX
 KW Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer; CPP32;
 KW aspartate-specific cysteine protease; ASCP; apoptosis; therapy;
 KW autoimmune disease; cerebellar degeneration; Alzheimer's disease;
 KW cytostatic; Parkinson's disease; immunomodulator; antimicrobial;
 KW viral infection; cell death-mediated disease; neuroprotective.
 XX
 OS Unidentified.
 XX
 PN US6271361-B1.
 XX
 PD 07-AUG-2001.
 XX
 PF 25-FEB-1999; 99US-0257218.
 XX
 PR 29-MAY-1997; 97US-0865579.
 XX
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX Alnemri ES, Fernandes-alnemri T, Litwack G;
 XX WPI; 2001-528686/58.
 XX New apoptotic genes and their apoptotic protease products, useful for
 PT modulating apoptosis for the therapeutic treatment of human diseases,
 PT e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's
 PT disease -

XX Disclosure; Column 39; 36pp; English.

XX The invention relates to an isolated gene encoding apoptotic protease, mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the aspartate-specific cysteine protease (ASCP) family. Mch6 DNA and protein sequences are useful for modulating apoptosis for the therapeutic treatment of human diseases. Mch6 sequences are useful for upregulating apoptosis (e.g. for treating cancers, autoimmune disease or viral infections) or downregulating apoptosis (e.g. for treating Alzheimer's disease, Parkinson's disease or cerebellar degeneration). The Mch6 sequence is useful for diagnosing, treating or reducing the severity of cell death-mediated diseases, as well as other diseases mediated by either increased or decreased programmed cell death. The present amino acid sequence is a fragment of CPP32 peptide which cleaves Mch6.

XX Sequence 6 AA;

Query Match 22.2%; Score 4; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13
|
|
|
|
Db 3 HGEE 6

RESULT 28
AAE08983
ID AAE08983 standard; peptide; 6 AA.
AC AAE08983;
XX
XX 15-NOV-2001 (first entry)
DT
DE CED-3 peptide fragment #2.
XX
XX Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer; CED-3; aspartate-specific cysteine protease; ASCP; apoptosis; therapy; autoimmune disease; cerebellar degeneration; Alzheimer's disease; cystostatic; Parkinson's disease; immunomodulator; antimicrobial; viral infection; cell death-mediated disease; neuroprotective.

XX Unidentified.

XX US6271361-B1.

XX 07-AUG-2001.

XX 25-FEB-1999; 99US-0257218.

XX 29-MAY-1997; 97US-0865579.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES, Fernandes-alnemri T, Litwack G;
PI
XX WPI; 2001-528686/58.

XX New apoptotic genes and their apoptotic protease products, useful for modulating apoptosis for the therapeutic treatment of human diseases, e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's disease -

XX Disclosure; Column 41; 36pp; English.

XX The invention relates to an isolated gene encoding apoptotic protease, mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the aspartate-specific cysteine protease (ASCP) family. Mch6 DNA and protein sequences are useful for modulating apoptosis for the therapeutic treatment of human diseases. Mch6 sequences are useful for upregulating apoptosis (e.g. for treating cancers, autoimmune

XX disease or viral infections) or downregulating apoptosis (e.g. for treating Alzheimer's disease, Parkinson's disease or cerebellar degeneration). The Mch6 sequence is useful for diagnosing, treating or reducing the severity of cell death-mediated diseases, as well as other diseases mediated by either increased or decreased programmed cell death. The present amino acid sequence is CED-3 peptide fragment.

XX Sequence 6 AA;

Query Match 22.2%; Score 4; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13
|
|
|
|
Db 3 HGEE 6

RESULT 29
AAB55642
ID AAB55642 standard; Peptide; 6 AA.
XX
XX AAB55642;
XX
XX 07-MAR-2001 (first entry)
DT
DE Monocyte surface receptor PDZ domain sequence #13.
XX
XX Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation; allergy; asthma; multiple sclerosis; cancer; infection.

XX Synthetic.

XX WO200069896-A2.

XX 23-NOV-2000.

XX 12-MAY-2000; 2000WO-US13161.

XX 14-MAY-1999; 99US-0134114.

XX 14-MAY-1999; 99US-0134117.

XX 14-MAY-1999; 99US-0134118.

XX 21-OCT-1999; 99US-0160860.

XX 29-OCT-1999; 99US-0162498.

XX 13-DEC-1999; 99US-0170453.

XX 14-JAN-2000; 2000US-0176195.

XX 14-FEB-2000; 2000US-0182296.

XX 11-APR-2000; 2000US-0196460.

XX 11-APR-2000; 2000US-0196527.

XX (AFBO-) ARBOR VITA CORP.

XX Lu PS;

XX WPI; 2001-080245/09.

XX Modulating a biological function of an endothelial cell or hematopoietic cell, useful for treating autoimmune diseases and infectious diseases, by administering an antagonist that inhibits binding between a PDZ protein and a PL protein -

XX Disclosure; Page 87-94; 14pp; English.

XX The present invention relates to a new method for modulating a biological function of an endothelial cell or hematopoietic cell. The method involves introducing into a cell, an antagonist that inhibits binding between a PDZ protein and a PL protein. The inhibitor is used to treat a disease mediated by hematopoietic cells, e.g. autoimmune disease. It may also be used to prevent transplantation rejection of a solid organ transplant. The method may also be used in the treatment of inflammation, allergy, inflammatory bowel diseases, ulcerative colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis,

CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,
 CC graft rejection, transplantation rejection), atherosclerosis, cancers,
 CC infectious diseases, ischemia, vasculitis and Crohn's disease.

SQ Sequence 6 AA;

Query Match 22.2%; Score 4; DB 22; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18

Db 2 LKSL 5

RESULT 30

AAB57489

ID AAB57489 standard; Peptide; 6 AA.

XX AAB57489;

AC AAB57489;

DT 12-MAR-2001 (first entry)

DE CD61 C-terminal core sequence #3.

XX Endothelial cell; haematopoietic cell; PDZ domain protein;

KW PL domain protein; leukocyte activation; T cell surface receptor;

KW synapse formation; transmembrane neurotransmitter receptor;

KW autoimmune disease; transplantation rejection; inflammation; allergy;

KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;

KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;

KW ischaemia; vasculitis; Crohn's disease.

XX Homo sapiens.

OS WO200069897-A2.

PN 23-NOV-2000.

PD 12-MAY-2000; 2000WO-US13166.

PF 14-MAY-1999; 99US-0134114.

PR 14-MAY-1999; 99US-0134117.

PR 14-MAY-1999; 99US-0134118.

PR 21-OCT-1999; 99US-0160860.

PR 29-OCT-1999; 99US-0162498.

PR 13-DEC-1999; 99US-0170453.

PR 14-JAN-2000; 2000US-0176195.

PR 14-FEB-2000; 2000US-0182296.

PR 11-APR-2000; 2000US-0196460.

PR 11-APR-2000; 2000US-0196527.

XX (ARBO-) ARBOR VITA CORP.

PA Lu PS;

XX WPI; 2001-025003/03.

DR New inhibitors of binding of a PDZ protein and PL protein for

PT inhibiting T cell-mediated response by haematopoietic cells, or for

PT treating diseases characterized by inflammatory and humoral immune

PT responses, e.g. inflammation, cancer -

XX Disclosure; Page 90; 139pp; English.

XX The present invention relates to a method for modulating a biological

CC function of an endothelial cell or haematopoietic cell, comprises

CC introducing into a cell an antagonist that inhibits binding between a

CC PDZ domain protein and a PL domain protein to result in inhibition of

CC leukocyte activation. The present sequence is a core sequence of a PL

CC domain protein (a T cell surface receptor). PDZ domains of proteins are

CC named after three prototypal proteins: PSD95, Drosophila large disc

CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved

CC in synapse formation by organising transmembrane neurotransmitter
 CC receptors through intracellular interactions. The inhibitors identified
 CC by the present invention can be used to treat a disease mediated by
 CC haematopoietic cells, e.g. autoimmune disease, inflammation, allergy
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The
 CC inhibitors can also be used to prevent transplantation rejection of a
 CC solid organ transplant.

XX Sequence 6 AA;

Query Match 22.2%; Score 4; DB 22; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18

Db 2 LKSL 5

RESULT 31

AAB57899

ID AAB57899 standard; Peptide; 6 AA.

XX AAB57899;

AC AAB57899;

DT 12-MAR-2001 (first entry)

DE CD61 C-terminal core sequence #3.

XX Endothelial cell; haematopoietic cell; PDZ domain protein;

KW PL domain protein; leukocyte activation; T cell surface receptor;

KW synapse formation; transmembrane neurotransmitter receptor;

KW autoimmune disease; transplantation rejection; inflammation; allergy;

KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;

KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;

KW ischaemia; vasculitis; Crohn's disease.

XX Homo sapiens.

OS WO200069898-A2.

PN 23-NOV-2000.

PD 12-MAY-2000; 2000WO-US13205.

PF 14-MAY-1999; 99US-0134114.

PR 14-MAY-1999; 99US-0134117.

PR 14-MAY-1999; 99US-0134118.

PR 21-OCT-1999; 99US-0160860.

PR 29-OCT-1999; 99US-0162498.

PR 13-DEC-1999; 99US-0170453.

PR 14-JAN-2000; 2000US-0176195.

PR 14-FEB-2000; 2000US-0182296.

PR 11-APR-2000; 2000US-0196460.

PR 11-APR-2000; 2000US-0196527.

XX (ARBO-) ARBOR VITA CORP.

PA Lu PS;

XX WPI; 2001-061214/07.

DR Modulating a biological function of a haematopoietic cell for treating

PT an allergic response, or diseases mediated by immune system cells,

PT comprises introducing into the cell a PDZ-PL interaction enhancer or

PT inhibitor -

XX Disclosure; Page 93; 143pp; English.

XX The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or haematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a
 CC PDZ domain protein and a PL domain protein to result in inhibition of a
 CC leukocyte activation. The present sequence is a core sequence of a PL
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are
 CC named after three prototypical proteins: PSD95, Drosophila large disc
 CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved
 CC in synapse formation by organising transmembrane neurotransmitter
 CC receptors through intracellular interactions. The inhibitors identified
 CC by the present invention can be used to treat a disease mediated by
 CC haematopoietic cells, e.g. autoimmune disease, inflammation, allergy
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The
 CC inhibitors can also be used to prevent transplantation rejection of a
 CC solid organ transplant.
 XX

SQ Sequence 6 AA;

Query Match 22.2%; Score 4; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
 ||||
 Db 2 LKSL 5

RESULT 32
 ABJ05121
 ID ABJ05121 standard; Peptide; 6 AA.
 XX
 AC ABJ05121;
 XX
 DT 07-NOV-2002 (first entry)
 XX
 DE T-cell surface receptor C-terminal core peptide SEQ ID No 116.
 XX
 KW Immunosuppressive; antiinflammatory; affinity; Kd; binding; PDZ domain;
 KW ligand; Ki; inhibitor; K-enhancer; leukocyte; autoimmune disease;
 KW inflammatory; humoral immune response; inflammation; C-terminal core;
 KW T-cell surface receptor.
 XX
 OS Unidentified.
 XX
 PN WO200231512-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 11-OCT-2001; 2001WO-US32150.
 XX
 PR 13-OCT-2000; 2000US-0688017.
 XX
 PA (ARBO-) ARBOR VITA CORP.
 XX
 PI Rabinowitz JD, Lu PS, Schweizer J;
 XX
 DR WPI; 2002-416878/44.
 XX
 PT Assays for determining the affinity of binding between a PDZ domain and
 PT a ligand, and determining the Ki of an inhibitor of the binding, PDZ
 PT comprises using a polypeptide comprising a PDZ domain and a non-PDZ
 PT domain -
 XX
 PS Disclosure; Page 114; 164pp; English.
 XX
 CC The invention relates to methods and reagents for determining the
 CC apparent affinity (Kd) of binding between a PDZ domain and a ligand. The

CC invention also relates to methods and reagents for determining the Ki of
 CC an inhibitor of binding between a PDZ domain and a ligand, identifying an
 CC agent that enhances binding of a PDZ domain and a ligand, and determining
 CC the potency (K-enhancer) of binding between a PDZ domain and a ligand, by
 CC determining the ligand bound with an immobilised polypeptide comprising a
 CC PDZ domain and a non-PDZ domain on a surface. The modulator (preferably,
 CC an inhibitor) of interaction between PDZ and PL is useful for treating a
 CC disease characterised by leukocyte activation, e.g., an autoimmune
 CC disease that is characterised by inflammatory or humoral immune response,
 CC and for reducing inflammation in a subject. This sequence represents a T-
 CC cell surface receptor C-terminal core peptide relating to the PDZ
 CC containing proteins of the invention.
 XX

SQ Sequence 6 AA;

Query Match 22.2%; Score 4; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
 ||||
 Db 2 LKSL 5

RESULT 33
 ABP63414
 ID ABP63414 standard; Peptide; 6 AA.
 XX

AC ABP63414;

DT 28-OCT-2002 (first entry)

DE Monocyte surface receptor PDZ motif (PL) peptide SEQ ID NO:116.

XX
 KW Molecular interaction; haematopoietic cell; immune response; T cell;
 KW PDZ domain; B cell; endothelial cell; PDZ protein; PSD95; PDZ ligand;
 KW Drosophila large disc protein; Zonula Occludin 1 protein; PL protein;
 KW immunosuppressive; antiinflammatory; antiallergic; antiatherosclerotic;
 KW antiulcer; antipsoriatic; dermatological; antiasthmatic; cytostatic;
 KW antimicrobial; vasotropic; inflammatory immune response; inflammation;
 KW humoral immune response; autoimmune disease; allergy; ulcerative colitis;
 KW inflammatory bowel disease; ileitis; enteritis; psoriasis; scleroderma;
 KW inflammatory dermatosis; respiratory allergic disease; asthma; cancer;
 KW allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia;
 KW angiogenesis-dependent disorder; infectious disease.

OS Homo sapiens.

OS Synthetic.

PN WO200242422-A2.

XX 30-MAY-2002.

XX 09-NOV-2001; 2001WO-US44138.

XX 11-NOV-2000; 2000US-0710059.

XX 24-NOV-2000; 2000US-0721915.

XX 24-NOV-2000; 2000US-0722069.

XX 28-NOV-2000; 2000US-0724553.

XX (ARBO-) ARBOR VITA CORP.

XX Lu P, Rabinowitz JD, Schweizer J;

XX WPI; 2002-608221/65.

XX Modulating the biological function of an endothelial cell or
 PT haematopoietic cell e.g., a T-cell or B-cell comprises introducing into
 PT the cell, an agent that inhibits binding of a PDZ protein and a PDZ
 PT ligand protein in the cell -

XX Disclosure; Page 132; 207pp; English.

XX

CC The present invention describes a method (M1) for modulating a biological
 CC function of an endothelial cell or haematopoietic cell. M1 comprises
 CC introducing into the cell, an agent that inhibits binding of a PDZ
 CC (PDS95, Drosophila large disc protein, and Zonula Occludin 1 protein)
 CC protein and a PDZ ligand (PL) protein, in the cell, and so modulates the
 CC biological function. Also described is a method (M2) for determining
 CC whether a test compound is an inhibitor of binding between a PDZ protein
 CC and a PL protein. M1 is used for modulating a biological function of an
 CC endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an
 CC inflammatory or humoral immune response, or an autoimmune disease. An
 CC inhibitor (I) is useful for treating a disease characterised by leukocyte
 CC activation, where the disease is characterised by an inflammatory or
 CC humoral immune response, e.g., an autoimmune disease. The compounds
 CC e.g., PL-PDZ interaction inhibitors are useful for treating (ameliorating
 CC symptoms of) a variety of diseases and conditions characterised by
 CC inflammatory and humoral immune responses e.g., inflammation, allergy,
 CC inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis,
 CC psoriasis and inflammatory dermatoses, scleroderma, respiratory allergic
 CC diseases such as asthma, allergic rhinitis, transplantation rejection
 CC (cardiac, kidney, lung, liver, small bowel, cornea, pancreas, cadaver,
 CC autologous, bone marrow, xenotransplantation), atherosclerosis, cancers,
 CC angiogenesis-dependent disorders, infectious diseases and ischaemia.
 CC ABQ96620 to ABQ96732 and ABP63153 to ABP63578 represent sequences used
 CC in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 22.2%; Score 4; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
 ||||
 DB 2 LKSL 5

RESULT 34
 ABJ01256
 ID ABJ01256 standard; Peptide; 6 AA.

XX AC ABJ01256;

XX DT 18-SEP-2002 (first entry)

XX DE Human caspase conserved region SEQ ID NO: 72.

XX KW Human; caspase; rev-caspase; gene therapy; protease; apoptosis;
 XX cancer; autoimmune disease; cytostatic; immunosuppressive.

XX OS Homo sapiens.

XX FN US6376226-B1.

XX PD 23-APR-2002.

XX PF 26-APR-2000; 2000US-0561756.

XX PR 09-JAN-1998; 98US-070897P.

XX PR 08-JAN-1999; 99US-0227721.

XX PA (UYJE-) UNIV JEFFERSON THOMAS.

XX PI Alnemri ES;

XX DR WPI; 2002-451275/48.

XX PT New rev-caspases engineered to contain the small subunit fused in frame
 XX N-terminal to the large subunit, which is in reverse order to the wild
 XX type caspases, are useful to treat cancer and autoimmune diseases -
 XX Disclosure; Fig 6; 81pp; English.

XX The present invention provides the protein and coding sequences of human

CC rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences
 CC can be used in the gene therapy of cancer and autoimmune diseases. The
 CC present sequence is a peptide described in the exemplification of the
 CC invention.

SQ Sequence 6 AA;

Query Match 22.2%; Score 4; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13
 ||||
 DB 3 HGEE 6

RESULT 35
 ABJ01267
 ID ABJ01267 standard; Peptide; 6 AA.

XX AC ABJ01267;

XX DT 18-SEP-2002 (first entry)

XX DE Human caspase conserved region SEQ ID NO: 83.

XX KW Human; caspase; rev-caspase; gene therapy; protease; apoptosis;
 XX cancer; autoimmune disease; cytostatic; immunosuppressive.

XX OS Homo sapiens.

XX FN US6376226-B1.

XX PD 23-APR-2002.

XX PF 26-APR-2000; 2000US-0561756.

XX PR 09-JAN-1998; 98US-070897P.

XX PR 08-JAN-1999; 99US-0227721.

XX PA (UYJE-) UNIV JEFFERSON THOMAS.

XX PI Alnemri ES;

XX DR WPI; 2002-451275/48.

XX PT New rev-caspases engineered to contain the small subunit fused in frame
 XX N-terminal to the large subunit, which is in reverse order to the wild
 XX type caspases, are useful to treat cancer and autoimmune diseases -
 XX Disclosure; Fig 6; 81pp; English.

XX The present invention provides the protein and coding sequences of human
 XX rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences
 XX can be used in the gene therapy of cancer and autoimmune diseases. The
 XX present sequence is a peptide described in the exemplification of the
 XX invention.

SQ Sequence 6 AA;

Query Match 22.2%; Score 4; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13
 ||||
 DB 3 HGEE 6

RESULT 36
 ABJ01272

ID ABJ01272 standard; Peptide; 6 AA.

XX

```

AC ABJ01272;
XX
XX 18-SEP-2002 (first entry)
XX
XX DE Human caspase conserved region SEQ ID NO: 88.
XX
XX KW Human; caspase; rev-caspase; gene therapy; protease; apoptosis;
XX KW cancer; autoimmune disease; cytostatic; immunosuppressive.
XX
XX OS Homo sapiens.
XX
XX PN US6376226-B1.
XX
XX PD 23-APR-2002.
XX
XX PF 26-APR-2000; 2000US-0561756.
XX
XX PR 09-JAN-1998; 98US-070897P.
XX PR 08-JAN-1999; 99US-0227721.
XX
XX PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX PI Alnemri ES;
XX
XX DR WPI; 2002-451275/48.
XX
XX PT New rev-caspases engineered to contain the small subunit fused in frame
XX PT N-terminal to the large subunit, which is in reverse order to the wild
XX PT type caspases, are useful to treat cancer and autoimmune diseases -
XX
XX PS Disclosure; Fig 6; 81pp; English.
XX
XX CC The present invention provides the protein and coding sequences of human
XX CC rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences
XX CC can be used in the gene therapy of cancer and autoimmune diseases. The
XX CC present sequence is a peptide described in the exemplification of the
XX CC invention.
XX
XX SQ Sequence 6 AA;
XX
XX Query Match 22.2%; Score 4; DB 23; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 10 HGEE 13
XX |||||
XX 3 HGEE 6
XX
XX DB
XX
XX RESULT 37
XX AAO17301
XX ID AAO17301 standard; Peptide; 6 AA.
XX
XX AC AAO17301;
XX
XX DT 08-JUL-2002 (first entry)
XX
XX DE A thaliana receptor kinase RKS11 peptide fragment.
XX
XX KW Vegetative propagation; plant; phytochrome; receptor kinase-like SERK;
XX KW RKS.
XX
XX OS Arabidopsis thaliana.
XX
XX PN EP1094113-A1.
XX
XX PD 25-APR-2001.
XX
XX PF 22-OCT-1999; 99EP-0203480.
XX
XX PR 22-OCT-1999; 99EP-0203480.
XX
XX PA (GENE-) GENETWISTER TECHNOLOGIES BV.
XX
XX Schmidt EDL, Van Der Kop DAM, De Boer AD;
XX WPI; 2002-228902/29.
XX
XX PT In vitro culture propagation of a plant from plant starting material,
XX PT comprises stimulating root/shoot initiation by introducing a
XX PT recombinant gene product into the starting material, thus reducing
XX PT phytochrome addition to culture -
XX
XX PS Disclosure; Page 100; 171pp; English.
XX
XX CC The present invention relates to a culture method for propagating a plant
XX CC from a plant starting material, where root or shoot initiation is
XX CC stimulated by introducing a gene into the starting material which allows
XX CC the reduction or absence of phytochrome addition to the culture. The
XX CC method is used for the propagation (preferably, seedless propagation) of
XX CC a plant from a plant starting material in an in vitro culture method.
XX CC Nucleic acids encoding receptor-like kinases are useful in the method.
XX CC The present sequence is a fragment of a receptor-like kinase protein.
XX
XX SQ Sequence 6 AA;
XX
XX Query Match 22.2%; Score 4; DB 23; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 11 GEEI 14
XX |||||
XX 2 GEEI 5
XX
XX DB
XX
XX RESULT 38
XX AAU28695
XX ID AAU28695 standard; Peptide; 7 AA.
XX
XX AC AAU28695;
XX
XX DT 03-JAN-2002 (first entry)
XX
XX DE DPI tryptic digest peptide #292.
XX
XX KW Human; depression associated protein isoform; tryptic digest peptide;
XX KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
XX KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
XX KW maniac-depressive illness; schizoaffective disorder.
XX
XX OS Homo sapiens.
XX
XX PN WO200162787-A1.
XX
XX PD 30-AUG-2001.
XX
XX PF 23-FEB-2001; 2001WO-GB00786.
XX
XX PR 24-FEB-2000; 2000GB-0004412.
XX PR 08-DEC-2000; 2000GB-0030050.
XX PR 12-DEC-2000; 2000US-0254830.
XX
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX PI Herath HMCAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
XX
XX DR WPI; 2001-570626/64.
XX
XX PT Novel nucleic acid encoding a protein associated with bipolar affective
XX PT disorder, which is used for diagnosis, prophylaxis and therapy of
XX PT neuropsychiatric disorders, such as bipolar affective disorder -
XX
XX PS Disclosure; Page 37; 153pp; English.
XX
XX CC The present invention relates to the identification of depression
XX CC associated protein isoforms (DPis), particularly the tryptic digest

```

CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)
 CC described are decreased in the cerebrospinal fluid (CSF) of BAD
 CC (bipolar affective disorder) subjects, whilst other DPIs
 CC (AAU28626-AAU28887) are increased in BAD subjects. Also described
 CC are peptide sequences identified from DPI-45 and DPI-213 and the
 CC nucleic acid sequences they are encoded by. The sequences of the
 CC invention are useful for clinical screening, diagnosis, prognosis,
 CC therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also
 CC known as bipolar mood disorder, BP), manic-depressive illnesses,
 CC attention deficit disorders, schizoaffective disorders, and unipolar
 CC affective disorders. The present sequence represents one of the DPI
 CC tryptic digest peptides of the present invention.

SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 BEIL 15
 Db |||||
 2 BEIL 5

RESULT 39
 AAU25065
 ID AAU25065 standard; Peptide; 7 AA.
 AC AAU25065;
 XX 18-DEC-2001 (first entry)
 DT
 DE Schizophrenia-Associated Protein Isoform (SPI) peptide #294.
 DE
 XX Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;
 KW neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
 KW
 XX Homo sapiens.
 OS
 XX WO200162785-A2.
 FN 30-AUG-2001.
 PD
 XX 23-FEB-2001; 2001WO-GB00792.
 PF
 XX 24-FEB-2000; 2000GB-0004415.
 PR
 XX 28-NOV-2000; 2000US-0750395.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA
 XX Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
 PI WPI; 2001-570624/64.
 XX
 DR New schizophrenia associated protein isoforms and encoding nucleic acid
 XX molecules, useful for treatment, diagnosis and prognosis of
 PT schizophrenia and screening for potential drugs for treatment and new
 PT drug targets -
 XX
 PS Disclosure; Page 35; 148pp; English.
 XX
 CC The sequence represents a schizophrenia-associated protein isoform (SPI).
 CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
 CC in cerebrospinal fluid, serum or plasma and are useful markers of
 CC schizophrenia. The sequences can be used for treatment and diagnosis of
 CC schizophrenia, screening, prognosis, monitoring the results of therapy,
 CC identifying patients most likely to respond to a particular therapy and
 CC identification of new targets for drug treatment. SPI DNA is useful as a
 CC nucleic acid probe to detect the presence of nucleic acids or SPIs.

SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 22; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 BEIL 15
 Db |||||
 2 BEIL 5

RESULT 40
 AAU26343
 ID AAU26343 standard; Peptide; 7 AA.
 XX AAU26343;
 AC AAU26343;
 XX 18-DEC-2001 (first entry)
 DT
 DE Depression-Associated Protein isoform DPI-174 #1.
 DE
 XX Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;
 KW DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;
 KW CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;
 KW attention deficient disorder; schizoaffective disorder;
 KW unipolar affective disorder.
 XX
 OS Homo sapiens.
 XX WO200163294-A2.
 FN 30-AUG-2001.
 PD
 XX 23-FEB-2001; 2001WO-GB00791.
 PF
 XX 24-FEB-2000; 2000GB-0004412.
 PR
 XX 08-DEC-2000; 2000GB-0030050.
 PR
 XX 12-DEC-2000; 2000US-0254830.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA
 XX Herath HMAC, Parekh RB, Rohlf C;
 PI WPI; 2001-582081/65.
 DR
 XX Preparation for diagnosing or treating bipolar affected disorder (BAD)
 PT or unipolar depression, or for screening for modulators, comprises a
 PT BAD-associated protein isoform -
 XX Claim 8; Page 37; 163pp; English.
 PS
 XX The invention relates to a preparation comprising an isolated Bipolar
 CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are
 CC used to screen, diagnose or prognose of BAD or unipolar depression,
 CC determine the stage or severity of BAD or unipolar depression, identify a
 CC subject at risk of developing BAD or unipolar depression, or monitor the
 CC effect of therapy in a subject. They are also used to screen for or
 CC identify agents that interact with a DPI. These agents, antibodies
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat
 CC or prevent BAD or unipolar depression. Diseases that can be treated are
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a
 CC unipolar affective disorder. The DPIs are used in proteomics. The
 CC proteomic approach of using DPIs for screening, diagnosis or prognosis of
 CC BAD or unipolar depression overcomes the problems of using gene
 CC expression analysis, such as not being able to obtain central nervous
 CC system (CNS) tissue from a living patient under normal circumstances.
 CC The present sequence is a DIP increased in the CSF (cerebro-spinal
 CC fluid) of subjects having BAD.

SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 BEIL 15

Db

|||||
2 EEIL 5

RESULT 41
AAM44583
ID AAM44583 standard; Peptide; 7 AA.
XX
AC AAM44583;
XX
25-OCT-2001 (first entry)
XX
H11 binding site consensus conforming peptide (CCP) #854.
XX
Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
CA2290722-A1.
XX
08-JUN-2001.
XX
08-DEC-1999; 99CA-2290722.
XX
08-DEC-1999; 99CA-2290722.
XX
(NOVO-) NOVOPHARM BIOTECH INC.
XX
Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
PI WPI; 2001-425937/46.
XX
Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX
Example 4; Page 104; 154pp; English.
XX
The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPFCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPFCs
CC or a population of different SPFCs consisting of immunogenic cancer cell
CC surface-associated SPFC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention.
XX
SQ Sequence 7 AA;
Query Match 22.2%; Score 4; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 RYQD 8
Db |||||
3 RYQD 6

RESULT 42
AAM44588
ID AAM44588 standard; Peptide; 7 AA.
XX
AC AAM44588;
XX
25-OCT-2001 (first entry)
XX
H11 binding site consensus conforming peptide (CCP) #859.
XX
Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
CA2290722-A1.
XX
08-JUN-2001.
XX
08-DEC-1999; 99CA-2290722.
XX
08-DEC-1999; 99CA-2290722.
XX
(NOVO-) NOVOPHARM BIOTECH INC.
XX
Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
PI WPI; 2001-425937/46.
XX
Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX
Example 4; Page 104; 154pp; English.
XX
The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPFCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPFCs
CC or a population of different SPFCs consisting of immunogenic cancer cell
CC surface-associated SPFC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention.
XX
SQ Sequence 7 AA;
Query Match 22.2%; Score 4; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 RYQD 8
Db |||||
3 RYQD 6

RESULT 43
AAU15409
ID AAU15409 standard; Peptide; 7 AA.
XX

AC AAU15409;
XX
DT 24-OCT-2001 (first entry)
XX
DE Schizophrenia-associated isoform peptide #294.
XX
KW Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
KW neurological disorder; neuropathy.
XX
OS Homo sapiens.
XX
PN WO200163293-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-GB00783.
XX
PR 24-FEB-2000; 2000GB-0004415.
PR 28-NOV-2000; 2000US-0750395.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMC, Parekh RB, Rohlf C;
XX
DR WPI; 2001-502868/55.
XX
PT Diagnosing and monitoring Schizophrenia by detecting the presence of
PT Schizophrenia Associated Features and Schizophrenia Associated Protein
PT isoforms in samples of cerebrospinal fluid -
XX
PS Claim 6; Page 35; 160pp; English.
XX
CC The invention relates to methods and compositions for screening,
CC diagnosis and prognosis of Schizophrenia. The method involves detecting
CC the presence of Schizophrenia (SCH) Associated Features (SfFs) and SCH
CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,
CC immunoassay or hybridisation assay, for diagnosing and monitoring SCH,
CC studying the effectiveness of treatments and for identifying potential
CC therapeutic agents. The method is used for (1) screening or diagnosis of
CC SCH and the relative abundance of at least 1 chosen feature correlates
CC with the presence or absence of SCH; and (2) monitoring the effect of
CC therapy administered to a subject with SCH and the relative abundance of
CC at least 1 chosen feature which correlates with the severity of SCH.
CC The expression and activity of the SPIs, SPIs and related molecules
CC (e.g. secondary messengers) are studied to diagnose SCH, monitor the
CC progress of the disorder and the effectiveness of treatment and as
CC targets to identify and produce potential therapeutic agents for the
CC treatment of SCH. The paucity of detectable neurologic defects
CC distinguishes neuropsychiatric disorders such as SCH from neurological
CC disorders, where manifestations of anatomical and biochemical changes
CC have been identified in many cases. Consequently the identification and
CC characterisation of cellular and/or molecular causative defects and
CC neuropathies are necessary for improved treatment of neuropsychiatric
CC disorders. AAU15114-AAU15762 represent the amino acid sequences of
CC schizophrenia-associated isoforms used in the method of the invention.
XX
SQ Sequence 7 AA;
Query Match 22.2%; Score 4; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 BEIL 15
Db 2 BEIL 5
RESULT 44
AAB55643
ID AAB55643 standard; Peptide; 7 AA.
XX
AC AAB55643;
XX

DT 07-MAR-2001 (first entry)
XX
DE Monocyte surface receptor PDZ domain sequence #14.
XX
KW Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;
KW allergy; asthma; multiple sclerosis; cancer; infection.
XX
OS Synthetic.
XX
PN WO200069896-A2.
XX
PD 23-NOV-2000.
XX
PF 12-MAY-2000; 2000WO-US13161.
XX
PR 14-MAY-1999; 99US-0134114.
PR 14-MAY-1999; 99US-0134117.
PR 14-MAY-1999; 99US-0134118.
PR 21-OCT-1999; 99US-0160860.
PR 29-OCT-1999; 99US-0162498.
PR 13-DEC-1999; 99US-0170453.
PR 14-JAN-2000; 2000US-0176195.
PR 14-FEB-2000; 2000US-0182296.
PR 11-APR-2000; 2000US-0196460.
PR 11-APR-2000; 2000US-0196527.
XX
PA (ARBO-) ARBOR VITA CORP.
XX
PI Lu PS;
XX
DR WPI; 2001-080245/09.
XX
PT Modulating a biological function of an endothelial cell or
PT hematopoietic cell, useful for treating autoimmune diseases and
PT infectious diseases, by administering an antagonist that inhibits
PT binding between a PDZ protein and a PL protein -
XX
PS Disclosure; Page 87-94; 141pp; English.
XX
CC The present invention relates to a new method for modulating a
CC biological function of an endothelial cell or hematopoietic cell. The
CC method involves introducing into a cell, an antagonist that inhibits
CC binding between a PDZ protein and a PL protein. The inhibitor is used
CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune
CC disease. It may also be used to prevent transplantation rejection of
CC a solid organ transplant. The method may also be used in the treatment
CC of inflammation, allergy, inflammatory bowel diseases, ulcerative
CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,
CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,
CC graft rejection, transplantation rejection), atherosclerosis, cancers,
CC infectious diseases, ischemia, vasculitis and Crohn's disease.
XX
SQ Sequence 7 AA;
Query Match 22.2%; Score 4; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 LKSL 18
Db 3 LKSL 6
RESULT 45
AAB57490
ID AAB57490 standard; Peptide; 7 AA.
XX
AC AAB57490;
XX
DT 12-MAR-2001 (first entry)
XX
DE CD61 C-terminal core sequence #4.

XX Endothelial cell; haematopoietic cell; PDZ domain protein;
 KW PL domain protein; leukocyte activation; T cell surface receptor;
 KW synapse formation; transmembrane neurotransmitter receptor;
 KW autoimmune disease; transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
 KW ischaemia; vasculitis; Crohn's disease.
 XX
 OS Homo sapiens.
 XX
 XX
 PN WO200069897-A2.
 XX
 XX 23-NOV-2000.
 XX
 PF 12-MAY-2000; 2000WO-US13166.
 XX
 PR 14-MAY-1999; 99US-0134114.
 PR 14-MAY-1999; 99US-0134117.
 PR 14-MAY-1999; 99US-0134118.
 PR 21-OCT-1999; 99US-0160860.
 PR 29-OCT-1999; 99US-0162498.
 PR 13-DEC-1999; 99US-0170453.
 PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.
 XX
 XX (ARBO-) ARBOR VITA CORP.
 PA
 Lu PS;
 XX
 XX WPI; 2001-025003/03.
 XX
 PT New inhibitors of binding of a PDZ protein and PL protein for
 PT inhibiting T cell-mediated response by hematopoietic cells, or for
 PT treating diseases characterized by inflammatory and humoral immune
 PT responses, e.g. inflammation, cancer -
 XX
 PS Disclosure; Page 90; 139pp; English.
 XX
 CC The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or haematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a
 CC PDZ domain protein and a PL domain protein to result in inhibition of
 CC leukocyte activation. The present sequence is a core sequence of a PL
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are
 CC named after three prototypical proteins: PSD95, Drosophila large disc
 CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved
 CC in synapse formation by organising transmembrane neurotransmitter
 CC receptors through intracellular interactions. The inhibitors identified
 CC by the present invention can be used to treat a disease mediated by
 CC haematopoietic cells, e.g. autoimmune disease, inflammation, allergy
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The
 CC inhibitors can also be used to prevent transplantation rejection of a
 CC solid organ transplant.
 XX
 SQ Sequence 7 AA;
 Query Match 22.2%; Score 4; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 15 LKSL 18
 Db 3 LKSL 6

RESULT 46
 AAB57900
 ID AAB57900 standard; Peptide; 7 AA.
 XX
 AC AAB57900;
 XX
 DT 12-MAR-2001 (first entry)
 XX
 DE CD61 C-terminal core sequence #4.
 XX
 XX
 KW Endothelial cell; haematopoietic cell; PDZ domain protein;
 KW PL domain protein; leukocyte activation; T cell surface receptor;
 KW synapse formation; transmembrane neurotransmitter receptor;
 KW autoimmune disease; transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
 KW ischaemia; vasculitis; Crohn's disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200069898-A2.
 XX
 XX 23-NOV-2000.
 XX
 PF 12-MAY-2000; 2000WO-US13205.
 XX
 PR 14-MAY-1999; 99US-0134114.
 PR 14-MAY-1999; 99US-0134117.
 PR 14-MAY-1999; 99US-0134118.
 PR 21-OCT-1999; 99US-0160860.
 PR 29-OCT-1999; 99US-0162498.
 PR 13-DEC-1999; 99US-0170453.
 PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.
 XX
 XX (ARBO-) ARBOR VITA CORP.
 PA
 Lu PS;
 XX
 XX WPI; 2001-061214/07.
 XX
 CC Modulating a biological function of a hematopoietic cell for treating
 CC an allergic response, or diseases mediated by immune system cells,
 CC comprises introducing into the cell a PDZ-PL interaction enhancer or
 CC inhibitor -
 XX
 PS Disclosure; Page 93; 143pp; English.
 XX
 CC The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or haematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a
 CC PDZ domain protein and a PL domain protein to result in inhibition of
 CC leukocyte activation. The present sequence is a core sequence of a PL
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are
 CC named after three prototypical proteins: PSD95, Drosophila large disc
 CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved
 CC in synapse formation by organising transmembrane neurotransmitter
 CC receptors through intracellular interactions. The inhibitors identified
 CC by the present invention can be used to treat a disease mediated by
 CC haematopoietic cells, e.g. autoimmune disease, inflammation, allergy
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The
 CC inhibitors can also be used to prevent transplantation rejection of a
 CC solid organ transplant.
 XX
 SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
 |||||
 Db 3 LKSL 6

RESULT 47
 ABJ05122
 ID ABJ05122 standard; Peptide; 7 AA.
 XX
 AC ABJ05122;
 XX
 DT 07-NOV-2002 (first entry)
 XX
 DE T-cell surface receptor C-terminal core peptide SEQ ID No 117.
 XX
 KW Immunosuppressive; antiinflammatory; affinity; Kd; binding; PDZ domain;
 KW ligand; Ki; inhibitor; K-enhancer; leukocyte; autoimmune disease;
 KW inflammatory; humoral immune response; inflammation; C-terminal core;
 KW T-cell surface receptor.
 XX
 OS Unidentified.
 XX
 PN WO200231512-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 11-OCT-2001; 2001WO-US32150.
 XX
 PR 13-OCT-2000; 2000US-0688017.
 XX
 PA (ARBO-) ARBOR VITA CORP.
 XX
 PI Rabinowitz JD, Lu PS, Schweizer J;
 XX
 DR WPI; 2002-416878/44.
 XX
 PT Assays for determining the affinity of binding between a PDZ domain and
 PT a ligand, and determining the Ki of an inhibitor of the binding.
 PT comprises using a polypeptide comprising a PDZ domain and a non-PDZ
 PT domain -
 XX
 PS Disclosure; Page 114; 164pp; English.
 XX
 CC The invention relates to methods and reagents for determining the
 CC apparent affinity (Kd) of binding between a PDZ domain and a ligand. The
 CC invention also relates to methods and reagents for determining the Ki of
 CC an inhibitor of binding between a PDZ domain and a ligand, identifying an
 CC agent that enhances binding of a PDZ domain and a ligand, and determining
 CC the potency (K-enhancer) of binding between a PDZ domain and a ligand, by
 CC determining the ligand bound with an immobilised polypeptide comprising a
 CC PDZ domain and a non-PDZ domain on a surface. The modulator (preferably,
 CC an inhibitor) of interaction between PDZ and PL is useful for treating a
 CC disease characterised by leukocyte activation, e.g., an autoimmune
 CC disease that is characterised by inflammatory or humoral immune response,
 CC and for reducing inflammation in a subject. This sequence represents a T-
 CC cell surface receptor C-terminal core peptide relating to the PDZ
 CC containing proteins of the invention.
 XX
 SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
 |||||
 Db 3 LKSL 6

RESULT 48
 ABP63415
 ID ABP63415 standard; Peptide; 7 AA.
 XX
 AC ABP63415;
 XX
 DT 28-OCT-2002 (first entry)
 XX
 DE Monocyte surface receptor PDZ motif (PL) peptide SEQ ID NO:117.
 XX
 KW Molecular interaction; haematopoietic cell; immune response; T cell;
 KW PDZ domain; B cell; endothelial cell; PDZ protein; PSD95; PDZ ligand;
 KW Drosophila large disc protein; Zonula Occludin 1 protein; PL protein;
 KW immunosuppressive; antiinflammatory; antiallergic; antiatherosclerotic;
 KW antiulcer; antipsoriatic; dermatological; antiasthmatic; cyostatic;
 KW antimicrobial; vasotropic; inflammatory immune response; inflammation;
 KW humoral immune response; autoimmune disease; allergy; ulcerative colitis;
 KW inflammatory bowel disease; ileitis; enteritis; psoriasis; scleroderma;
 KW inflammatory dermatosis; respiratory allergic disease; asthma; cancer;
 KW allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia;
 KW angiogenesis-dependent disorder; infectious disease.
 XX
 OS Homo sapiens.
 XX
 OS Synthetic.
 XX
 PN WO200242422-A2.
 XX
 PD 30-MAY-2002.
 XX
 PF 09-NOV-2001; 2001WO-US44138.
 XX
 PR 11-NOV-2000; 2000US-0710059.
 PR 24-NOV-2000; 2000US-0721915.
 PR 24-NOV-2000; 2000US-0722069.
 PR 28-NOV-2000; 2000US-0724553.
 XX
 PA (ARBO-) ARBOR VITA CORP.
 XX
 PI Lu P, Rabinowitz JD, Schweizer J;
 XX
 DR WPI; 2002-608221/65.
 XX
 CC Modulating the biological function of an endothelial cell or
 CC haematopoietic cell e.g., a T-cell or B-cell comprises introducing into
 CC the cell, an agent that inhibits binding of a PDZ protein and a PDZ
 CC ligand protein in the cell -
 XX
 PS Disclosure; Page 132; 207pp; English.
 XX
 CC The present invention describes a method (M1) for modulating a biological
 CC function of an endothelial cell or haematopoietic cell. M1 comprises
 CC introducing into the cell, an agent that inhibits binding of a PDZ
 CC (PSD95, Drosophila large disc protein, and Zonula Occludin 1 protein)
 CC protein and a PDZ ligand (PL) protein in the cell, and so modulates the
 CC biological function. Also described is a method (M2) for determining
 CC whether a test compound is an inhibitor of binding between a PDZ protein
 CC and a PL protein. M1 is used for modulating a biological function of an
 CC endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an
 CC inflammatory or humoral immune response, or an autoimmune disease. An
 CC inhibitor (I) is useful for treating a disease characterised by leukocyte
 CC activation, where the disease is characterised by an inflammatory or
 CC humoral immune response, e.g., an autoimmune disease. The compounds
 CC e.g., PL-PDZ interaction inhibitors are useful for treating (ameliorating
 CC symptoms of) a variety of diseases and conditions characterised by
 CC inflammatory and humoral immune responses e.g., inflammation, allergy,
 CC inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis,
 CC psoriasis and inflammatory dermatoses, scleroderma, respiratory allergic
 CC diseases such as asthma, allergic rhinitis, transplantation rejection
 CC (cardiac, kidney, liver, small bowel, cornea, pancreas, cadaver,
 CC autologous, bone marrow, xenotransplantation), atherosclerosis, cancers,
 CC angiogenesis-dependent disorders, infectious diseases and ischaemia.
 CC ABQ96620 to ABQ96732 and ABP63153 to ABP63578 represent sequences used
 CC in the exemplification of the present invention.


```

XX SQ Sequence 7 AA;
Query Match 22.2%; Score 4; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
Db 3 LKSL 6

RESULT 49
ABP11644
ID ABP11644 standard; Peptide; 8 AA.
XX AC ABP11644;
XX AC ABP11644;
XX DT 15-JUL-2002 (first entry)
XX HIV A01 super motif gag peptide #16.
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; virucide.
XX Human immunodeficiency virus type 1.
XX WO200124810-A1.
XX 12-APR-2001.
XX 05-OCT-2000; 2000WO-US27766.
XX 05-OCT-1999; 99US-0412863.
XX (EPIM-) EPIMMUNE INC.
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Cellis E, Kubo RT, Grey HM;
XX WPI; 2001-354887/37.
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1 -
XX Claim 32; Page 107; 448pp; English.
XX The present invention describes a composition (I) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (ABP25347 to
XX ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX may be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumour-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines.
XX An additional advantage of an group-based vaccine approach is the ability
XX to combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP11501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention.
XX SQ Sequence 8 AA;
Query Match 22.2%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Query Match 22.2%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
Db 4 LKSL 7

RESULT 50
ABP12644
ID ABP12644 standard; Peptide; 8 AA.
XX AC ABP12644;
XX AC ABP12644;
XX DT 15-JUL-2002 (first entry)
XX HIV A02 super motif gag peptide #115.
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; virucide.
XX Human immunodeficiency virus type 1.
XX WO200124810-A1.
XX 12-APR-2001.
XX 05-OCT-2000; 2000WO-US27766.
XX 05-OCT-1999; 99US-0412863.
XX (EPIM-) EPIMMUNE INC.
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Cellis E, Kubo RT, Grey HM;
XX WPI; 2001-354887/37.
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1 -
XX Claim 32; Page 128; 448pp; English.
XX The present invention describes a composition (I) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (ABP25347 to
XX ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX may be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumour-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines.
XX An additional advantage of an group-based vaccine approach is the ability
XX to combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP11501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention.
XX SQ Sequence 8 AA;
Query Match 22.2%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      15 LKSL 18
Db      ||||
        5 LKSL 8

RESULT 51
ABP12645
ID ABP12645 standard; Peptide; 8 AA.
XX
XX AC
XX ABP12645;
XX
XX DT
XX 15-JUL-2002 (first entry)
XX
XX DE
XX HIV A02 super motif gag peptide #116.
XX
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; virucide.
XX
XX OS Human immunodeficiency virus type 1.
XX
XX PN WO200124810-A1.
XX
XX PD 12-APR-2001.
XX
XX PF 05-OCT-2000; 2000WO-US27766.
XX
XX PR 05-OCT-1999; 99US-0412863.
XX
XX PA (EPIM-) EPIMUNE INC.
XX
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX DR WPI; 2001-354887/37.
XX
XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV-1 -
XX
XX PS Claim 32; Page 128; 448pp; English.
XX
XX CC The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (ABL25347 to
XX CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines,
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group-based vaccine approach is the ability
XX CC to combine selected groups (CTL and HTL), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be modulated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. ABP11501 to ABP25412
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX
XX SQ Sequence 8 AA;

Query Match 22.2%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 LKSL 18
Db      ||||
        5 LKSL 8

RESULT 52
ABP15564
ID ABP15564 standard; Peptide; 8 AA.
XX
XX AC ABP15564;
XX
XX DT 15-JUL-2002 (first entry)
XX
XX DE HIV A24 super motif gag peptide #50.
XX
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; virucide.
XX
XX OS Human immunodeficiency virus type 1.
XX
XX PN WO200124810-A1.
XX
XX PD 12-APR-2001.
XX
XX PF 05-OCT-2000; 2000WO-US27766.
XX
XX PR 05-OCT-1999; 99US-0412863.
XX
XX PA (EPIM-) EPIMUNE INC.
XX
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX DR WPI; 2001-354887/37.
XX
XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV-1 -
XX
XX PS Claim 32; Page 187; 448pp; English.
XX
XX CC The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (ABL25347 to
XX CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines,
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group-based vaccine approach is the ability
XX CC to combine selected groups (CTL and HTL), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be modulated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. ABP11501 to ABP25412
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX
XX SQ Sequence 8 AA;

Query Match 22.2%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


DT 15-JUL-2002 (first entry)
 XX HIV B58 super motif gag peptide #49.
 DE
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US27766.
 XX
 PR 05-OCT-1999; 99US-0412863.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-354887/37.
 DR
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 XX
 PS Claim 32; Page 234; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 8 AA;
 Query Match 22.2%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 LKSL 18
 Db 5 LKSL 8
 RESULT 56
 ABP17849
 ID ABP17849 standard; Peptide; 8 AA.
 XX
 AC ABP17849;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV B58 super motif gag peptide #68.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US27766.
 XX
 PR 05-OCT-1999; 99US-0412863.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-354887/37.
 DR
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 XX
 PS Claim 32; Page 234; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 8 AA;
 Query Match 22.2%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 LKSL 18
 Db 4 LKSL 7
 RESULT 57
 ABP17869
 ID ABP17869 standard; Peptide; 8 AA.
 XX
 AC ABP17869;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV B58 super motif gag peptide #88.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;

KW antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1.

XX WO200124810-A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27766.

XX 05-OCT-1999; 99US-0412863.

XX (EPIM-) EPIMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -

XX Claim 32; Page 235; 448pp; English.

CC The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABP25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention.

XX Sequence 8 AA;

Query Match 22.2%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18

Db 4 LKSL 7

RESULT 58

ABP20480
ID ABP20480 standard; Peptide; 8 AA.

XX AC ABP20480;

XX 15-JUL-2002 (first entry)

DE HIV A03 motif gag peptide #143.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.

OS Human immunodeficiency virus type 1.

XX WO200124810-A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27766.

XX 05-OCT-1999; 99US-0412863.

XX (EPIM-) EPIMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM,

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -

XX Claim 32; Page 289; 448pp; English.

CC The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABP25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention.

XX Sequence 8 AA;

Query Match 22.2%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18

Db 4 LKSL 7

RESULT 59

ABP20520
ID ABP20520 standard; Peptide; 8 AA.

XX AC ABP20520;

XX 15-JUL-2002 (first entry)

XX HIV A03 motif gag peptide #183.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.

OS Human immunodeficiency virus type 1.

XX WO200124810-A1.

XX

```

PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
XX (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 290; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC an group-based vaccine escape may be selected from conserved regions of
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 8 AA;
Query Match 22.2%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 LKSL 18
Db 4 LKSL 7
|||||
RESULT 60
ABP23517
ID ABP23517 standard; Peptide; 8 AA.
XX
AC ABP23517;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A11 motif pol peptide #459.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
XX WO200124810-A1.
PN
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.

```

```

XX 05-OCT-1999; 99US-0412863.
XX (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX WPI; 2001-354887/37.
XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 350; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC an group-based vaccine escape may be selected from conserved regions of
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 8 AA;
Query Match 22.2%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 ILK 16
Db 1 ILK 4
|||||
RESULT 61
AAB55644
ID AAB55644 standard; Peptide; 8 AA.
XX
AC AAB55644;
XX
DT 07-MAR-2001 (first entry)
XX
DE Monocyte surface receptor PDZ domain sequence #15.
XX
KW Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;
KW allergy; asthma; multiple sclerosis; cancer; infection.
XX
OS Synthetic.
XX
XX WO200069896-A2.
PN
PD 23-NOV-2000.
XX
XX 12-MAY-2000; 2000WO-US13161.
PF
PR 14-MAY-1999; 99US-0134114.
PR 14-MAY-1999; 99US-0134117.
PR 14-MAY-1999; 99US-0134118.

```

PR 21-OCT-1999; 99US-0160860.
 PR 29-OCT-1999; 99US-0162498.
 PR 13-DEC-1999; 99US-0170453.
 PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.
 XX
 PA (ARBO-) ARBOR VITA CORP.
 XX
 PI Lu PS;
 XX
 DR WPI; 2001-080245/09.
 XX
 PT Modulating a biological function of an endothelial cell or
 PT hematopoietic cell, useful for treating autoimmune diseases and
 PT infectious diseases, by administering an antagonist that inhibits
 PT binding between a PDZ protein and a PL protein -
 XX
 PS Disclosure; Page 87-94; 14pp; English.
 XX
 CC The present invention relates to a new method for modulating a
 CC biological function of an endothelial cell or hematopoietic cell. The
 CC method involves introducing into a cell, an antagonist that inhibits
 CC binding between a PDZ protein and a PL protein. The inhibitor is used
 CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune
 CC disease. It may also be used to prevent transplantation rejection of
 CC a solid organ transplant. The method may also be used in the treatment
 CC of inflammation, allergy, inflammatory bowel diseases, ulcerative
 CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,
 CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,
 CC graft rejection, transplantation rejection), atherosclerosis, cancers,
 CC infectious diseases, ischemia, vasculitis and Crohn's disease.
 XX
 SQ Sequence 8 AA;
 Query Match 22.2%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 LKSL 18
 ||||
 Db 4 LKSL 7
 RESULT 62
 AAB57491
 ID AAB57491 standard; Peptide; 8 AA.
 XX
 AC AAB57491;
 XX
 DT 12-MAR-2001 (first entry)
 XX
 DE CD61 C-terminal core sequence #5.
 XX
 KW Endothelial cell; haematopoietic cell; PDZ domain protein;
 KW PL domain protein; leukocyte activation; T cell surface receptor;
 KW synapse formation; leukocyte activation; T cell surface receptor;
 KW autoimmune disease; transmembrane neurotransmitter receptor;
 KW inflammatory disease; transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
 KW ischaemia; vasculitis; Crohn's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200069897-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 12-MAY-2000; 2000WO-US13166.
 XX
 PR 14-MAY-1999; 99US-0134114.

PR 14-MAY-1999; 99US-0134117.
 PR 14-MAY-1999; 99US-0134118.
 PR 21-OCT-1999; 99US-0160860.
 PR 29-OCT-1999; 99US-0162498.
 PR 13-DEC-1999; 99US-0170453.
 PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.
 XX
 PA (ARBO-) ARBOR VITA CORP.
 XX
 PI Lu PS;
 XX
 DR WPI; 2001-025003/03.
 XX
 PT New inhibitors of binding of a PDZ protein and PL protein for
 PT inhibiting T cell-mediated response by hematopoietic cells, or for
 PT treating diseases characterized by inflammatory and humoral immune
 PT responses, e.g. inflammation, cancer -
 XX
 PS Disclosure; Page 90; 139pp; English.
 XX
 CC The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or haematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a
 CC PDZ domain protein and a PL domain protein to result in inhibition of
 CC leukocyte activation. The present sequence is a core sequence of a PL
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are
 CC named after three prototypical proteins: PSD95, Drosophila large disc
 CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved
 CC in synapse formation by organising transmembrane neurotransmitter
 CC receptors through intracellular interactions. The inhibitors identified
 CC by the present invention can be used to treat a disease mediated by
 CC haematopoietic cells, e.g. autoimmune disease, inflammation, allergy
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The
 CC inhibitors can also be used to prevent transplantation rejection of a
 CC solid organ transplant.
 XX
 SQ Sequence 8 AA;
 Query Match 22.2%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 LKSL 18
 ||||
 Db 4 LKSL 7
 RESULT 63
 AAB57901
 ID AAB57901 standard; Peptide; 8 AA.
 XX
 AC AAB57901;
 XX
 DT 12-MAR-2001 (first entry)
 XX
 DE CD61 C-terminal core sequence #5.
 XX
 KW Endothelial cell; haematopoietic cell; PDZ domain protein;
 KW PL domain protein; leukocyte activation; T cell surface receptor;
 KW synapse formation; leukocyte activation; T cell surface receptor;
 KW autoimmune disease; transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
 KW ischaemia; vasculitis; Crohn's disease.
 XX

OS Homo sapiens.
 XX WO2000069898-A2.
 PN 23-NOV-2000.
 XX 12-MAY-2000; 2000WO-US13205.
 XX 14-MAY-1999; 99US-0134114.
 PR 14-MAY-1999; 99US-0134117.
 PR 14-MAY-1999; 99US-0134118.
 PR 21-OCT-1999; 99US-0160860.
 PR 29-OCT-1999; 99US-0162498.
 PR 13-DEC-1999; 99US-0170453.
 PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.
 XX (ARBO-) ARBOR VITA CORP.
 PA Lu PS;
 XX WPI; 2001-061214/07.
 DR Modulating a biological function of a hematopoietic cell for treating
 PT an allergic response, or diseases mediated by immune system cells,
 PT comprises introducing into the cell a PDZ-PL interaction enhancer or
 PT inhibitor -
 XX Disclosure; Page 93; 143pp; English.
 PS The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or haematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a
 CC PDZ domain protein and a PL domain protein to result in inhibition of
 CC leukocyte activation. The present sequence is a core sequence of a PL
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are
 CC named after three prototypical proteins: PSD95, Drosophila large disc
 CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved
 CC in synapse formation by organising transmembrane neurotransmitter
 CC receptors through intracellular interactions. The inhibitors identified
 CC by the present invention can be used to treat a disease mediated by
 CC haematopoietic cells, e.g. autoimmune disease, inflammation, allergy
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The
 CC inhibitors can also be used to prevent transplantation rejection of a
 CC solid organ transplant.
 XX Sequence 8 AA;
 SQ Query Match 22.2%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 15 LKSL 18
 Db 4 LKSL 7
 RESULT 64
 ABJ05123
 ID ABJ05123 standard; Peptide; 8 AA.
 XX AC ABJ05123;
 XX 07-NOV-2002 (first entry)
 DT T-cell surface receptor C-terminal core peptide SEQ ID No 118.
 DE

XX Immunosuppressive; antiinflammatory; affinity; Kd; binding; PDZ domain;
 KW ligand; Ki; inhibitor; K-enhancer; leukocyte; autoimmune disease;
 KW inflammatory; humoral immune response; inflammation; C-terminal core;
 KW T-cell surface receptor.
 XX Unidentified.
 OS WO200231512-A2.
 XX 18-APR-2002.
 PD 11-OCT-2001; 2001WO-US32150.
 PF 13-OCT-2000; 2000US-0688017.
 PR (ARBO-) ARBOR VITA CORP.
 XX Rabinowitz JD, Lu PS, Schweitzer J;
 XX WPI; 2002-416878/44.
 DR Assays for determining the affinity of binding between a PDZ domain and
 PT a ligand, and determining the Ki of an inhibitor of the binding, PDZ
 PT comprises using a polypeptide comprising a PDZ domain and a non-PDZ
 PT domain -
 XX Disclosure; Page 114; 164pp; English.
 PS The invention relates to methods and reagents for determining the
 CC apparent affinity (Kd) of binding between a PDZ domain and a ligand. The
 CC invention also relates to methods and reagents for determining the Ki of
 CC an inhibitor of binding between a PDZ domain and a ligand, identifying an
 CC agent that enhances binding of a PDZ domain and a ligand, and determining
 CC the potency (K-enhancer) of binding between a PDZ domain and a ligand, by
 CC determining the ligand bound with an immobilised polypeptide comprising a
 CC PDZ domain and a non-PDZ domain on a surface. The modulator (preferably,
 CC an inhibitor) of interaction between PDZ and PL is useful for treating a
 CC disease characterised by leukocyte activation, e.g., an autoimmune
 CC disease that is characterised by inflammatory or humoral immune response,
 CC and for reducing inflammation in a subject. This sequence represents a T-
 CC cell surface receptor C-terminal core peptide relating to the PDZ
 CC containing proteins of the invention.
 XX Sequence 8 AA;
 SQ Query Match 22.2%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 15 LKSL 18
 Db 4 LKSL 7
 RESULT 65
 ABJ06021
 ID ABJ06021 standard; Peptide; 8 AA.
 XX AC ABJ06021;
 XX 14-NOV-2002 (first entry)
 DT Hepatitis B virus epitope #239.
 DE Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 KW virucide; hepatotropic; antiinflammatory.
 XX Hepatitis B virus.
 OS WO200219986-A1.
 PN 14-MAR-2002.
 PD

XX 08-SEP-2000; 2000WO-US24802.
XX
PR 08-SEP-2000; 2000WO-US24802.
XX
XX (EPIM-) EPIMMUNE INC.
PA (SETT/) SETTE A.
XX
XX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
PI Cellis E, Kubo RT, Grey HM, Chesnut RW;
XX
XX WPI; 2002-643192/69.
XX
XX Vaccine composition for treating or preventing hepatitis B virus (HBV)
PT infection, and/or for stimulating an immune response to HBV, comprises
PT a HBV peptide epitope -
XX
XX Disclosure; Page 114; 228pp; English.
XX
XX The present invention relates to a composition comprising at least one
CC hepatitis B virus epitope. This can be used in the production of a
CC vaccine for use in preventing or treating hepatitis B virus infection.
CC The present sequence is a peptide described in the exemplification of the
CC invention.
XX
XX Sequence 8 AA;
SQ
Query Match 22.2%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GEEI 14
DB 3 GEEI 6
RESULT 66
ID ABJ06547
XX AC ABJ06547;
XX
XX 14-NOV-2002 (first entry)
XX
XX Hepatitis B virus epitope #765.
XX
XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
KW virucide; hepatotropic; antiinflammatory.
XX
XX Hepatitis B virus.
XX
XX WO200219986-A1.
XX
XX 14-MAR-2002.
XX
XX 08-SEP-2000; 2000WO-US24802.
XX
XX 08-SEP-2000; 2000WO-US24802.
XX
XX (EPIM-) EPIMMUNE INC.
PA (SETT/) SETTE A.
XX
XX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
PI Cellis E, Kubo RT, Grey HM, Chesnut RW;
XX
XX WPI; 2002-643192/69.
XX
XX Vaccine composition for treating or preventing hepatitis B virus (HBV)
PT infection, and/or for stimulating an immune response to HBV, comprises
PT a HBV peptide epitope -
XX
XX Disclosure; Page 127; 228pp; English.

XX The present invention relates to a composition comprising at least one
CC hepatitis B virus epitope. This can be used in the production of a
CC vaccine for use in preventing or treating hepatitis B virus infection.
CC The present sequence is a peptide described in the exemplification of the
CC invention.
XX
XX Sequence 8 AA;
SQ
Query Match 22.2%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GEEI 14
DB 3 GEEI 6
RESULT 67
ID ABJ07394
XX AC ABJ07394;
XX
XX 14-NOV-2002 (first entry)
XX
XX Hepatitis B virus epitope #1612.
XX
XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
KW virucide; hepatotropic; antiinflammatory.
XX
XX Hepatitis B virus.
XX
XX WO200219986-A1.
XX
XX 14-MAR-2002.
XX
XX 08-SEP-2000; 2000WO-US24802.
XX
XX 08-SEP-2000; 2000WO-US24802.
XX
XX (EPIM-) EPIMMUNE INC.
PA (SETT/) SETTE A.
XX
XX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
PI Cellis E, Kubo RT, Grey HM, Chesnut RW;
XX
XX WPI; 2002-643192/69.
XX
XX Vaccine composition for treating or preventing hepatitis B virus (HBV)
PT infection, and/or for stimulating an immune response to HBV, comprises
PT a HBV peptide epitope -
XX
XX Disclosure; Page 143; 228pp; English.
XX
XX The present invention relates to a composition comprising at least one
CC hepatitis B virus epitope. This can be used in the production of a
CC vaccine for use in preventing or treating hepatitis B virus infection.
CC The present sequence is a peptide described in the exemplification of the
CC invention.
XX
XX Sequence 8 AA;
SQ
Query Match 22.2%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GEEI 14
DB 3 GEEI 6
RESULT 68
ID ABP63416

ID ABP63416 standard; Peptide; 8 AA.
XX AC ABP63416;
XX DT 28-OCT-2002 (first entry)
XX DE Monocyte surface receptor PDZ motif (PL) peptide SEQ ID NO:118.
XX KW Molecular interaction; haematopoietic cell; immune response; T cell;
KW PDZ domain; B cell; endothelial cell; PDZ protein; PSD95; PDZ ligand;
KW Drosophila large disc protein; Zonula Occludin 1 protein; PL protein;
KW immunosuppressive; antiinflammatory; antiallergic; antiatherosclerotic;
KW anticancer; antipsoriatic; dermatological; antiasthmatic; cytostatic;
KW antimicrobial; vasotropic; inflammatory immune response; inflammation;
KW humoral immune response; autoimmune disease; allergy; ulcerative colitis;
KW inflammatory bowel disease; ileitis; enteritis; psoriasis; scleroderma;
KW inflammatory dermatosis; respiratory allergic disease; asthma; cancer;
KW allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia;
KW angiogenesis-dependent disorder; infectious disease.
XX OS Homo sapiens.
OS Synthetic.
XX PN WO200242422-A2.
XX PD 30-MAY-2002.
XX PF 09-NOV-2001; 2001WO-US44138.
XX PR 11-NOV-2000; 2000US-0710059.
PR 24-NOV-2000; 2000US-0721915.
PR 24-NOV-2000; 2000US-0722069.
PR 28-NOV-2000; 2000US-0724553.
XX PA (ARBO-) ARBOR VITA CORP.
XX PI Lu P, Rabinowitz JD, Schweizer J;
XX WPI; 2002-608221/55.
XX PT Modulating the biological function of an endothelial cell or
PT hematopoietic cell e.g., a T-cell or B-cell comprises introducing into
PT the cell, an agent that inhibits binding of a PDZ protein and a PDZ
PT ligand protein in the cell -
XX PS Disclosure; Page 132; 207pp; English.
XX CC The present invention describes a method (M1) for modulating a biological
CC function of an endothelial cell or haematopoietic cell. M1 comprises
CC introducing into the cell, an agent that inhibits binding of a PDZ
CC (PS95, Drosophila large disc protein, and Zonula Occludin 1 protein)
CC protein and a PDZ ligand (PL) protein in the cell, and so modulates the
CC biological function. Also described is a method (M2) for determining
CC whether a test compound is an inhibitor of binding between a PDZ protein
CC and a PL protein. M1 is used for modulating a biological function of an
CC endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an
CC inflammatory or humoral immune response, or an autoimmune disease. An
CC inhibitor (I) is useful for treating a disease characterised by leukocyte
CC activation, where the disease is characterised by an inflammatory or
CC humoral immune response, e.g., an autoimmune disease. The compounds
CC e.g., PL-PDZ interaction inhibitors are useful for treating (ameliorating
CC symptoms of) a variety of diseases and conditions characterised by
CC inflammatory and humoral immune responses e.g., inflammation, allergy,
CC inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis,
CC psoriasis and inflammatory dermatoses, scleroderma, respiratory allergic
CC diseases such as asthma, allergic rhinitis, transplantation rejection
CC (cardiac, kidney, lung, liver, small bowel, cornea, pancreas, cadaver,
CC autologous, bone marrow xenotransplantation), atherosclerosis, cancers,
CC angiogenesis-dependent disorders, infectious diseases and ischaemia.
CC ABQ96620 to ABQ96732 and ABP63153 to ABP63578 represent sequences used
CC in the exemplification of the present invention.
XX SQ Sequence 8 AA;

Query Match 22.2%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 LKSL 18
DB 4 LKSL 7
RESULT 69
AAR66006
ID AAR66006 standard; peptide; 9 AA.
XX AC AAR66006;
XX DT 30-JUN-1995 (first entry)
XX DE Peptide which binds immune complexes.
XX KW Immune complex; immunoadsorbent.
XX OS Synthetic.
XX PN JP06263795-A.
XX PD 20-SEP-1994.
XX PF 30-SEP-1993; 93JP-0245367.
PR 30-SEP-1992; 92JP-0261821.
PR 18-JAN-1993; 93JP-0006099.
XX PA (KURS) KURARAY CO LTD.
XX DR WPI; 1994-338300/42.
XX PT Peptide(s) capable of binding to immune complex, and adsorbents
PT contg them - useful for removal of immune complexes from body
PT fluid and for treatment of associated diseases.
XX PS Example 8; Page 6; 15pp; Japanese.
XX CC The invention relates to new peptides of formula H-X-A-Y-Z in which
CC A is a peptide fragment of 6-12 amino acids containing the sequence
CC Ala-B-C-Glu-Ile-Leu, where B and C are Trp, Tyr and/or Phe; X and Y
CC are each a single bond, or an amino acid or peptide composed of 2-10
CC amino acids selected from Asp, Glu, Arg, Lys and His, provided at
CC least one of X and Y is not a bond; and Z is OH or amide.
CC The peptides can bind to immune complexes. They can be fixed to a
CC support and used for selective removal of immune complexes from body
CC fluids without removal of useful components. They can thus be used for
CC treating diseases involving the complexes. In Examples, the
CC activity of the peptides is compared to that of reference peptides
CC in which neither X nor Y is present.
XX CC The present sequence is a specific example of the new peptides.
XX SQ Sequence 9 AA;
Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 BILK 16
DB 5 BILK 8
RESULT 70
AAR65863
ID AAR65863 standard; peptide; 9 AA.
XX AC AAR65863;

XX DT 26-JUN-1995 (first entry)

XX DE Antideoxyribonucleic acid antibody adsorbent peptide.

XX KW Antideoxyribonucleic acid adsorbent peptide; kidney inflammation;

XX KW systemic lupus erythematosus.

XX OS Synthetic.

XX PN JP06261941-A.

XX PD 20-SEP-1994.

XX PF 13-OCT-1993; 93JP-0256111.

XX PR 18-JAN-1993; 93JP-0006100.

XX PA (KURS) KURARAY CO LTD.

XX WPI; 1994-337461/42.

XX DR Adsorbents of antideoxyribonucleic - comprising a peptide,

PT immobilised on a carrier.

XX PS Claim 1; Page 14; 16pp; Japanese.

XX CC AAR65841-R65879 are antideoxyribonucleic (ADN) acid adsorbent peptides

CC derived from the highly generic peptide in the specification. When these

CC peptides are immobilised on a carrier (either cellulose, porous

CC glass, polyvinyl alcohol or polyacrylamide) they can be used to

CC remove ADN antibodies, which can result in kidney inflammation and

CC systemic lupus erythematosus.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 15; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16

DB 5 EILK 8

|||||

RESULT 71

AAR70537

ID AAR70537 standard; Peptide; 9 AA.

XX AC AAR70537;

XX DT 09-JAN-1996 (first entry)

XX DE HIV peptide fragment 6 capable of binding to HLA-B3501.

XX KW HLA; human lymphocyte antigen; HIV; human immunodeficiency virus;

KW binding peptide; induce killer cell; prevention; treatment; AIDS;

KW autoimmune disease syndrome; vaccine.

XX OS Human immunodeficiency virus.

XX PN WO9511255-A1.

XX PD 27-APR-1995.

XX PF 19-OCT-1994; 94WO-JP01756.

XX PR 19-OCT-1993; 93JP-0261302.

XX PA (AJIN) AJINOMOTO CO INC.

PA (AJIN) AJINOMOTO KK.

XX PI Miwa K, Takiguchi M;

XX DR WPI; 1995-170188/22.

XX PT HLA-binding peptide fragments from HIV proteins - induce killer

PT cells which target HIV-infected cells and can be incorporated into

PT anti-HIV vaccines

XX PS Claim 1; Page 27; 61pp; Japanese.

XX CC AAR70537 is a peptide fragment derived from an HIV (Human

CC Immunodeficiency Virus) protein which is capable of binding to human

CC lymphocyte antigen (HLA) B*3501. Peptides shown in AAR70519-42 are all

CC capable of binding to HLA-B*3501, and other peptide fragments bind to

CC other specific HLA's. Pref. peptides have Pro, Ala or Gly as the second

CC residue (from the N-terminal) and Leu, Ile, Met, Phe, Val (or Tyr or Ala)

CC at the carboxy terminal. The peptides induce killer cells which target

CC HIV-infected cells. They are useful in the prevention and treatment of

CC HIV and AIDS. Anti-HIV vaccines may incorporate the peptides, or may

CC incorporate a vector (such as vaccinia or BCG) contg. DNA encoding the

CC peptides.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 16; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18

DB 6 LKSL 9

|||||

RESULT 72

AAR70544

ID AAR70544 standard; Peptide; 9 AA.

XX AC AAR70544;

XX DT 11-JAN-1996 (first entry)

XX DE HIV peptide fragment 12 capable of binding to HLA-B51.

XX KW HLA; human lymphocyte antigen; HIV; human immunodeficiency virus;

KW binding peptide; induce killer cell; prevention; treatment; AIDS;

KW autoimmune disease syndrome; vaccine.

XX OS Human immunodeficiency virus.

XX PN WO9511255-A1.

XX PD 27-APR-1995.

XX PF 19-OCT-1994; 94WO-JP01756.

XX PR 19-OCT-1993; 93JP-0261302.

XX PA (AJIN) AJINOMOTO CO INC.

PA (AJIN) AJINOMOTO KK.

XX PI Miwa K, Takiguchi M;

XX DR WPI; 1995-170188/22.

XX PT HLA-binding peptide fragments from HIV proteins - induce killer

PT cells which target HIV-infected cells and can be incorporated into

PT anti-HIV vaccines

XX PS Claim 1; Page 29; 61pp; Japanese.

XX CC AAR70544 is a peptide fragment derived from an HIV (Human

CC Immunodeficiency Virus) protein and is capable of binding to human

CC lymphocyte antigen (HLA) B51. Peptides shown in AAR70543-64 are all

CC capable of binding to HLA-B51, and other peptide fragments bind to other

CC specific HLA's. Pref. peptides have Pro, Ala or Gly as the second residue
 CC (from the N-terminal) and Leu, Ile, Met, Phe, Val (or Tyr or Ala) at the
 CC carboxy terminal. The peptides induce killer cells which target
 CC HIV-infected cells. They are useful in the prevention and treatment of
 CC HIV and AIDS. Anti-HIV vaccines may incorporate the peptides, or may
 CC incorporate a vector (such as vaccinia or BCG) contg. DNA encoding the
 CC peptides.
 XX
 XX

SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 16; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
 ||||
 Db 6 LKSL 9

RESULT 73

AAAR77554
 ID AAR77554 standard; Peptide; 9 AA.

XX
 AC AAR77554;

XX
 DT 14-FEB-1996 (first entry)

DE HIV(B35)GAG-29, human immunodeficiency virus epitope.

XX HLA; human lymphocyte antigen; HIV; human immunodeficiency virus;
 KW binding peptide; induce killer cell; prevention; treatment; AIDS;
 KW autoimmune disease syndrome; vaccine.
 XX

OS Human immunodeficiency virus (MN isolate).

XX
 PN WO9511255-A1.

XX
 PD 27-APR-1995.

XX
 PF 19-OCT-1994; 94WO-JF01756.

XX
 PR 19-OCT-1993; 93JP-0261302.

XX
 PA (AJIN) AJINOMOTO CO INC.

XX
 PA (AJIN) AJINOMOTO KK.

XX
 PI Miwa K, Takiguchi M;

XX
 DR WPI; 1995-170188/22.

XX HLA-binding peptide fragments from HIV proteins - induce killer
 PT cells which target HIV-infected cells and can be incorporated into
 PT anti-HIV vaccines
 XX

PS Example 1; Page 16; 61pp; Japanese.

XX R775540 is a peptide fragment derived from an HIV (Human
 CC immunodeficiency virus) gag protein (residues 490-498) and is capable of
 CC binding to a human lymphocyte antigen. The peptide can induce killer
 CC cells which target HIV-infected cells. It is also useful in the
 CC prevention and treatment of HIV and AIDS. Anti-HIV vaccines may
 CC incorporate the peptides, or may incorporate a vector (such as vaccinia
 CC or BCG) contg. DNA encoding the peptides.
 XX

SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 16; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
 ||||
 Db 6 LKSL 9

RESULT 74
 AAW49244

ID AAW49244 standard; peptide; 9 AA.

XX
 AC AAW49244;

XX
 DT 05-JUN-1998 (first entry)

XX Human leucocyte antigen DQ4 binding peptide #135.

XX Human leucocyte antigen; HLA-DQ4; combinatorial library;
 KW autoimmune disease; Chronic articular rheumatism.
 XX

OS Synthetic.

XX
 PN JP08151396-A.

XX
 PD 11-JUN-1996.

XX
 PF 28-NOV-1994; 94JP-0292657.

XX
 PR 28-NOV-1994; 94JP-0292657.

XX
 PA (TEIJ) TEIJIN LTD.

XX
 DR WPI; 1996-329479/33.

XX HLA-binding oligopeptide and an immuno:regulator contg it - used in
 PT the treatment of auto:immune disease
 XX

PS Claim 4; Page 23; 61pp; Japanese.

XX This peptide is an example of a peptide which binds to a human leucocyte
 CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagenid
 CC combinatorial library comprising the sequence AAV05953, by screening
 CC with an HLA-DQ4 molecule. The peptide is used for the treatment of
 CC autoimmune disease, or especially for treatment of viral diseases.
 XX

SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 17; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GEEI 14
 ||||
 Db 1 GEEI 4

RESULT 75

AAAY96353
 ID AAY96353 standard; peptide; 9 AA.

XX
 AC AAY96353;

XX
 DT 29-AUG-2000 (first entry)

XX HLA-A3 binding peptide hTERT R535.

XX hTERT; telomerase complex; reverse transcriptase; MHC; HLA; CTL; cancer;
 KW human leucocyte antigen; tumour-associated antigen; cytostatic; vaccine;
 KW major histocompatibility complex; cytotoxic T lymphocyte; immunotherapy.
 XX

OS Homo sapiens.

XX
 PN WO200025813-A1.

XX
 PD 11-MAY-2000.

XX
 PF 29-OCT-1999; 99WO-US25438.

XX

PR 29-OCT-1998; 98US-0106106.
XX
XX (DAND) DANA FARBER CANCER INST INC.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Nadler LM, Hahn WC, Schultze JL, Vonderheide RH;
PI
XX WPI; 2000-365402/31.
DR
XX Universal tumor-associated antigens such as telomerase catalytic
PT subunit capable of binding major histocompatibility complex molecule
PT useful for diagnosis, prevention and treatment of cancer
XX
XX Disclosure; Page 74; 136pp; English.
PS
XX Human telomerase complex reverse transcriptase (hTERT) is expressed in
CC more than 85 percent of human cancers. hTERT is useful as a universal
CC tumour-associated antigen (TAA) that binds to a major histocompatibility
CC complex molecule (MHC). hTERT peptides were analyzed for the ability to
CC bind to HLA (human leukocyte antigen) class I molecules. Cytotoxic T
CC lymphocytes (CTL) were then generated that kill a cell expressing hTERT
CC or a hTERT-TAA, in a hTERT or TAA specific MHC-restricted fashion.
CC Antigen presenting cells (APC) were also generated ex vivo for
CC presentation of a TAA peptide or hTERT. The APC can be used to activate
CC CTL to kill cells expressing the TAA. The TAA, hTERT peptides, APC and
CC CTL are useful for cancer immunotherapy. Measuring the level of CTL in a
CC sample is useful for assessing the level of immunity of a patient to a
CC TAA or a peptide, where the sample is obtained before or after a cancer
CC treatment is given to the patient. TAA peptides (e.g. hTERT) are also
CC useful for diagnosis and prophylactic treatment of cancer.
XX
SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EEIL 15
|
|
|
|
Db 4 EEIL 7

Search completed: November 25, 2003, 19:27:19
Job time : 46.9419 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 28.8937 Seconds
(without alignments)
114.943 Million cell updates/sec

Title: US-09-641-801-30

Perfect score: 18

Sequence: 1 ATFNRQDGHGEILKSL 18

Scoring table: OLIGO

Gapex 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	15	US-10-281-652-30
2	6	33.3	18	10	US-09-734-520-33
3	6	33.3	18	14	US-10-012-034A-33
4	5	27.8	9	14	US-10-153-159-28
5	5	27.8	9	15	US-10-153-176-28
6	4	22.2	5	10	US-09-976-736-56
7	4	22.2	5	10	US-09-976-736-60
8	4	22.2	5	10	US-09-976-736-64
9	4	22.2	6	9	US-09-952-768-23
10	4	22.2	6	9	US-09-952-768-33
11	4	22.2	6	9	US-09-952-768-38
12	4	22.2	6	10	US-09-954-697-72
13	4	22.2	6	10	US-09-954-697-83
14	4	22.2	6	10	US-09-954-697-88
15	4	22.2	6	10	US-09-867-852-205
16	4	22.2	6	10	US-09-867-852-207
17	4	22.2	6	14	US-10-059-749-34
18	4	22.2	6	14	US-10-059-749-45
19	6	14	US-10-059-749-50		
20	4	22.2	7	10	US-09-791-378-294
21	4	22.2	7	11	US-09-791-393-189
22	4	22.2	7	11	US-09-791-389-189
23	4	22.2	9	10	US-09-753-831-6
24	4	22.2	9	10	US-09-791-378-204
25	4	22.2	9	12	US-10-282-960-87
26	4	22.2	9	12	US-09-942-052-132
27	4	22.2	9	12	US-09-942-052-137
28	4	22.2	9	12	US-09-942-052-215
29	4	22.2	9	12	US-09-942-052-241
30	4	22.2	9	12	US-09-942-052-310
31	4	22.2	9	12	US-09-942-052-317
32	4	22.2	9	12	US-09-942-052-343
33	4	22.2	9	12	US-09-942-052-405
34	4	22.2	9	12	US-09-942-052-421
35	4	22.2	9	12	US-09-942-052-513
36	4	22.2	9	12	US-09-942-052-517
37	4	22.2	9	12	US-09-942-052-603
38	4	22.2	9	12	US-09-942-052-635
39	4	22.2	9	14	US-10-153-159-21
40	4	22.2	9	14	US-10-153-159-24
41	4	22.2	9	14	US-10-153-159-29
42	4	22.2	9	14	US-10-153-159-30
43	4	22.2	9	15	US-10-153-176-21
44	4	22.2	9	15	US-10-153-176-24
45	4	22.2	9	15	US-10-153-176-29
46	4	22.2	9	15	US-10-153-176-30
47	4	22.2	10	9	US-09-912-917-3
48	4	22.2	10	11	US-09-572-404B-722
49	4	22.2	10	11	US-09-572-404B-724
50	4	22.2	10	12	US-09-572-270A-611
51	4	22.2	10	12	US-09-572-270A-948
52	4	22.2	10	12	US-09-572-270A-950
53	4	22.2	10	12	US-09-942-052-152
54	4	22.2	10	12	US-09-942-052-269
55	4	22.2	10	12	US-09-942-052-282
56	4	22.2	10	12	US-09-942-052-294
57	4	22.2	10	12	US-09-942-052-367
58	4	22.2	10	12	US-09-942-052-375
59	4	22.2	10	12	US-09-942-052-474
60	4	22.2	10	12	US-09-942-052-484
61	4	22.2	10	12	US-09-942-052-488
62	4	22.2	10	12	US-09-942-052-493
63	4	22.2	10	12	US-09-942-052-560
64	4	22.2	10	12	US-09-942-052-566
65	4	22.2	10	12	US-09-942-052-582
66	4	22.2	10	12	US-09-942-052-597
67	4	22.2	10	12	US-09-942-052-667
68	4	22.2	10	12	US-09-942-052-681
69	4	22.2	10	12	US-09-942-052-682
70	4	22.2	10	12	US-09-942-052-692
71	4	22.2	10	12	US-10-239-313A-5
72	4	22.2	10	12	US-10-239-313A-80
73	4	22.2	10	12	US-10-200-708-39
74	4	22.2	10	12	US-10-200-708-440
75	4	22.2	10	12	US-10-200-708-594
76	4	22.2	10	12	US-09-573-822C-22
77	4	22.2	10	12	US-09-573-822C-58
78	4	22.2	10	12	US-09-573-822C-265
79	4	22.2	10	12	US-10-277-292-58
80	4	22.2	10	12	US-10-277-292-296
81	4	22.2	10	12	US-10-277-292-394
82	4	22.2	10	12	US-10-280-340-58
83	4	22.2	10	12	US-10-280-340-296
84	4	22.2	10	12	US-10-280-340-394
85	4	22.2	10	15	US-10-133-210-53
86	4	22.2	10	15	US-10-133-210-88
87	4	22.2	11	10	US-09-795-006A-137
88	4	22.2	11	11	US-09-852-910-149

Sequence 207, App
Sequence 34, Appl
Sequence 45, Appl
Sequence 50, Appl
Sequence 294, App
Sequence 189, App
Sequence 189, App
Sequence 6, Appl
Sequence 204, App
Sequence 87, Appl
Sequence 132, App
Sequence 137, App
Sequence 215, App
Sequence 241, App
Sequence 310, App
Sequence 343, App
Sequence 345, App
Sequence 405, App
Sequence 421, App
Sequence 513, App
Sequence 517, App
Sequence 603, App
Sequence 635, App
Sequence 21, Appl
Sequence 24, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 21, Appl
Sequence 24, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 3, Appl
Sequence 722, App
Sequence 724, App
Sequence 611, App
Sequence 948, App
Sequence 950, App
Sequence 152, App
Sequence 269, App
Sequence 282, App
Sequence 294, App
Sequence 367, App
Sequence 375, App
Sequence 474, App
Sequence 484, App
Sequence 488, App
Sequence 493, App
Sequence 560, App
Sequence 566, App
Sequence 582, App
Sequence 597, App
Sequence 667, App
Sequence 681, App
Sequence 682, App
Sequence 692, App
Sequence 5, Appl
Sequence 80, Appl
Sequence 29, Appl
Sequence 440, App
Sequence 594, App
Sequence 22, Appl
Sequence 98, Appl
Sequence 265, App
Sequence 58, Appl
Sequence 296, App
Sequence 394, App
Sequence 296, App
Sequence 394, App
Sequence 53, Appl
Sequence 88, Appl
Sequence 137, App
Sequence 149, App

89 4 22.2 12 15 US-10-033-662-16 Sequence 16, Appl
90 4 22.2 12 15 US-10-055-711-13 Sequence 13, Appl
91 4 22.2 13 9 US-09-813-329-39 Sequence 39, Appl
92 4 22.2 13 9 US-09-813-329-49 Sequence 49, Appl
93 4 22.2 13 9 US-09-813-329-60 Sequence 60, Appl
94 4 22.2 13 9 US-09-873-676-13 Sequence 13, Appl
95 4 22.2 13 12 US-10-153-244-61 Sequence 61, Appl
96 4 22.2 13 12 US-10-153-244-124 Sequence 124, App
97 4 22.2 13 12 US-10-153-244-174 Sequence 174, App
98 4 22.2 13 12 US-10-153-244-224 Sequence 224, App
99 4 22.2 14 10 US-09-957-143-5 Sequence 5, Appl
100 4 22.2 15 11 US-09-907-969-502 Sequence 502, App

ALIGNMENTS

RESULT 1

US-10-281-652-30
; Sequence 30, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-30

Query Match 100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATFNRYQDHGEILKSL 18
 |||||
Db 1 ATFNRYQDHGEILKSL 18

RESULT 2

US-09-734-520-33
; Sequence 33, Application US/09734520
; Patent No. US20020115173A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel
; TITLE OF INVENTION: SHORT PEPTIDES FROM THE A-REGION OF
; TITLE OF INVENTION: PROTEIN KINASES WHICH SELECTIVELY MODULATE PROTEIN KINASE
; FILE REFERENCE: 1242.2003-000
; CURRENT FILING DATE: 2000-12-11
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:

; OTHER INFORMATION: Jak2
US-09-734-520-33

Query Match 33.3%; Score 6; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EILKSL 18
 |||||
Db 2 EILKSL 7

RESULT 3

US-10-012-034A-33
; Sequence 33, Application US/10012034A
; Publication No. US20020137141A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel
; TITLE OF INVENTION: SHORT PEPTIDES FROM THE A-REGION OF
; TITLE OF INVENTION: PROTEIN KINASES WHICH SELECTIVELY MODULATE PROTEIN KINASE
; FILE REFERENCE: BEN-SASSON-5A
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US/10/012,034A
; PRIOR FILING DATE: 2000-12-11
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Jak2
; NAME/KEY: MYRISTATE
; LOCATION: (1)...(0)
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (0)...(18)
US-10-012-034A-33

Query Match 33.3%; Score 6; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EILKSL 18
 |||||
Db 2 EILKSL 7

RESULT 4

US-10-153-159-28
; Sequence 28, Application US/10153159
; Publication No. US20020177170A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY
; FILE REFERENCE: 26050-704
; CURRENT APPLICATION NUMBER: US/10/153,159
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 9


```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/952,768
; APPLICATION NUMBER: US/09/952,768
; FILING DATE: 10-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen, William T.
; REGISTRATION NUMBER: 44,614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "CED-3"
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-952-768-38

Query Match          22.2%; Score 4; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 HGEE 13
      |||||
Db       3 HGEE 6

RESULT 12
US-09-954-697-72
; Sequence 72, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-72

Query Match          22.2%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 HGEE 13
      |||||
Db       3 HGEE 6

RESULT 13
US-09-954-697-83
; Sequence 83, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697

```

```

; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-83

Query Match          22.2%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 HGEE 13
      |||||
Db       3 HGEE 6

RESULT 14
US-09-954-697-88
; Sequence 88, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-88

Query Match          22.2%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 HGEE 13
      |||||
Db       3 HGEE 6

RESULT 15
US-09-867-852-205
; Sequence 205, Application US/09867852
; Patent No. US20020147324A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/867,852
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205

```

```
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-867-852-205

Query Match          22.2%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
Db 3 LKSL 6

RESULT 16
US-09-867-852-207
; Sequence 207, Application US/09867852
; Patent No. US20020147324A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/867,852
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-867-852-207

Query Match          22.2%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
Db 3 LKSL 6

RESULT 17
US-10-059-749-34
; Sequence 34, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-10-059-749-34

Query Match          22.2%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13
Db 3 HGEE 6

RESULT 18
US-10-059-749-45
; Sequence 45, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
```

TELEFAX: (619) 535-9849

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-10-059-749-45

Query Match 22.2%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13

|||||

Db 3 HGEE 6

RESULT 19

US-10-059-749-50

Sequence 50, Application US/10059749

Publication No. US20020183504A1

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

Fernandes-Alnemri, Teresa

Litwack, Gerald

TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids

CORRESPONDENCE ADDRESS: Encoding Same and Methods of Use

NUMBER OF SEQUENCES: 87

ADDRESS: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/059,749

FILING DATE: 29-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/865,579

FILING DATE: 29-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-ID 2180

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-9849

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 50:

US-10-059-749-50

Query Match 22.2%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13

|||||

Db 3 HGEE 6

RESULT 20

US-09-791-378-234

Sequence 234, Application US/09791378

Patent No. US20020142303A1

GENERAL INFORMATION:

APPLICANT: Parekh, Rajesh

TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF

SCHIZOPHRENIA

FILE REFERENCE: 9195-061-999

CURRENT APPLICATION NUMBER: US/09/791,378

CURRENT FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: 09/750,395

PRIOR FILING DATE: 2000-12-28

NUMBER OF SEQ ID NOS: 677

SOFTWARE: Patent in version 3.0

SEQ ID NO 294

LENGTH: 7

TYPE: PRT

ORGANISM: Homo sapiens

US-09-791-378-234

Query Match 22.2%; Score 4; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EBIL 15

|||||

Db 2 EBIL 5

RESULT 21

US-09-791-393-189

Sequence 189, Application US/09791393

Publication No. US20030032200A1

GENERAL INFORMATION:

APPLICANT: Herath, Rajesh Bhikhu

APPLICANT: Rohlf, Christian

TITLE OF INVENTION: Proteins, Genes and Their Use for

Diagnosis and Treatment of Bipolar Affective Disorder (BAD)

TITLE OF INVENTION: and Unipolar Depression

FILE REFERENCE: 2543-1-001 N1

CURRENT APPLICATION NUMBER: US/09/791,393

CURRENT FILING DATE: 2002-01-02

EARLIER APPLICATION NUMBER: GB 0004412.3

EARLIER FILING DATE: 2000-02-24

EARLIER APPLICATION NUMBER: GB 0030050.9

EARLIER FILING DATE: 2000-12-08

EARLIER APPLICATION NUMBER: US 60/254,830

EARLIER FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 308

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 189

LENGTH: 7

TYPE: PRT

ORGANISM: homo sapien

US-09-791-393-189

Query Match 22.2%; Score 4; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EBIL 15

|||||

Db 2 EBIL 5

RESULT 22

US-09-791-389-189

Sequence 189, Application US/09791389

Publication No. US20030032773A1

GENERAL INFORMATION:

; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhiknu
; APPLICANT: Rohlf, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-189

Query Match 22.2%; Score 4; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.1e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 12 EEIL 15
|
|
|
|
Db 2 EEIL 5

RESULT 23

US-09-753-831-6
; Sequence 6, Application US/09753831
; Patent No. US20020137683A1
; GENERAL INFORMATION:
; APPLICANT: Hogan, Kevin T.
; APPLICANT: Ross, Mark M.
; TITLE OF INVENTION: C-SKI Oncogene-Derived Peptides for Prevention,
; TITLE OF INVENTION: Treatment and Diagnosis of Cancer
; FILE REFERENCE: 26747-27
; CURRENT APPLICATION NUMBER: US/09/753,831
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: U.S. 60/174296
; PRIOR FILING DATE: 2000-01-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence.No. US20020137683Alapeptide
; OTHER INFORMATION: Derived from the human C-SKI oncoprotein.
US-09-753-831-6

Query Match 22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EILK 16
|
|
|
|
Db 6 EILK 9

RESULT 24

US-09-791-378-204
; Sequence 204, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:

; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 204
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-204

Query Match 22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EEIL 15
|
|
|
|
Db 1 EEIL 4

RESULT 25

US-10-282-960-87
; Sequence 87, Application US/10282960
; Publication No. US20030143228A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Si-Yi
; APPLICANT: Zhaoyang, You
; APPLICANT: Schroers, Roland
; TITLE OF INVENTION: Human Telomerase Reverse Transcriptase as a Class-II Restrict-
; TITLE OF INVENTION: Associated Antigen
; FILE REFERENCE: P02193US1
; CURRENT APPLICATION NUMBER: US/10/282,960
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/345,012
; PRIOR FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human
US-10-282-960-87

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TFNR 5
|
|
|
|
Db 4 TFNR 7

RESULT 26

US-09-942-052-132
; Sequence 132, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28

; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-132

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
|||
Db 6 LKSL 9

RESULT 27

US-09-942-052-137
; Sequence 137, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 137
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-137

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
|||
Db 2 LKSL 5

RESULT 28

US-09-942-052-215
; Sequence 215, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052

; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 215
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-215

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
|||
Db 2 LKSL 5

RESULT 29

US-09-942-052-241
; Sequence 241, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 241
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-241

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
|||
Db 4 LKSL 7

RESULT 30

US-09-942-052-310
; Sequence 310, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00

; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 310
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-310

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
|
|
|
|
Db 4 LKSL 7

RESULT 31
US-09-942-052-343
; Sequence 343, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 343
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-343

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
|
|
|
|
Db 2 LKSL 5

RESULT 32
US-09-942-052-345
; Sequence 345, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 345
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-345

; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 345
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-345

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
|
|
|
|
Db 6 LKSL 9

RESULT 33
US-09-942-052-405
; Sequence 405, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 405
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-405

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
|
|
|
|
Db 2 LKSL 5

RESULT 34
US-09-942-052-421
; Sequence 421, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 421
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-421

; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 421
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-421

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
|||
Db 6 LKSL 9

RESULT 35
US-09-942-052-513
; Sequence 513, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 513
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-513

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
|||
Db 6 LKSL 9

RESULT 36
US-09-942-052-517
; Sequence 517, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 517
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-517

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
|||
Db 2 LKSL 5

RESULT 37
US-09-942-052-603
; Sequence 603, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 603
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-603

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
|||
Db 2 LKSL 5

RESULT 38
US-09-942-052-635
; Sequence 635, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao


```
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 635
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-635

Query Match          22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 LKSL 18
      |||||
Db      6 LKSL 9

RESULT 39
US-10-153-159-21
; Sequence 21, Application US/10153159
; Publication No. US20020177170A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIE
; TITLE OF INVENTION: SILICO
; FILE REFERENCE: 26050-704
; CURRENT APPLICATION NUMBER: US/10/153,159
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR1 Variant
US-10-153-159-21

Query Match          22.2%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 FNNY 6
      |||||
Db      4 FNNY 7

RESULT 40
US-10-153-159-24
; Sequence 24, Application US/10153159
; Publication No. US20020177170A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
```

```
; TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY
; FILE REFERENCE: 26050-704
; CURRENT APPLICATION NUMBER: US/10/153,159
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR1 Variant
US-10-153-159-24

Query Match          22.2%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 FNNY 6
      |||||
Db      4 FNNY 7

RESULT 41
US-10-153-159-29
; Sequence 29, Application US/10153159
; Publication No. US20020177170A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY
; TITLE OF INVENTION: SILICO
; FILE REFERENCE: 26050-704
; CURRENT APPLICATION NUMBER: US/10/153,159
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR1 Variant
US-10-153-159-29

Query Match          22.2%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 FNNY 6
      |||||
Db      4 FNNY 7

RESULT 42
US-10-153-159-30
; Sequence 30, Application US/10153159
; Publication No. US20020177170A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
```

```

; APPLICANT: Wang, Caili
; TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIB
; FILE REFERENCE: 26050-704
; CURRENT APPLICATION NUMBER: US/10/153,159
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR1 Variant
US-10-153-159-30

Query Match          22.2%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FNRY 6
Db 4 FNRY 7

RESULT 43
US-10-153-176-21
; Sequence 21, Application US/10153176
; Publication No. US20030022240A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; APPLICANT: Cao, Yicheng
; APPLICANT: Li, Shengfeng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
; FILE REFERENCE: 26050-701
; CURRENT APPLICATION NUMBER: US/10/153,176
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR1 Variant
US-10-153-176-21

Query Match          22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FNRY 6
Db 4 FNRY 7

RESULT 44
US-10-153-176-24
; Sequence 24, Application US/10153176
; Publication No. US20030022240A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Caili
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; APPLICANT: Cao, Yicheng
; APPLICANT: Li, Shengfeng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
; FILE REFERENCE: 26050-701
; CURRENT APPLICATION NUMBER: US/10/153,176
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR1 Variant
US-10-153-176-29

Query Match          22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FNRY 6
Db 4 FNRY 7

RESULT 45
US-10-153-176-29
; Sequence 29, Application US/10153176
; Publication No. US20030022240A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; APPLICANT: Cao, Yicheng
; APPLICANT: Li, Shengfeng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
; FILE REFERENCE: 26050-701
; CURRENT APPLICATION NUMBER: US/10/153,176
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR1 Variant
US-10-153-176-29

Query Match          22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FNRY 6
Db 4 FNRY 7

```

```

; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; APPLICANT: Cao, Yicheng
; APPLICANT: Li, Shengfeng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
; FILE REFERENCE: 26050-701
; CURRENT APPLICATION NUMBER: US/10/153,176
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR1 Variant
US-10-153-176-24

Query Match          22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FNRY 6
Db 4 FNRY 7

RESULT 45
US-10-153-176-29
; Sequence 29, Application US/10153176
; Publication No. US20030022240A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; APPLICANT: Cao, Yicheng
; APPLICANT: Li, Shengfeng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
; FILE REFERENCE: 26050-701
; CURRENT APPLICATION NUMBER: US/10/153,176
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR1 Variant
US-10-153-176-29

Query Match          22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FNRY 6
Db 4 FNRY 7

```

RESULT 46
US-10-153-176-30
; Sequence 30, Application US/10153176
; Publication No. US2003002240A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Calli
; APPLICANT: Cao, Yicheng
; APPLICANT: Li, Shengfeng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
; FILE REFERENCE: 26050-701
; CURRENT APPLICATION NUMBER: US/10/153,176
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR1 Variant
US-10-153-176-30

Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 3 FNRY 6
|
|
|
Db 4 FNRY 7

RESULT 47
US-09-912-917-3
; Sequence 3, Application US/09912917
; Patent No. US20020028487A1
; GENERAL INFORMATION:
; APPLICANT: Latnangue, Nicholas B
; APPLICANT: Shikama, No. US20020028487A1iko
; TITLE OF INVENTION: The University Court of the University of Glasgow
; TITLE OF INVENTION: JMY, a co-activator for p300/CBP, nucleic acid encoding
; FILE REFERENCE: JMY and uses thereof
; CURRENT APPLICATION NUMBER: US/09/912,917
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 09/311,236
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: GB 9818235.5
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-912-917-3

Query Match 22.2%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 13 EILK 16
|
|
|
Db 5 EILK 8

RESULT 48
US-09-572-404B-722
; Sequence 722, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 722
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in PRKAR2A OR PKR2 OR PRKAR2 at 273-282 and
; OTHER INFORMATION: interact with Sequence 721 in this patent.
US-09-572-404B-722

Query Match 22.2%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 15 LKSL 18
|
|
|
Db 4 LKSL 7

RESULT 49
US-09-572-404B-724
; Sequence 724, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 724
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in PRKAR2A OR PKR2 OR PRKAR2 at 272-281 and
; OTHER INFORMATION: interact with Sequence 723 in this patent.
US-09-572-404B-724

Query Match 22.2%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 15 LKSL 18
|
|
|
Db 5 LKSL 8

RESULT 50
US-09-572-270A-611
; Sequence 611, Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572,270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 611

```
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in Unknown at 379-388 and may interact with
US-09-572-270A-611
```

```
Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      14 ILKS 17
        ||||
Db       7 ILKS 10
```

RESULT 51

```
US-09-572-270A-948
; Sequence 948, Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572,270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 948
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in PYRB. at 115-124 and may interact with
US-09-572-270A-948
```

```
Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      13 EILK 16
        ||||
Db       5 EILK 8
```

RESULT 52

```
US-09-572-270A-950
; Sequence 950, Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572,270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 950
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in PYRB. at 114-123 and may interact with
US-09-572-270A-950
```

```
Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      13 EILK 16
        ||||
Db       6 EILK 9
```

RESULT 53

```
US-09-942-052-152
```

```
; Sequence 152, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: USEFUL IN TREATMENT AND DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 152
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-152
```

```
Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      15 LKSL 18
        ||||
Db       7 LKSL 10
```

RESULT 54

```
US-09-942-052-269
; Sequence 269, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: USEFUL IN TREATMENT AND DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 269
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-269
```

```
Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      15 LKSL 18
        ||||
Db       7 LKSL 10
```

RESULT 55

US-09-942-052-282
; Sequence 282, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 282
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-282

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
|||
Db 2 LKSL 5

RESULT 56
US-09-942-052-294
; Sequence 294, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 294
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-294

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
|||
Db 5 LKSL 8

RESULT 57
US-09-942-052-367
; Sequence 367, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 367
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-367

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
|||
Db 5 LKSL 8

RESULT 58
US-09-942-052-375
; Sequence 375, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 375
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-375

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
|||
Db 6 LKSL 9

RESULT 59
US-09-942-052-474
; Sequence 474, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 474
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-474

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
|||
Db 7 LKSL 10

RESULT 60
US-09-942-052-484
; Sequence 484, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 484
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-484

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
|||
Db 4 LKSL 7

RESULT 61
US-09-942-052-488
; Sequence 488, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 488
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-488

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
|||
Db 3 LKSL 6

RESULT 62
US-09-942-052-493
; Sequence 493, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 493
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-493

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
|||

Db 6 LKSL 9

RESULT 63

US-09-942-052-560
; Sequence 560, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 560
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-560

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18

Db 7 LKSL 10

RESULT 64

US-09-942-052-566
; Sequence 566, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 566
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-566

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18

Db 4 LKSL 7

RESULT 65

US-09-942-052-582
; Sequence 582, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 582
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-582

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18

Db 6 LKSL 9

RESULT 66

US-09-942-052-597
; Sequence 597, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 597
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-597

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
|||||
Db 3 LKSL 6

RESULT 67

US-09-942-052-667
; Sequence 667, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 667
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-667

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
|||||
Db 6 LKSL 9

RESULT 68

US-09-942-052-681
; Sequence 681, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 681
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-681

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
|||||
Db 4 LKSL 7

RESULT 69

US-09-942-052-682
; Sequence 682, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 682
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-682

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
|||||
Db 7 LKSL 10

RESULT 70

US-09-942-052-692
; Sequence 692, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 692
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-692

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
||||
Db 2 LKSL 5

RESULT 71
US-10-239-313A-5
; Sequence 5, Application US/10299313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-239-313A-5

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16
||||
Db 1 EILK 4

RESULT 72
US-10-239-313A-80
; Sequence 80, Application US/10299313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-239-313A-80

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16
||||
Db 7 EILK 10

RESULT 73
US-10-200-708-29
; Sequence 29, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-29

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16
||||
Db 6 EILK 9

RESULT 74
US-10-200-708-440
; Sequence 440, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 440
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-440

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16
||||

Db 2 EILK 5

RESULT 75

US-10-200-708-594
; Sequence 594, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 594
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-594

Query Match 22.2%; Score 4; DS 12; Length 10;
Best Local Similarity 100.0%; Pred.No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 13 EILK 16
|||
Db 7 EILK 10

Search completed: November 25, 2003, 20:37:07
Job time : 29.8837 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 14.5465 Seconds
(without alignments)
52.356 Million cell updates/sec

Title: US-09-641-801-30
Perfect score: 18
Sequence: 1 ATFNRYODDHGEEILKSL 18

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

```
Minimum DB seq length: 3
Maximum DB seq length: 20
```

Post-processing: Listing first 100 summaries

```
Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/aaa/5A_COMB.pcp.*
2: /cgn2_6/ptodata/1/aaa/5B_COMB.pcp.*
3: /cgn2_6/ptodata/1/aaa/6A_COMB.pcp.*
4: /cgn2_6/ptodata/1/aaa/6B_COMB.pcp.*
5: /cgn2_6/ptodata/1/aaa/PCTus_COMB.pcp.*
6: /cgn2_6/ptodata/1/aaa/backfiles1.pcp.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	18	100.0	18	4	US-09-641-803-30	Sequence 30, Appl	
2	4	22.2	5	3	US-08-510-133A-17	Sequence 17, Appl	
3	4	22.2	5	3	US-08-585-895-17	Sequence 17, Appl	
4	4	22.2	5	4	US-09-161-241-56	Sequence 60, Appl	
5	4	22.2	5	4	US-09-161-241-60	Sequence 60, Appl	
6	4	22.2	5	4	US-09-161-241-64	Sequence 64, Appl	
7	4	22.2	5	4	US-08-601-132-17	Sequence 17, Appl	
8	4	22.2	6	1	US-08-665-220-23	Sequence 23, Appl	
9	4	22.2	6	1	US-08-665-220-33	Sequence 33, Appl	
10	4	22.2	6	1	US-08-665-220-38	Sequence 38, Appl	
11	4	22.2	6	2	US-08-618-408B-23	Sequence 23, Appl	
12	4	22.2	6	2	US-08-618-408B-33	Sequence 33, Appl	
13	4	22.2	6	2	US-08-618-408B-38	Sequence 38, Appl	
14	4	22.2	6	2	US-08-310-912A-205	Sequence 205, Appl	
15	4	22.2	6	2	US-08-310-912A-207	Sequence 207, Appl	
16	4	22.2	6	3	US-09-301-085-205	Sequence 205, Appl	
17	4	22.2	6	3	US-09-301-085-207	Sequence 207, Appl	
18	4	22.2	6	3	US-09-257-218-34	Sequence 34, Appl	
19	4	22.2	6	3	US-09-257-218-45	Sequence 45, Appl	
20	4	22.2	6	3	US-09-257-218-50	Sequence 50, Appl	
21	4	22.2	6	3	US-09-311-760-34	Sequence 34, Appl	
22	4	22.2	6	3	US-09-311-760-45	Sequence 45, Appl	
23	4	22.2	6	3	US-09-311-760-50	Sequence 50, Appl	
24	4	22.2	6	3	US-09-291-692-23	Sequence 23, Appl	
25	4	22.2	6	3	US-09-291-692-33	Sequence 33, Appl	
26	4	22.2	6	3	US-09-291-692-38	Sequence 38, Appl	
27	4	22.2	6	4	US-09-561-756-72	Sequence 72, Appl	

ALIGNMENTS

```
RESULT 1
US-09-641-803-30
; Sequence 30, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEROF, AND
; TITLE OF INVENTION: ANALOGS THEROF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-30

Query Match          100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATENRYODDHGEILKSL 18
Db 1 ATENRYODDHGEILKSL 18

RESULT 2
US-08-510-133A-17
; Sequence 17, Application US/08510133A
; Patent No. 6221839
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Receptor Ligand
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28113/32863
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
;
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-585-895-17

Query Match          22.2%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16
Db 2 EILK 5

RESULT 3
US-08-585-895-17
; Sequence 17, Application US/08585895
; Patent No. 6245530
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Receptor Ligand
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28113/33072
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
;
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-585-895-17

Query Match          22.2%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16
Db 2 EILK 5

RESULT 4
US-09-161-241-56
; Sequence 56, Application US/09161241
```

```
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-510-133A-17

Query Match          22.2%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16
Db 2 EILK 5

RESULT 3
US-08-585-895-17
; Sequence 17, Application US/08585895
; Patent No. 6245530
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Receptor Ligand
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28113/33072
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
;
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-585-895-17

Query Match          22.2%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16
Db 2 EILK 5

RESULT 4
US-09-161-241-56
; Sequence 56, Application US/09161241
```

```
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daquang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human
US-09-161-241-56

Query Match      22.2%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 GEEI 14
Db      2 GEEI 5

RESULT 5
US-09-161-241-60
; Sequence 60, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daquang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human
US-09-161-241-60

Query Match      22.2%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 GEEI 14
Db      2 GEEI 5

RESULT 6
US-09-161-241-64
; Sequence 64, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daquang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64

; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daquang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64

; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human
US-09-161-241-64

Query Match      22.2%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 GEEI 14
Db      2 GEEI 5

RESULT 7
US-08-601-132-17
; Sequence 17, Application US/08601132
; Patent No. 6403088
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Receptor Ligand
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/601,132
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28113/33118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-601-132-17

Query Match      22.2%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 BILK 16
Db      2 BILK 5

RESULT 8
US-08-665-220-23
; Sequence 23, Application US/08665220
; Patent No. 5786173
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
```

```

; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,
; Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/665,220
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/618,408
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "Mch3"
; US-08-665-220-23

Query Match 22.2%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13
Db 3 HGEE 6

RESULT 9
US-08-665-220-33
; Sequence 33, Application US/08665220
; Patent No. 5786173
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,
; Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/665,220
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/618,408
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/665,220
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/618,408
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "CPP32"
; US-08-665-220-33

Query Match 22.2%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13
Db 3 HGEE 6

RESULT 10
US-08-665-220-38
; Sequence 38, Application US/08665220
; Patent No. 5786173
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,
; Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/665,220
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/618,408
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.

```

```

; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "CED-3"
US-08-665-220-38

Query Match 22.2%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13
   ||||
Db 3 HGEE 6

RESULT 11
US-08-618-408B-23
; Sequence 23, Application US/08618408B
; Patent No. 5851815
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, No. 5851815el Apoptotic
; TITLE OF INVENTION: Proteases, Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,408B
; FILING DATE: 19-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; ADDRESSES: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,408B
; FILING DATE: 19-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1957
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "Mch3"
US-08-618-408B-23

Query Match 22.2%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13
   ||||
Db 3 HGEE 6

RESULT 12
US-08-618-408B-33
; Sequence 33, Application US/08618408B
; Patent No. 5851815
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, No. 5851815el Apoptotic
; TITLE OF INVENTION: Proteases, Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,408B
; FILING DATE: 19-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1957
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "CPP32"
US-08-618-408B-33

Query Match 22.2%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13
   ||||
Db 3 HGEE 6

RESULT 13
US-08-618-408B-38
; Sequence 38, Application US/08618408B
; Patent No. 5851815
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Alnemri, Emad S.
```

```
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, No. 5851815el Apoptotic
; TITLE OF INVENTION: Proteases, Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,408B
; FILING DATE: 19-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1957
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "CED-3"
; US-08-618-408B-38

Query Match 22.2%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13
Db 3 HGEE 6
|||||

RESULT 14
US-08-310-912A-205
; Sequence 205, Application US/08310912A
; Patent No. 5981730
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,912A
; FILING DATE: September 22, 1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/227,360
```

```
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,912A
; FILING DATE: September 22, 1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/227,360
; FILING DATE: April 13, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/254001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-310-912A-205

Query Match 22.2%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
Db 3 LKSL 6
|||||

RESULT 15
US-08-310-912A-207
; Sequence 207, Application US/08310912A
; Patent No. 5981730
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,912A
; FILING DATE: September 22, 1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/227,360
```



```

; FILING DATE: April 13, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/254001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 207:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-310-912A-207

```

```

Query Match          22.2%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      15 LKSL 18
Db      3 LKSL 6

```

RESULT 16

```

US-09-301-085-205
; Sequence 205, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang

```

```

; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/301,085
; EARLIER FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: 08/310,912
; EARLIER FILING DATE: 1994-09-22
; EARLIER APPLICATION NUMBER: 08/227,360
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-301-085-205

```

```

Query Match          22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      15 LKSL 18
Db      3 LKSL 6

```

RESULT 17

```

US-09-301-085-207
; Sequence 207, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.

```

```

; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/301,085
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: 08/310,912
; EARLIER FILING DATE: 1994-09-22
; EARLIER APPLICATION NUMBER: 08/227,360
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-301-085-207

```

```

Query Match          22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      15 LKSL 18
Db      3 LKSL 6

```

RESULT 18

```

US-09-257-218-34
; Sequence 34, Application US/09257218
; Patent No. 6271361
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/257,218
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid

```

```
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-257-218-34

Query Match      22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13
Db 3 HGEE 6

RESULT 19
US-09-257-218-45
; Sequence 45, Application US/09257218
; Patent No. 6271361
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,218
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-257-218-50

Query Match      22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13
Db 3 HGEE 6

RESULT 21
US-09-311-760-34
; Sequence 34, Application US/09311760
; Patent No. 6274318
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/311,760
```

; FILING DATE: 13-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/865,579
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-311-760-34
Query Match 22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy 10 HGE 13
Db 3 HGE 6
RESULT 22
US-09-311-760-45
; Sequence 45, Application US/09311760
; Patent No. 6274318
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; Fernandes-Alnemri, Teresa
; Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/311,760
; FILING DATE: 13-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/865,579
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-311-760-50
Query Match 22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy 10 HGE 13
Db 3 HGE 6
RESULT 24
US-09-291-692-23
; Sequence 23, Application US/09291692
; Patent No. 6287795
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.

; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-311-760-45
Query Match 22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy 10 HGE 13
Db 3 HGE 6
RESULT 23
US-09-311-760-50
; Sequence 50, Application US/09311760
; Patent No. 6274318
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; Fernandes-Alnemri, Teresa
; Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/311,760
; FILING DATE: 13-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/865,579
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-311-760-50
Query Match 22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy 10 HGE 13
Db 3 HGE 6
RESULT 24
US-09-291-692-23
; Sequence 23, Application US/09291692
; Patent No. 6287795
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.

APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
APPLICANT: Armstrong, Robert
APPLICANT: Tomaselli, Kevin
TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING AND METHODS OF USE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: Use
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,692
FILING DATE: 04-13-1999
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 480140.424C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..6
OTHER INFORMATION: /note= "Mch3"
US-09-291-692-23
Query Match 22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 HGEE 13
Db 3 HGEE 6
RESULT 25
US-09-291-692-33
Sequence 33, Application US/09291692
Patent No. 6287795
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
APPLICANT: Armstrong, Robert
APPLICANT: Tomaselli, Kevin
TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING AND METHODS OF USE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: Use
ZIP: 98104
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,692
FILING DATE: 04-13-1999
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 480140.424C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..6
OTHER INFORMATION: /note= "CPP32"
US-09-291-692-33
Query Match 22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 HGEE 13
Db 3 HGEE 6
RESULT 26
US-09-291-692-38
Sequence 38, Application US/09291692
Patent No. 6287795
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
APPLICANT: Armstrong, Robert
APPLICANT: Tomaselli, Kevin
TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING AND METHODS OF USE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: Use
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,692
FILING DATE: 04-13-1999
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 480140.424C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note="CED-3"
US-09-291-692-38

Query Match 22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13
|||
Db 3 HGEE 6

RESULT 27
US-09-561-756-72
; Sequence 72, Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561,756
; CURRENT FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 09/227,721
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-561-756-72

Query Match 22.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13
|||
Db 3 HGEE 6

RESULT 28
US-09-561-756-83
; Sequence 83, Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561,756
; CURRENT FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 09/227,721
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-561-756-83

Query Match 22.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13
|||
Db 3 HGEE 6

RESULT 29
US-09-561-756-88
; Sequence 88, Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561,756
; CURRENT FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 09/227,721
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-561-756-88

Query Match 22.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13
|||
Db 3 HGEE 6

RESULT 30
US-09-227-721-72
; Sequence 72, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227,721
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-227-721-72

Query Match 22.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13
|||
Db 3 HGEE 6

RESULT 31
US-09-227-721-83
; Sequence 83, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.

; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227,721
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-227-721-83

Query Match 22.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13
Db 3 HGEE 6

RESULT 32

US-09-227-721-88
; Sequence 88, Application US/09227721

; Patent No. 6379950

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES

; FILE REFERENCE: 480140.431

; CURRENT APPLICATION NUMBER: US/09/227,721

; CURRENT FILING DATE: 1999-01-08

; NUMBER OF SEQ ID NOS: 116

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 88

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-227-721-88

Query Match 22.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13
Db 3 HGEE 6

RESULT 33

US-08-865-579-34

; Sequence 34, Application US/08865579

; Patent No. 6455296

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; APPLICANT: Fernandes-Alnemri, Teresa

; APPLICANT: Litwack, Gerald

; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids/

; TITLE OF INVENTION: Encoding Same and Methods of Use

; NUMBER OF SEQUENCES: 87

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-865-579-34

Query Match 22.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13
Db 3 HGEE 6

RESULT 34

US-08-865-579-45

; Sequence 45, Application US/08865579

; Patent No. 6455296

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; APPLICANT: Fernandes-Alnemri, Teresa

; APPLICANT: Litwack, Gerald

; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids

; TITLE OF INVENTION: Encoding Same and Methods of Use

; NUMBER OF SEQUENCES: 87

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/865,579

; FILING DATE: 29-MAY-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-ID 2180

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-9849

; INFORMATION FOR SEQ ID NO: 45:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-865-579-45

Query Match 22.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      10 HGEE 13
      |||||
Db       3 HGEE 6

RESULT 35
US-08-865-579-50
; Sequence 50, Application US/08865579
; Patent No. 6455296
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-865-579-50

Query Match      22.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 HGEE 13
      |||||
Db       3 HGEE 6

RESULT 36
US-10-059-749-34
; Sequence 34, Application US/10059749
; Patent No. 6566505
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California

```

```

; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-10-059-749-34

Query Match      22.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 HGEE 13
      |||||
Db       3 HGEE 6

RESULT 37
US-10-059-749-45
; Sequence 45, Application US/10059749
; Patent No. 6566505
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Query Match 22.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13
|||||
Db 3 HGEE 6

RESULT 38
US-10-059-749-50
; Sequence 50, Application US/10059749
; Patent No. 6566505
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; Fernandes-Alnemri, Teresa
; Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Query Match 22.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13
'. |||||

Db 3 HGEE 6
RESULT 39
US-08-615-181-19
; Sequence 19, Application US/08615181
; Patent No. 5756666
; GENERAL INFORMATION:
; APPLICANT: MASAFUMI, TAKIGUCHI
; APPLICANT: MIWA, KIYOSHI
; TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE
; TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND
; TITLE OF INVENTION: CURING AIDS
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,181
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/01756
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 261302/1993
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-796-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
; US-08-615-181-19

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
|||||
Db 6 LKSL 9

RESULT 40
US-08-615-181-26
; Sequence 26, Application US/08615181
; Patent No. 5756666
; GENERAL INFORMATION:
; APPLICANT: MASAFUMI, TAKIGUCHI
; APPLICANT: MIWA, KIYOSHI
; TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE
; TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND

;; TITLE OF INVENTION: CURING AIDS
;; NUMBER OF SEQUENCES: 115
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OBLON, SHIVAK, MCCLELLAND, MAIER & NEUSTADT,
;; P.C.
;; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;; CITY: ARLINGTON
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/615,181
;; FILING DATE: 04-APR-1996
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/JP94/01756
;; FILING DATE: 19-OCT-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 261302/1993
;; FILING DATE: 19-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OBLON, NORMAN F.
;; REGISTRATION NUMBER: 24,618
;; REFERENCE/DOCKET NUMBER: 10-796-0 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-413-3000
;; TELEFAX: 703-413-2220
;; INFORMATION FOR SEQ ID NO: 26:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; ORIGINAL SOURCE:
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
;; US-08-615-181-26

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
Db 6 LKSL 9

RESULT 41
US-08-518-967-7
; Sequence 7, Application US/08518967
; Patent No. 5861307
; GENERAL INFORMATION:
; APPLICANT: Kuchino, Y. et al.
; TITLE OF INVENTION: HUMAN s-MYC-LIKE POLYPEPTIDE AND
; TITLE OF INVENTION: A GENE CODING FOR SAID POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIELDS & LEMACK
; STREET: 176 East Main Street, Suite 8
; CITY: Westboro
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01581
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/518,967
;; FILING DATE: August 24, 1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 6-207236
;; FILING DATE: 31-AUG-94
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lemack, Kevin S.
;; REGISTRATION NUMBER: 32,579
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (508) 898-1818
;; TELEFAX: (508) 898-2020
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal
;; US-08-518-967-7

Query Match 22.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GEEI 14
Db 5 GEEI 8

RESULT 42
US-08-159-339A-287
; Sequence 287, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 287:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-287

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16
|||
Db 7 EILK 10

RESULT 43
US-09-188-579-66

Sequence 66, Application US/09188579B
Patent No. 6107040
GENERAL INFORMATION:
APPLICANT: Shuman, Stewart
TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
FILE REFERENCE: D6185
CURRENT APPLICATION NUMBER: US/09/188,579B
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 114
SEQ ID NO 66
LENGTH: 10
TYPE: PRT
ORGANISM: vaccinia virus
FEATURE:
OTHER INFORMATION: Motif VI of RNA guanylyltransferase.
US-09-188-579-66

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16
|||
Db 2 EILK 5

RESULT 44
US-09-315-444-66

Sequence 66, Application US/09315444A
Patent No. 6232070
GENERAL INFORMATION:
APPLICANT: Shuman, Stewart
TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
FILE REFERENCE: D6185C1P
CURRENT APPLICATION NUMBER: US/09/315,444A
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: US 09/188,579
PRIOR FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 66
LENGTH: 10
TYPE: PRT
ORGANISM: vaccinia virus
FEATURE:
OTHER INFORMATION: Motif VI of RNA guanylyltransferase.
US-09-315-444-66

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16
|||
Db 2 EILK 5

RESULT 45

US-09-319-730-8
Sequence 8, Application US/09319730
Patent No. 6310176
GENERAL INFORMATION:
APPLICANT: Barra, Donatella
APPLICANT: SIMMACO, Maurizio
TITLE OF INVENTION: ANTIMICROBIALY ACTIVE POLYPEPTIDES
FILE REFERENCE: 003300-574
CURRENT APPLICATION NUMBER: US/09/319,730
CURRENT FILING DATE: 1999-08-24
PRIOR APPLICATION NUMBER: PCT/SE97/02075
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: SE 9604593-5
PRIOR FILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 10
TYPE: PRT
ORGANISM: Rana Temporaria
US-09-319-730-8

Query Match 22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
|||
Db 6 LKSL 9

RESULT 46

US-09-319-730-9
Sequence 9, Application US/09319730
Patent No. 6310176
GENERAL INFORMATION:
APPLICANT: Barra, Donatella
APPLICANT: SIMMACO, Maurizio
TITLE OF INVENTION: ANTIMICROBIALY ACTIVE POLYPEPTIDES
FILE REFERENCE: 003300-574
CURRENT APPLICATION NUMBER: US/09/319,730
CURRENT FILING DATE: 1999-08-24
PRIOR APPLICATION NUMBER: PCT/SE97/02075
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: SE 9604593-5
PRIOR FILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 10
TYPE: PRT
ORGANISM: Rana Temporaria
US-09-319-730-9

Query Match 22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
|||
Db 6 LKSL 9

RESULT 47

US-09-311-236-3
Sequence 3, Application US/09311236
Patent No. 6376215

```

; GENERAL INFORMATION:
; APPLICANT: Lathangue, Nicholas B
; APPLICANT: Shikama, No. 6376215iko
; APPLICANT: The University Court of the University of Glasgow
; TITLE OF INVENTION: JMY, a co-activator for p300/CBP, nucleic acid encoding
; TITLE OF INVENTION: JMY and uses thereof
; FILE REFERENCE: AHB/LP5731500
; CURRENT FILING DATE: 1999-05-13
; EARLIER APPLICATION NUMBER: US/09/311,236
; EARLIER FILING DATE: 1997-10-21
; EARLIER APPLICATION NUMBER: GB 9722238.4
; EARLIER FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-311-236-3

Query Match      22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 BILK 16
Db 5 BILK 8

RESULT 48
US-09-721-362-66
; Sequence 66, Application US/09721362
; Patent No. 6420163
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185CIP/D
; CURRENT APPLICATION NUMBER: US/09/721,362
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/315,444
; PRIOR FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: vaccinia virus
; FEATURE:
; OTHER INFORMATION: Motif VI of RNA guanylyltransferase.
US-09-721-362-66

Query Match      22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 BILK 16
Db 2 BILK 5

RESULT 49
US-09-489-847-344
; Sequence 344, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657

```

```

; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 344
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-344

Query Match      22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
Db 2 LKSL 5

RESULT 50
US-08-652-877-75
; Sequence 75, Application US/08652877
; Patent No. 6187548
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjaln, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd., 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.5.1
; SOFTWARE: Word 6.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,877
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15203
; FILING DATE: 22-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,314
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355E-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808

```

```
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; US-08-652-877-75

Query Match                22.2%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GBEI 14
Db      2 GBEI 5

RESULT 51
US-08-476-515A-75
; Sequence 75, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Akersstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjalim, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Martin Savitzky
; STREET: 3C43,
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 7.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,515A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE94/00483
; FILING DATE: 24-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9301764-8
; FILING DATE: 24-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:

; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; FRAGMENT TYPE: internal
; US-08-476-515A-75

Query Match                22.2%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GBEI 14
Db      2 GBEI 5

RESULT 52
5194592-76
; Patent No. 5194592
; APPLICANT: YOSHIDA, HAJIME
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO NOVEL
; POLYPEPTIDES DERIVATIVES OF HUMAN GRANULOCYTE COLONY
; STIMULATING FACTOR
; NUMBER OF SEQUENCES: 83
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/318,527
; FILING DATE: 3-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 136,647
; FILING DATE: 22-DEC-1987
; SEQ ID NO: 76:
; LENGTH: 11
; 5194592-76

Query Match                22.2%; Score 4; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 LKSL 18
Db      4 LKSL 7

RESULT 53
5489533-12
; Patent No. 5489533
; APPLICANT: SPRINGER, TIMOTHY A.;STAUNTON, DONALD E.;
; DUSTIN, MICHAEL L.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; ICAM-2
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/384,814
; FILING DATE: 06-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 89,3075
; FILING DATE: 12-JUL-1995
; APPLICATION NUMBER: 89,307
; FILING DATE: 12-JUL-1993
; APPLICATION NUMBER: 454,294
; FILING DATE: 22-DEC-1989
; APPLICATION NUMBER: 45,963
; FILING DATE: 04-MAY-1987
; APPLICATION NUMBER: 115,798
; FILING DATE: 02-NOV-1987
; APPLICATION NUMBER: 155,943
; FILING DATE: 16-FEB-1988
; APPLICATION NUMBER: 189,815
; FILING DATE: 03-MAY-1988
; APPLICATION NUMBER: 250,446
; FILING DATE: 28-SEP-1988
; SEQ ID NO: 12:
; LENGTH: 12
; 5489533-12
```

Query Match 22.2%; Score 4; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATFN 4
Db 2 ATFN 5

RESULT 54
5512660-12
; Patent No. 5512660
; APPLICANT: SPRINGER, TIMOTHY A.; STAUNTON, DONALD E.;
; DUSTIN, MICHAEL L.
; TITLE OF INVENTION: PURIFIED ICAM-2 AND FRAGMENT THEREOF
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,613
; FILING DATE: 10-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 89,307
; FILING DATE: 12-JUL-1993
; APPLICATION NUMBER: 454,294
; FILING DATE: 22-DEC-1989
; APPLICATION NUMBER: 45,963
; FILING DATE: 04-MAY-1987
; APPLICATION NUMBER: 115,798
; FILING DATE: 02-NOV-1987
; APPLICATION NUMBER: 155,943
; FILING DATE: 16-FEB-1988
; APPLICATION NUMBER: 189,815
; FILING DATE: 03-MAY-1988
; APPLICATION NUMBER: 250,446
; FILING DATE: 28-SEP-1988
; SEQ ID NO: 12;
; LENGTH: 12
5512660-12

Query Match 22.2%; Score 4; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATFN 4
Db 2 ATFN 5

RESULT 55
US-09-206-059-13
; Sequence 13, Application US/09206059
; Patent No. 6201104
; GENERAL INFORMATION:
; APPLICANT: MacDonald, Nicholas
; APPLICANT: Sim, Kim Lee
; TITLE OF INVENTION: Angiogenesis-Inhibiting Protein Binding Peptides and
; TITLE OF INVENTION: Proteins and Methods of Use
; FILE REFERENCE: 05213-0370
; CURRENT APPLICATION NUMBER: US/09/206,059
; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: binding peptides
US-09-206-059-13

Query Match 22.2%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 EILK 16
Db 5 EILK 8

RESULT 56
US-09-319-730-2
; Sequence 2, Application US/09319730
; Patent No. 6310176
; GENERAL INFORMATION:
; APPLICANT: BARRA, Donatella
; APPLICANT: SIMMACO, Maurizio
; TITLE OF INVENTION: ANTIMICROBIALY ACTIVE POLYPEPTIDES
; FILE REFERENCE: 003300-574
; CURRENT APPLICATION NUMBER: US/09/319,730
; CURRENT FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: PCT/SE97/02075
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: SE 9604593-5
; PRIOR FILING DATE: 1996-12-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Rana Temporaria
US-09-319-730-2

Query Match 22.2%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
Db 9 LKSL 12

RESULT 57
PCT-US93-06751-66
; Sequence 66, Application PC/TUS9306751
; GENERAL INFORMATION:
; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
; TITLE OF INVENTION: Immunological Conjugates of OMPC and
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06751
; FILING DATE: 19930719
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meredith, Roy D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: 18614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4678
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:


```
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EIL 15
Db 10 EIL 13

RESULT 61
US-09-148-030-4
; Sequence 4, Application US/09148030C
; Patent No. 6458357
; GENERAL INFORMATION:
; APPLICANT: White, Michael T.
; APPLICANT: O'Brien, John S.
; APPLICANT: Wright, David E.
; TITLE OF INVENTION: RETRO-INVERSO NEUTROTROPIC AND ANALGESIC
; FILE REFERENCE: MYELOS.004CP1
; CURRENT FILING DATE: 1998-09-03
; PRIOR FILING DATE: 1997-09-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (2)...(2)
; OTHER INFORMATION: D-Ala
US-09-148-030-4

Query Match 22.2%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EIL 15
Db 10 EIL 13

RESULT 62
US-08-467-083-32
; Sequence 32, Application US/08467083
; Patent No. 5726023
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,083
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/414,417
```

```
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-467-083-32

Query Match 22.2%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16
Db 6 EILK 9

RESULT 63
US-08-414-417B-32
; Sequence 32, Application US/08414417B
; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-414-417B-32

Query Match 22.2%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16
Db 6 EILK 9
```

```

RESULT 64
US-08-486-348A-32
; Sequence 32, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/486,348A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-486-348A-32

Query Match 22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EILK 16
Db 6 EILK 9

RESULT 65
US-08-486-545B-32
; Sequence 32, Application US/08486545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/466,680B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-466-680B-32

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EILK 16
Db 6 EILK 9

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,545B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-468-545B-32

Query Match 22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EILK 16
Db 6 EILK 9

RESULT 66
US-08-466-680B-32
; Sequence 32, Application US/08466680B
; Patent No. 6075122
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,680B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-466-680B-32

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


QY 13 EILK 16
|||||
Db 6 EILK 9

RESULT 67

US-09-009-953-91
; Sequence 91, Application US/09009953
; Patent No. 6413517
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Identification of Broadly
; REACTIVE DR RESTRICTED EPITOPES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 21-Jan-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,713
; FILING DATE: 23-JAN-1997
; APPLICATION NUMBER: US 60/037,432
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-011520US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 91:
US-09-009-953-91

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 13 EILK 16
|||||
Db 3 EILK 6

RESULT 68

US-09-418-780A-5
; Sequence 5, Application US/09418780A
; Patent No. 6504009
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/09/418,780A
; CURRENT FILING DATE: 1999-10-15

; PRIOR APPLICATION NUMBER: PCT/JP98/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-780A-5

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 13 EILK 16
|||||
Db 3 EILK 6

RESULT 69

US-09-418-780A-8
; Sequence 8, Application US/09418780A
; Patent No. 6504009
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/09/418,780A
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-780A-8

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 13 EILK 16
|||||
Db 3 EILK 6

RESULT 70

US-09-418-780A-24
; Sequence 24, Application US/09418780A
; Patent No. 6504009
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/09/418,780A
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-418-780A-24

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 11 GEEI 14
|||
db 9 GEEI 12

Query Match	22 24	Score	4
US-08-795-430-9			
peptide			
MOLECULE TYPE:			

RESULT 74
US-09-355-700-9

```
; Sequence 9, Application US/09355700
; Patent No. 6361946
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
;               Heisinki University Licensing
;               Alitalo, Kari (U.S. only)
;               Joukov, Vladimir (U.S. only)
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
;               Protein and Gene, Mutants Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/355,700
; FILING DATE: 05-NOV-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,430
; FILING DATE: 05-FEB-1997
; APPLICATION NUMBER: PCT/FI96/00427
; FILING DATE: 01-AUG-1996
; APPLICATION NUMBER: 08/671,573
; FILING DATE: 28-JUN-1996
; APPLICATION NUMBER: 08/601,132
; FILING DATE: 14-FEB-1996
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; APPLICATION NUMBER: 08/510,133
; FILING DATE: 01-AUG-1995
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/34140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-355-700-9

Query Match      22.2%; Score 4; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 BILK 16
        ||||
Db      14 BILK 17

RESULT 75
US-08-601-132-39
; Sequence 39, Application US/08601132
; Patent No. 6403088
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Receptor Ligand
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/601,132
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28113/33118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-601-132-39

Query Match      22.2%; Score 4; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 BILK 16
        ||||
Db      14 BILK 17

Search completed: November 25, 2003, 20:30:06
Job time : 15.5465 secs
```